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The spread of rabies in Ethiopian wolves: from field data to transmission parameters

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**Book of Abstracts
of the 13th International Symposium on
Veterinary Epidemiology and Economics**

Book of Abstracts

of the 13th International Symposium on Veterinary Epidemiology and Economics

2012 – Maastricht



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P u b l i s h e r s

Dear colleagues,

Welcome at ISVEE; the 13th international symposium on veterinary epidemiology and economics. Welcome to Maastricht.

Decision makers dealing with animal health problems, at the herd, regional or (inter)national level are increasingly faced with new challenges. New pathogens like the Schmallenberg virus, increasing demand for animal protein in developing countries, climate change, increasing interest in the risks of animals for human health, and increasing questions of the society at large about the way we keep animals are only a few out of many. Veterinary epidemiology and veterinary economics are the scientific disciplines that can help taking the best decision, because they provide crucial quantitative information about animal health at the population level.

Nevertheless, veterinary epidemiology and economics cannot do that alone, because we would just be providing statistical associations from a black box. Only by **crossing the border** with other disciplines like microbiology, immunology, veterinary and animal sciences, communication and others and by focussing on the **bridges that connect** them with veterinary epidemiology and economics we can create the multi-disciplinary approach needed to solve many of today's research questions.

Crossing borders, building bridges is the motto of this symposium and you will encounter this motto throughout the conference, in the keynote lectures as well as in many of the oral and poster sessions. A variety of topics will be presented to you from sophisticated statistical modelling over socio-economic impact of diseases to the application of veterinary epidemiology in daily practice.

Thanks to the many contributions and excellent key note speakers, you will hear state of the art presentations and see posters with top of the bill science originating from over 70 different countries and covering animal health and diseases from a wide variety of species. Sessions and breaks will give you ample opportunities to discuss with your colleagues and, moreover, we are convinced that our attractive social programme will help you expand and strengthen your network. We encourage you to look, listen and discuss and to build new scientific and personal bridges so that veterinary epidemiology and economics can further flourish in a multi-disciplinary scientific world.

We thank the scientific committee for their invaluable help in designing a very interesting programme. Moreover, we thank our sponsors for making this conference possible. Most of all we thank you, participants of ISVEE, for your contributions and your presence at ISVEE 2012. We wish you an inspiring conference.

On behalf of the Organizing Committee,



Arjan Stegeman
President



Jeroen Dewulf
Vice-President and Chair of Scientific Committee

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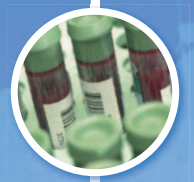
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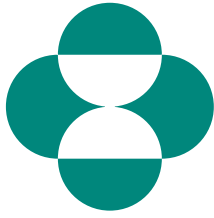
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ISVEE 13 Bursary awards

We are proud to announce that a total of 21 bursary awards have been awarded to students from developing countries to participate in ISVEE 13. The ISVEE 13 Bursary awards have been sponsored by:

- **Nordic Society for Veterinary Epidemiology** (1 bursary award);
- **Flemish Society for Veterinary Epidemiology and Economics** (3 bursary awards);
- **Dutch Society for Veterinary Epidemiology and Economics** (3 bursary awards);
- **Society for Veterinary Epidemiology and Preventive Medicine** (3 bursary awards);
- **Boerenbond Belgium** (2 bursary awards);
- **Food and Agricultural Organisation (FAO) of the United Nations** (4 bursary awards);
- **Dr. Salman** (3 bursary awards);
- **Instavet** (1 bursary award);
- **Belgian Embassy in South Africa, Pretoria** (1 bursary award).

The following persons received a bursary award:

Familyname	Initials	Firstname	Company/Institute	City	Country
Adesokan	H.K.	Hezekiah	University of Ibadan		Nigeria
Baljinnyam	Z.	Zolzaya	Institute of Veterinary Medicine, MSUA	Ulaanbaatar	Mongolia
Brito Rodriquez	B.P.	Barbara Patricia	Universidad Nacional de Rosario, Centre for Animal Disease Modelling and Surveil	Davis	United States of America
Chaka	H.	Hassen	National Animal Health Diagnostic and Investigation Centre	Sebeta	Ethiopia
De Hildebrand E Grisi Filho	J.H.	Jose Henrique	University of Sao Paulo	Sao Paolo	Brazil
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Fasina	F.O.	Folorunso Oludayo	University of Pretoria	Pretoria	South Africa
Gachohi	J.	J.	International Livestock Research Institute	Nairobi	Kenya
Jemberu	W.T.	Wudu Temesgen	University of Gondar	Gondar	Ethiopia
Lankaster	F.	Felix	University of Glasgow	Arusha	Tanzania
Marufu	M.C.	Munyaradzi Christoph	University of Kwazulu-Natal	Pietermaritzburg	South Africa
Mersinaj	K.	Kujtim	Food Safety and Veterinary Institute	Isuv	Albania
Nekouei Jahromi	O.A.	Omid Ali	University of Theran	Theran	Iran
Nicolino	R.	Rafael	Federal University of Minas Gerais UFMG	Belo horizonte	Brazil
Niedersberg de Avila	L.	Luciana	Agencia Defesa Agropecuaria da Bahia		Brazil
Patanasatienkul	T.	Thitiwan	Atlantic Veterinary College, UPEI	Charlottetown	Canada
Salih	H.	Huyam	Ministry of animal resources & fisheries	Khartoum	Sudan
Seric-Haracic	S.	Sabina	Veterinary Faculty of the University of Sarajevo	Sarajevo	Bosnia and Herzegovina
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Van Eeden	C.	Charmaine	University of Pretoria	Pretoria	South Africa
Wera	E.	Ewaldus	Kupang State Agricultural Polytechnic	Kupang	Indonesia

Keynote speakers

Prof. Derek Smith

Cambridge University, UK

A bridge between molecular research and veterinary epidemiology

Prof. David Rogers

Oxford University, UK

The link between climate change, global warming and animal diseases

Prof. Theresa Bernardo

Michigan State University, USA

The applications of social media and social networks in epidemiology

Prof. Ynte Hein Schukken

Cornell University, USA

Epidemiology in veterinary practice

Dr. Katinka de Balogh

FAO – selected by the European college on Veterinary Public Health

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Genomic epidemiology of zoonotic pathogens

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Next generation sequencing has vastly increased the availability of pathogen genome sequence data. By developing evolutionary and epidemiological models and applying them to sequence data, new insights are gained into how pathogens are evolving, the nature of host association and aspects of between-host transmission. Advances in statistical methods have improved model choice and parameter estimation for models of evolutionary ancestry, resulting in better reconstructions of pathogen genealogies, and improved estimates of evolutionary parameters. These models are valuable: they provide estimates of when and where key events occurred, such as the emergence of new variants; they improve our understanding of population growth and how it relates to the basic reproduction number; and they enable the contribution of different sources and transmission pathways to be determined. New Zealand's relative isolation and unique patterns of colonisation with humans and animals provides a test bed for exploring the evolution of pathogens such as *Campylobacter*. In this study we demonstrate the power of marrying rich data sets with modern statistical methods, and how different types of data can be used to learn about evolution. Our datasets include over 4,000 *Campylobacter* isolates from a range of hosts with low genome coverage (7 loci) and 59 isolates with high coverage (>1000 genes). Our analysis indicates multiple introductions (pre-human and post Polynesian and European colonisation) and provides revised estimates of the relative rates of recombination and mutation. Further, by informing our understanding of host-association and the relative rates of transmission between animals and humans, the melding of statistical genetics and epidemiology, combined with partial and full genome sequence data, has informed successful control strategies in New Zealand.

Unravelling the fine-scale transmission of bovine tuberculosis in Northern Ireland

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Bovine tuberculosis (bTB) poses a major health and economic problem in many areas of the world. Where eradication programmes have failed, infection in a wildlife reservoir is often implicated, and in the British Isles bTB in cattle has been linked to infection in the Eurasian badger *Meles meles*. Despite extensive research effort involving laboratory studies, ecology, epidemiology and large-scale intervention trials, the exact roles of badgers and cattle in maintaining bTB in the British Isles remains not only unclear but also mired in controversy. Here we present recent work on Northern Irish data, using whole genome sequences of the causal agent of bTB, *Mycobacterium bovis*, to elucidate transmission dynamics among cattle and badgers at the farm scale. Combining these molecular data with detailed information on cattle birth, death and movement, we are able to identify with unprecedented resolution the fine spatial and temporal scales at which the pathogen is transferred between the two hosts, and thus demonstrate the predominance of local processes in bTB persistence. Extending our approach to bTB in the British Isles more widely should enable valuable progress to be made in understanding and quantifying the role of badgers as a wildlife reservoir, and the risk they pose for the disease in cattle.

Spatial epidemiology of *Escherichia coli* O157:H7 in dairy cattle in relation to night roosts of *Sturnus vulgaris* (European starling) in Ohio, USA (2007-2009)

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The goal of our study was to determine if the night roosts of European starlings (*Sturnus vulgaris*) act as foci for the dissemination of *Escherichia coli* O157:H7 among dairy farms. From 2007-2009, we collected bovine fecal samples (n=9,000) and starling gastrointestinal contents (n=430) from 150 dairy farms in northeastern Ohio. Isolates of *E. coli* O157:H7 that were recovered from these samples were sub-typed using multilocus variable number tandem repeat analysis (MLVA). Generated MLVA-types were used to construct a dendrogram based on a categorical multistate coefficient and unweighted pair group method with arithmetic mean (UPGMA). Using a focused spatial scan statistic, we identified statistically significant spatial clusters around starling night roosts of dairy cattle with an increased prevalence of *E. coli* O157:H7 positive fecal pats, an increased diversity of distinguishable MLVA-types, and a greater number of isolates with MLVA-types from bovine-starling clades versus bovine-only clades. These results support our hypothesis that starlings contribute to the dissemination of this bacterium among dairy farms.

Transmission dynamics of *Mannheimia haemolytica* and *Mycoplasma bovis* in beef bulls at fattening operations

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Mannheimia haemolytica and *Mycoplasma bovis* are the principal bacteria isolated from cattle suffering from bovine respiratory disease (BRD) in fattening operations. Little information is available on their transmission dynamics within pens during BRD outbreaks. Such information is nevertheless crucial to adapt control measures. The objective of this study was to characterize by molecular typing *M. haemolytica* and *M. bovis* isolates collected from bulls' lungs during BRD outbreaks to determine whether a single or multiple clones are present within pens. 12 groups of 8 to 12 beef bulls (n=112) were studied during the 40 days following their arrival at fattening operations. Bulls were purchased at auction markets and came from different farms. As soon as a BRD case was detected in a group, a trans-tracheal aspiration (TTA) was performed on each bull of the group to isolate bacteria. TTA were then repeated every 3 days on non-treated bulls until no new BRD case was detected in the group. *M. haemolytica* and *M. bovis* isolates were characterized by pulsed-field gel electrophoresis (PFGE). *M. haemolytica* and *M. bovis* isolates were collected during 14 and 6 BRD outbreaks respectively. The within-pen prevalence of bulls positive for *M. haemolytica* and *M. bovis* during BRD outbreaks ranged respectively from 11% to 89% (mean=60%) and from 8% to 100% (mean=54%). During 10 of the 14 outbreaks, 2 to 4 different clones of *M. haemolytica* were recovered whereas only 1 clone was recovered in the 4 remaining outbreaks. Concerning *M. bovis*, only one clone was recovered during 5 of the 6 BRD outbreaks. Molecular typing revealed, for *Mannheimia haemolytica* isolates, a high within-pen genetic variability during BRD outbreaks indicating a low occurrence of horizontal transmission, and a unique clone of *M. bovis*, indicating a frequent transmission among penmates.

Using strain typing to determine vertical infections of *Mycobacterium avium* subspecies *paratuberculosis*
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Daughters of *Mycobacterium avium* subspecies *paratuberculosis* (MAP)-infected dairy cattle are assumed to be at high risk of vertical infection. Alternatively, genetics can account for increased susceptibility to MAP, therefore dam and daughter can be both infected but not necessarily due to vertical transmission. Analyzing strain diversity using multi locus short sequence repeat (MLSSR) typing in longitudinal datasets allows us a potential distinction between vertical transmission and genetic susceptibility. In this study we examine the strain types of MAP in dam-daughter pairs to evaluate whether these pairs have the same strain. We identified 12 MAP-infected dam-daughter pairs from the Regional Dairy Quality Management Alliance study herd in NY. All adult animals on the farm were tested for MAP via fecal culture semi-annually for seven years and tissue samples were available on a subset of cull animals. Positive cultures were sub-streaked and processed for MLSSR typing. Following genotyping, isolates from each dam-daughter pair were compared to determine whether they shared the same MAP genotype. Of the 12 infected dam-daughter pairs, 9 had identical strains shared between the dams and daughters. In addition, 2 daughters had the dam's strain as well as another circulating strain. Overall, 8 strains were represented in the daughters that did not come from dams. Of the 12 daughters, 5 carried different strains of MAP than their dams, even when concurrently infected with the dam's strain. Even though the majority of transmission was of the dominant on-farm strain of MAP, there was still an association between dam status and MAP strain in daughters. It appears that some strains of MAP may transmit vertically more commonly than others.

The molecular diversity of *Mycobacterium avium* subsp. *paratuberculosis* on Alberta dairy farms determined using MALDI-TOF mass spectrometry

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Johne's disease (JD) is primarily controlled through prevention. However, this requires a thorough understanding of the transmission patterns and sources of *Mycobacterium avium* subspecies *paratuberculosis* (Map). Strain typing of Map isolates can provide valuable insight into the epidemiology of JD that can ultimately be used to design and evaluate regional control programs. A number of strain typing techniques have been used to discriminate Map isolates, though many have proven too impractical to encourage large scale studies. Short sequence repeats (SSR) found in the Map genome were previously determined to be the most discriminatory compared with other techniques to investigate Map strain variability between and within herds. Unfortunately, accurate sequence analysis of mono- and di-nucleotide repeats is still moderately difficult, expensive, and laborious. We used DNA MALDI-TOF analysis as alternative to Sanger sequencing for typing Map using multiple SSR loci. We applied this technique to isolates originating from the Alberta Johne's Disease Initiative in which six environmental samples taken at different sites in the cow barn are cultured from a projected 80% of all the dairy farms in the province (n=480). Genomic DNA was extracted from Map colonies obtained from cultures. Short sequences surrounding the SSR regions were amplified by PCR using a biotinylated primer. DNA was purified using streptavidin beads and eluted before processing for MALDI-TOF analysis. Differentiating spectra were obtained for the different alleles of the tested SSR loci. The provincial distribution of the identified Map genotypes based on the SSR profiles will be presented. Typing of SSRs provides valuable information regarding the molecular epidemiology of Map. Resolving the genotypes present on 80% of the dairy farms in Alberta will provide unprecedented insight into Map diversity, distribution and transmission, a critical step in the prevention of JD in dairy herds.

Site-specific biosafety and biosecurity risk assessment for the national bio and agro-defense facility
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Foreign animal, emerging, and zoonotic diseases present a significant threat to the United States economy, agricultural security, and public health. To address this threat, the Department of Homeland Security is designing a state of the art biocontainment facility, the National Bio and Agro-Defense Facility, where comprehensive scientific research on the pathogens that may be involved would be performed. As part of the facility design and planning process, DHS used a highly integrated multi-disciplinary probabilistic risk assessment methodology involving facility engineering design evaluation, source term analysis, site specific climatology development and analysis, fate and transport modelling, epidemiological modelling, economic impact modelling, and quantitative risk analytics. In this presentation, the research team will detail the multifaceted economic approach used. Specifically, a partial equilibrium multi-market model evaluated producer and consumer welfare impacts to the agricultural sector resulting from unintentional releases of FMDv. Costs and disruptions to the non-agricultural activities were estimated using an Input-Output model and costs of response (e.g. surveillance, quarantine, euthanasia, etc.) were calculated. Preliminary results (approved for release by DHS) and associated conclusions will be presented.

A financial cost-benefit analysis of the Norwegian ‘Healthier goats’ sanitation program using stochastic simulation to analyse risks

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In 2001 the Goat Health Services in Norway initiated a program to sanitize for caprine arthritis encephalitis, paratuberculosis (Johne’s disease) and caseous lymphadenitis in dairy goat herds (‘Healthier goats’). The program is largely financed by the government. A financial cost-benefit analysis (CBA) has been conducted by calculating the net present value (NPV) of costs and returns of the program over 5, 10 and 20 years. The calculations are based on a study showing average milk yield increase by 21% (from 627 to 756 kg) per goat in sanitized herds. Sanitized goats also last longer resulting in lower costs of replacement. The costs, gathered via a survey, comprised farmers’ work on sanitation, feed costs, farm building and other investments, and temporary production problems. Benefits due to increased milk yield are restricted by a milk quota and affected by governmental animal premium payments. A substantial part of farmers’ costs were reimbursed by the program. Still the value of NPV for the first 5 year period is negative (-160,000 NOK) while for the 10 year perspective NPV is 132,000 NOK which shows the program to be beneficial at a 4.5% discount rate. The CBA is supported by a risk analysis using @Risk© to examine the effects of uncertainty in input variables such as milk yield, milk quality and investment costs. The importance of farmers’ investments and risks as well as government participation in relation to preventive veterinary medicine and animal disease control are discussed.

The economics of animal health surveillance: translating principles into practice: a case study from Switzerland

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To inform their resource allocation decisions, the Swiss federal veterinary service required a practical tool for the economic assessment of animal health surveillance. Building on established economic concepts and criteria, a generic theoretical framework and practical guide were developed. It was shown that disease mitigation must be conceptualized as a three-variable process involving recovery of output losses, surveillance and intervention. Moreover, the relative contributions of surveillance and intervention resources must be investigated with regard to the substitution possibilities between them. The approach allows optimal net benefit accruing to society from allocating scarce mitigation resources to be identified. Applying the framework, policy makers have more comprehensive information about the economic efficiency of their resource allocation decisions than is possible with conventional cost-benefit or cost-effectiveness analysis. Having developed the framework and practical guide, the next step was knowledge transfer to analysts and decision-makers. An implementation strategy was proposed to representatives of the Swiss federal veterinary service. This included veterinary staff training in economics, the creation of decision frameworks that fully integrate economic criteria, communication and collaboration between epidemiologists, economists and decision-makers, and utilisation of research results. A training workshop was organised for researchers and government officials to explain the economic principles and to illustrate the practical use of the guide. In this paper, we report on the implementation process to date. Discussion focuses on impediments to applying economic efficiency criteria in practice, and difficulties encountered in communication and collaboration across disciplines and between policy makers. In conclusion, we suggest ways to make further progress in the light of experience gained.

Session 02**Theatre 4****Enhancing passive surveillance: an economic evaluation of alternative methods**

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Surveillance for new and re-emerging animal disease in England and Wales is based on *post-mortem* and laboratory investigation of diagnostic submissions to the Animal Health and Veterinary Laboratories Agency and the systematic analysis of submission data; the aim, to provide early warning of animal disease events. This surveillance system is passive, based on the voluntary submission of carcase and sample material to a laboratory network, with submission rates encouraged by partial subsidy. Recent stricture on Government spending has driven investigation of methods to provide surveillance on a reduced budget with no loss of efficacy. Complementary generic economic and compartmental epidemiological models were developed using parameters defined by real-world data to assess the effect of changes in resource allocation. The models were applied to a BSE-like syndrome with zoonotic potential, and the national economic impact measured relative to a baseline of current surveillance for two scenarios: (1) subsidised carcase collection, (2) integration of database entries generated by telephone consultation between state and private veterinarians. Stochastic economic models were run as Monte-Carlo simulations with 10000 iterations and sensitivity analysis performed to identify key input parameters. Mean undiscounted net values for both scenarios were positive, ranging from 4 to 7 million pounds. Mean cost per infected animal saved was £338 and £153 respectively, and cost per infected carcass removed from the food chain was £475 and £217. Both scenarios therefore provided good value for money. The integrated modelling approach presented facilitates understanding of the economic efficiency of passive surveillance and highlights critical factors in the on-farm decision making processes which underlie disease reporting. The generic nature of the approach allows its application to a wide range of diseases and scenarios.

Biosecurity in pig herds is associated with production- and treatment-characteristics

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It is generally assumed that biosecurity measures in pig production improve performance and health status of the pigs, and may thus decrease the need for antimicrobial treatments. However, limited quantitative data is available to support this hypothesis. In the present study, 95 randomly selected closed pig herds were visited to quantify the biosecurity status of the herd by means of a risk-based weighted biosecurity scoring system. This score ranges from 0 (= total absence of biosecurity measures) to 100 (= perfect biosecurity). During the same visit, data concerning herd-, farmer- and production-characteristics and the use of antimicrobials (quantified as treatment incidences) were collected. The external biosecurity score (measures preventing pathogens from entering the herd) was on average 65/100 (min 45; max 89), whereas the internal biosecurity score (measures reducing within-herd spread of pathogens) was on average 52/100 (min 18; max 87). Herd size was positively associated with the external biosecurity score and a negative association was observed between the internal biosecurity score and the age of the buildings as well as the experience of the farmer. These results indicate that biosecurity is generally better implemented in larger herds, more modern facilities and by younger farmers. The overall, external and internal biosecurity score were positively associated with the daily weight gain and feed conversion ratio of fattening pigs (both $P < 0.01$), indicating that in herds with higher biosecurity the production is also better. Whereas the internal biosecurity was negatively associated with treatment incidence ($P < 0.05$), indicating an improved biosecurity is associated with a reduction of antimicrobial drug use. This study demonstrated clear associations between the biosecurity and both production and treatment characteristics in pig production.

Session 02**Theatre 6****Assessment of the biosecurity risks posed by the poultry exhibition sector in Australia**

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Poultry exhibitors are perceived to pose a risk of disease introduction and spread due to the high frequency of movements of birds and the close contact between birds at poultry shows. This cross-sectional study assesses the biosecurity risks posed by poultry exhibitors in Australia. Interviews with 46 exhibitors at eight poultry shows and a postal survey were used to gather information on poultry exhibitors. Logistic regression was used to investigate associations between age, gender, location, number of birds and number of shows attended per year, with biosecurity and communication practices. A total of 357 (29.1%) exhibitors responded to the postal survey. Over 80% of all exhibitors kept less than 200 birds and did not have commercial poultry operations within 5 km of their property; while 68.0% reported having some small poultry keepers in their proximity. Despite most exhibitors (90.8%) having knowledge of some biosecurity principles; some of their practices could pose a risk for disease introduction and spread. For example 67.0% reported contact of wild birds with domestic birds and only 60.0% cleaned transport cages after each use and 40.6% isolated birds for over two weeks. Most exhibitors (75.0%) attended more than 5 shows per year, travelling long distances (up to 1000 km) to attend a show. Contact with veterinarians was low (23.1%), with younger exhibitors and women more likely ($P < 0.05$) to contact a veterinarian than older exhibitors and men. Older exhibitors identified other poultry exhibitors and poultry clubs as useful sources of information; while, younger exhibitors and women were more likely to use internet and veterinarians to seek information on their birds ($P < 0.01$). Findings from this study will be used to quantify the risk of disease introduction and spread among poultry exhibitors and identify those practices posing the highest risk. Additionally, results could support the development of an effective extension strategy to enhance biosecurity among this sector of the industry.

Bluetongue in Switzerland: an investigation modeling within-herd population dynamics, vaccination strategies and herd immunity

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In 2006 Bluetongue virus serotype 8 (BTV8), a vector-borne disease of ruminants transmitted by *Culicoides* midges, was first reported in north-western Europe and spread rapidly, prompting many countries to initiate vaccination programmes. In order to implement an efficient vaccination programme, a thorough understanding of the host, the vector and the environment is required. To contribute to the understanding of BTV8 control in Switzerland, a stochastic compartmental model was developed to simulate within-herd population dynamics and examine its effect on immunity levels after vaccination. This model was combined with the basic reproduction number to estimate the within-herd effective reproduction number, R_e , for three Swiss farm-types: a dairy herd, a dairy herd with a suckler calf unit and a sheep flock. The results indicated that the high levels of immunity required to control BTV8 within a herd can be difficult to achieve. While annual vaccination reduced the R_e in the two cattle herd types, it remained above one during the vector season at altitudes below 1500 meters. In sheep flocks, where the time of lambing varies yearly, R_e is dependent upon the interaction of vaccination date, lambing date and vector season. Sensitivity analysis determined that the influential parameters for R_e were (1) the probability of disease transmission from host to vector; and (2) the ratio used to convert midge trap numbers to the density of midges present on the farm. This is partly a reflection of the difficulty in determining the true value of these parameters. This study demonstrated that herd immunity levels and local climate have major implications for effective BTV8 control and suggests regional and farm-type specific strategies would be more appropriate than a uniform approach at the national level.

Session 03**Theatre 2****Developing rules of thumb for between-farm transmission and control of avian influenza, classical swine fever, and foot-and-mouth disease**

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Large epidemics of highly-pathogenic avian influenza (HPAI), foot-and-mouth disease (FMD) and classical swine fever (CSF) have struck livestock farming in a number European countries in the past 10-15 years. Analyzing the epidemic data, mathematical models of the between-farm transmission dynamics have been constructed that are now being used to assess the impact of control strategies against future epidemics. We review between-farm transmission probabilities estimated from recent epidemics in The Netherlands of CSF (1997/1998), FMD (2001) and HPAI (2003), and use these to make a comparison of these three diseases in terms of their between-farm transmission risks and the options for control by pre-emptive culling and emergency vaccination. The main epidemiological quantities determining the differences in transmission risk between these diseases are three: (1) the distance-dependent transmission probability; (2) the farm density distribution; and (3) the generation time of infection. In order to develop a rule of thumb for disease 'controllability' based on quantities 1 and 2, we develop a new approach to define and estimate critical farm densities. A second rule of thumb, specific for disease control using emergency vaccination, is based on comparing quantity 3 to the protection delay determined in vaccination-transmission experiments.

Rs, a counterpart of the basic reproduction number in a seasonal context

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Arboviruses are responsible for vector-borne diseases of major concern in human and animal health. Their spread is seasonal in temperate regions, due to variation in host availability, such as for migratory birds, or vector availability, arthropod life cycle being governed by temperature and humidity. Virus transmission is reduced during the unfavourable season because of a lack of contact between hosts and vectors. However, virus persistence is observed during winter despite a dramatic reduction in vector abundance. Therefore, the effectiveness of control strategies against these vector-borne diseases should be evaluated in a seasonal context. The basic reproduction number, R_0 , the expected number of secondary cases generated by the primary case during its infection period when introduced into a fully susceptible population, enquires about the invasion ability of a pathogen in a host population. It is used commonly to evaluate the ability of control strategies to prevent disease spread, i.e. their ability to decrease R_0 to below one. Nevertheless, numerically assessing R_0 from models is a difficult task in a seasonal context due to likely large amplitude oscillations in vector population sizes transforming any numerical procedure into a 'stiff' problem. We propose a counterpart (R_S) of R_0 in a seasonal context. Our numerical calculation of R_S is easy to implement and has been validated for a vector-borne disease model with a periodic transmission function. In addition, we propose to use simultaneously to R_S another indicator of the epidemic risk, A^* , the largest eigenvalue of the seasonal next-generation matrices defined over a period. We advise to use both these indicators to evaluate control strategies of the spread of any vector-borne disease for which the vector seasonality plays a major role in the disease spread and illustrate it by evaluating vaccination strategies to control bluetongue spread.

The interaction of genetics and epidemiological processes in ovine footrot

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Footrot (FR) is a bacterial disease of sheep that is detrimental to welfare, adversely affects production, and can recur throughout life. Susceptibility is partly under genetic control and heritability estimates have been made using pedigree and phenotype data. However, true underlying heritabilities for genetically influenced traits are challenging to estimate because phenotypic variation between individuals depends on exposure, which itself is dependent on infection. Thus, heritability estimates differ at high and low disease prevalence because epidemiological processes interact recursively with genetic effects. To fully understand endemic diseases such as FR, and work towards long term solutions for control, genetics and epidemiology must be considered simultaneously. A stochastic, individual-based, simulation model of FR in a flock of 200 ewes was developed that included flock demography, disease processes, bacterial contamination of the environment and host genetic variation for traits influencing infection and disease processes. Sensitivity analyses were performed using ANOVA to examine the contribution of unknown parameters to outcome variation. Infection rate and bacterial death rate were the most significant factors determining the observed prevalence of FR, and the estimated heritability of resistance. The dominance of infection parameters in determining outcomes implies that observational data cannot be used to accurately assess the strength of genetic control of underlying traits describing the infection process, i.e. resistance. Current work involves the implementation of epidemiological interventions (pasture rotation, selective culling, antibiotic treatment and vaccination) and genetic selection processes, to determine their effects on the incidence and prevalence of FR in a sheep flock.

Evaluating vaccination for foot-and-mouth disease control: an international study

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Vaccination is increasingly being recognised as an important tool for managing foot-and-mouth disease (FMD) outbreaks. However, there is considerable uncertainty, which is of particular relevance to previously free countries, as to when and how vaccination should be optimally used, and how vaccinated animals should be managed. The study is an international collaboration between modellers from Australia, New Zealand, Canada, United States and United Kingdom, and uses a multi-model comparison approach to: The study uses four modelling platforms to compare a range of vaccination strategies with a standard control (no-vaccination) approach. Data from the 2010 UK FMD exercise, Exercise Silver Birch, is being used as the basis for the study. Key factors being investigated include vaccination approach (suppressive versus protective vaccination), timing (when vaccination is introduced), species vaccinated, priorities for vaccination and deployment methods, and resource issues. The work is strengthening international collaboration and providing a better understanding of the key issues and parameters influencing the effectiveness of vaccination as a control tool for FMD. The study aims to enhance the credibility of simulation modeling in disease control decision making. Findings will be used to: (1) support and develop more robust and acceptable policies for FMD control; (2) identify the conditions under which vaccination may offer significant benefits in controlling an FMD outbreak; (3) identify the key features and parameters that influence effectiveness of vaccination; (4) describe any differences between QUAD member's models relating to policy decision making around vaccination effectiveness.

An outbreak of highly pathogenic avian influenza in domestic ostriches: the current situation in South Africa

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Avian influenza devastated the ostrich industry of South Africa in 2011, resulting in the cessation of exports of fresh ostrich meat to the European Union as well as the stamping-out slaughter of 37,000 ostriches, representing approximately 15% of the domestic ostrich population of the country. The outbreak also adversely affected 20,000 people who rely directly on the industry for their livelihood. The virus was first detected in March 2011, when birds on five relatively unconnected and geographically distant farms in the Oudtshoorn valley in the south-western region of the country tested seropositive for the H5 subtype. A highly pathogenic strain of avian influenza (HPAI) subtype H5N2 was isolated in April 2011 from one of these properties, and surveillance using serological and PCR techniques revealed a further 29 infected farms in the following three months, 13 of which were confirmed HPAI H5N2 positive using DNA sequencing of the H5 cleavage site. Despite subsequent efforts to contain the disease, using methods such as slaughter, movement control and declaration of an infected area, birds with positive H5 serology were still being detected on new properties in November 2011. Owing to the unique circumstances of this outbreak, and the interaction between several role-players: the National Department of Agriculture, Forestry and Fisheries; the Provincial Department of Agriculture; the Ostrich Business Chamber and private and state laboratory services, many challenges were encountered in the management of this disease outbreak campaign. This presentation will provide a brief overview of the situation to date.

Evaluating non statutory sampling schemes in red meat chemical residue surveillance in Northern Ireland

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Residues in animal products have implications for consumers and international trade. Statutory testing for residues at slaughter is carried out as a result of Directive 96/23/EC (NRCP). This is supplemented in Northern Ireland with two non statutory random sampling schemes (Bovine Quality Assurance Scheme-BQA and Pig Testing Scheme-PTS). PTS was set up to control the abuse of in-feed antimicrobials within pig production while BQA is aimed to increase the statistical robustness of statutory testing for cattle, as this testing has a underlying assumption that the prevalence is homogeneous throughout the Member State. Using 2010 data, we evaluated the performance of these sampling schemes by assessing the current scheme usage/results and estimated the effectiveness using two methods: a decision tree analysis and a simulation study. We estimated the animal level sampling sensitivity and the surveillance system sampling sensitivity. The 'true' prevalence of residues in slaughter pigs and cattle was then approximated using a Bayesian approach. Results from both schemes showed a low apparent animal prevalence in 2010 with 0.15% in PTS and BQA finding no positive animals in 2010. The animal level sampling sensitivity was low for both schemes-BQA=0.004/PTS=0.003. The 'true' prevalence of residue positive cattle and pigs were 0.3% and 0.1% respectively. For a given year with a true prevalence of 0.1%, statutory testing would fail to find any positive pigs 91% of the time and positive cattle 35% of the time compared to <0.1% of the time for NRCP with PTS and 10% of the time for NRCP with BQA. Given the low 'true' prevalence, there should be a move towards a more cost effective targeted sampling approach for non statutory testing. Also the study highlighted the need for testing to match the current drug usage patterns within production.

Sensitivity and specificity of ELISA and PCR tests for identifying *Coxiella burnetii* seropositive and shedder cows using Bayesian analysis

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The objective was to estimate sensitivity (Se) and specificity (Sp) of milk and blood antibody ELISA and milk PCR tests to determine *Coxiella burnetii* status in dairy cows. Milk samples from 454 randomly selected cows from 12 dairy herds were included in this study. At the beginning of the study, bulk tank milk (BTM) samples from each herd were tested for the level of *C. burnetii* antibodies using ELISA and the herds were stratified according to high and low antibody levels. Among the 454 cows, samples from 230 cows included both blood and milk and were tested by all three tests and milk samples from the remaining 224 cows were tested by PCR and ELISA. Se and Sp of the tests were estimated in absence of a gold standard using latent class modeling in Bayesian analysis assuming conditional dependency between the two ELISAs. Conditional covariance (COC) was calculated to validate this assumption. A scenario of combined cut off values for the three tests was evaluated. The best set of results was revealed at cut offs at 33 quantification cycles for PCR and at antibody level (S/P ratio) 30 for the ELISA tests. Se and Sp values and 95% posterior credibility interval (PCI) were: PCR: 0.87 (0.71-0.99) and 0.99 (0.95-1.00); Milk ELISA: 0.57 (0.48-0.67) and 0.88 (0.84-0.93); Blood ELISA: 0.42 (0.31-0.53) and 0.86 (0.81-0.91). PCR Se and Sp were significantly higher than those of both ELISAs, and Se of milk ELISA was significantly higher than Se of blood ELISA, but without significant differences between their Sp estimates. Estimate of COC confirmed that the ELISAs were conditionally dependent in terms of both Se (COC 0.15; PCI 0.10-0.19) and Sp (COC 0.09; PCI 0.06-0.12). PCR quantification cycles ≥ 33 behaved constant and had higher Se and Sp than both ELISAs. Therefore PCR is considered a better test for identifying shedder cows.

Serological surveillance for avian influenza infections in poultry: is the gold standard really ‘golden’?

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Avian influenza (AI) control in areas at high risk of exposure should be centred on risk-based surveillance programs to promptly identify the infection in poultry populations. Diagnostic tests are fundamental to surveillance. Serological tests coupled with clinical inspection of poultry holdings are among the methods currently applied for low pathogenicity AI (LPAI) surveillance. Serological diagnosis of LPAI can be performed using different methods, yet the hemagglutination inhibition (HI) test is considered as the “gold standard” for AI antibody subtyping. Although alternative diagnostic assays have been developed, in most cases their accuracy has been evaluated in comparison to HI test results, whose performance for poultry has not been properly evaluated. In this study, we estimated the sensitivity (Se) and specificity (Sp) of the HI test and six other diagnostic assays for the detection of AI antibodies in the absence of a gold standard. We applied a Bayesian version of Latent Class Analysis to compare the results of multiple tests from different study settings reported in the literature. The results showed that the HI test has nearly perfect accuracy (i.e. 98.8% Se and 99.5% Sp). It performed well in both chickens and turkeys yet was less accurate in experimentally infected poultry, compared to naturally infected. Blocking ELISA and the indirect immunofluorescence assay also performed very well. In conclusion, given its very high Se and Sp, the HI test may be effectively considered as a gold standard. However, in the framework of LPAI surveillance, where large numbers of samples have to be processed, the blocking ELISA could be a valid alternative to the HI test, in that it is almost as accurate as the HI test yet quicker and easier to automate.

Bayesian latent models with random effects to estimate test accuracies of six different serological tests for *Brucella abortus*

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For bovine brucellosis, an important zoonotic disease occurring almost worldwide and causing production losses and public health concern, a perfect diagnostic test (‘gold standard’) is not available. Latent class models provide a potential approach to estimating diagnostic accuracy in the absence of a gold standard. The aim of the present study was to estimate test accuracies of six different serological tests for *Brucella abortus* originating from a field study of 19444 bovine samples tested with six different serological tests (SAT cut-off 31 iu, CFT, RBT, iELISA, cELISA, EDTA cut-off 51 iu) – all of them EU approved – undertaken in Northern Ireland. Different combinations of five tests with uninformative prior distributions on key model parameters were investigated. Population prevalence was estimated using a hierarchical beta-binomial approach, that is the (true but unknown) prevalence on each individual farm was allowed to vary as a farm level random effect. Effects of two-way covariances between tests were assessed by formal model selection using DIC as the goodness-of-fit criterion. Models were fitted using Markov chain Monte Carlo estimation through JAGS software and the output analysed with the package coda within the software R. The ranking order of the posterior means of sensitivities remained constant across all models and all combinations tested (SAT>RBT>EDTA>CFT>iELISA>cELISA). With the exception of SAT with a mean posterior estimate of 98.2, the other tests showed specificities of at least 99.9%. The estimated prevalence was 3.7% (95% CI [3.2;4.5]).

Within herd transmission and evaluation of the performance of clinical and serological diagnosis of foot and mouth disease virus during an outbreak in vaccinated cattle

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In 2000 Bolivia started a foot and mouth disease FMD eradication programme based on a mass vaccination campaign, control movement and clinical and serological surveillance. Guidelines for the implementation of such surveillance activities had been established intuitively and although these proved useful, better scientific evidence was needed to refine them. The objectives of this study were to evaluate 1) the diagnostic performance of clinical inspection and serological tests for detection of FMD virus non-structural proteins (NSP), and 2) the possible within-herd transmission of virus in vaccinated cattle. Data came from twenty three affected herds monitored during an epidemic of FMD type O in 2007. Clinical inspections were made regularly. All cattle from every herd were serum sampled one month after the last animal with clinical signs was detected. These samples were tested for the presence of antibodies against NSP of FMDV using the PANAFTOSA's 3ABC-ELISA test and the EITB test. Data from clinical and serological diagnosis were analysed using a Bayesian model. Parameters such as the sensitivity Se and specificity Sp of the tests and the 'true' prevalence p of FMD in the affected herds were estimated. The latter parameter was used to estimate the within herd reproduction ratio R of the virus. The Se of clinical inspections, the 3ABC-ELISA and the EITB tests were estimated to be 0.36, 0.87 and 0.92 respectively. The various estimated Sp 's; were 0.88, 0.93 and 0.93 respectively. The within-herd prevalence of infected animals ranged from 0.06 to 0.91 and R from 1.03 to 2.69. The estimates determined in this study can be used to refine current surveillance guidelines and inform simulation models for surveillance and control of FMD in vaccinated cattle populations.

False attribution: bias in probabilistic source attribution models for *Salmonella* infections

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The objective of probabilistic food source attribution models is to quantify the relative contribution of specific foods to the overall burden of human disease. In 2004, Hald *et al.* developed a model to estimate the number of human salmonellosis cases annually from contaminated animal-food sources. In this model and other subsequent models based on the Hald model, the ability to accurately estimate the burden of illness associated with specific foods could be dramatically affected by the implicit assumptions of the models. A validation of these attribution models is necessary but challenging to perform. The objective of this study was therefore to simulate causal datasets of *Salmonella* infections in people derived from various food sources and then run a modified Hald attribution model to determine the accuracy of attribution. Factors such as differential *Salmonella* strain prevalence across food commodities, number of colonies selected for analysis from each sample, differences in consumption quantities across food commodities, and potential biases of *Salmonella* cultivation protocols were included in these simulations. The modified model was run in WinBUGS 14. In general, the attribution model attributed more cases to a particular source when the prevalence of *Salmonella* in that source increased, regardless of whether the actual number of cases 'caused' by that source increased. The potential bias of *Salmonella* cultivation methods had a dramatic effect on the accuracy of attribution. Accuracy increased asymptotically with increasing number of colonies analyzed per sample. Given these results, it appears that interventions based on attribution models could be misguided due to the fact that these models have not been validated and are sensitive to fluctuations in *Salmonella* distributions. Future versions of the models should account for potential biases inherent in the acquisition of the data that populate the models.

Good practice in conducting and reporting quantitative risk assessments: a problem-oriented approach

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Quantitative risk assessment (QRA) models are required in many risk analysis frameworks such as for example international trade with animals, animal products and food. QRA models aim at an evaluation of the risk of an adverse consequence (endpoint) associated with a given hazard and risk scenario. The use of QRA is governed by international guidelines, which encourage the use of stochastic (probabilistic) methods if suitable data are available for model parameterisation. The transparency of the risk model is an important pre-requirement for scientific review and mutual acceptability of QRA results by trading partners and competent authorities. Both the conduct and the review of QRA models require an interdisciplinary approach. A well-structured and comprehensive model documentation is often difficult to achieve in practice and a lack of clarity in the reporting of the evidence, the modelling concepts, model assumptions and results are not uncommon. Against this background, a tool in R (www.r-project.org) is currently developed that (1) guides the modeller through comprehensive and consistent model documentation; (2) ensures the identity between definition, implementation and documentation of the model; and (3) automatically generates a technical model documentation. The open source licence under which the tool is distributed guarantees transparency to the level of source code. The presentation summarises the stage of development and illustrates unique functions such as Bayesian domains within the scenario models using example applications. The tool is available from the author and information can be obtained from http://www.bfr.bund.de/en/r/risk_risk_modelling_and_auto_reporting_in_r-52162.html.

Risk of African swine fever introduction into the European Union through illegal importation of pork and products

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Diseases such as African swine fever (ASF), classical swine fever or foot-and-mouth disease have severe socio-economic impacts when introduced into new regions. The history of disease incursions in the European Union (EU) suggests that initial outbreaks were often due to illegal importation of meat and meat products, and that the EU's surveillance strategy would benefit from decision-support tools for evaluating the risk of disease introduction through illegal imports. Due to the difficulty in quantifying illegal movements of animal products however, few studies have been conducted on this topic. We present an innovative risk assessment framework for disease introduction into the EU through illegal importation of meat products, using ASF as an example. The semi-quantitative model considered proxy indicators (PI), i.e. factors likely to influence the release of contaminated smuggled pork and pork products, and the exposure of the domestic pig population. PIs were weighted using expert opinion so as to reflect their influence on the risk of release or exposure. Suitable datasets available in the public domain or information easily obtained for all EU member states (MS) were identified for each PI, and their values across MS were categorized into scores from 0 to 5. Release and exposure risk scores were obtained by weighted linear combination of the PIs' scores and weights, and then converted into qualitative risk categories. The model identified differences in risk levels for EU MS with five MS at high or moderate risk of ASF release, two MS at high risk of exposure and twelve MS at moderate risk of exposure. The results highlight regions where illegal import is of particular concern, and might be useful to inform surveillance systems.

A comparative assessment of the risks of introduction and spread of foot and mouth disease among pig farms in Australia

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Small-scale pig producers are believed to pose higher biosecurity risks for the introduction and spread of exotic diseases than the mainstream pig industry. This study is a comparative assessment of the risk of introduction and spread of foot and mouth disease (FMD) through different sectors of the pig industry: (1) large-scale producers (LS); (2) small-scale producers (<100 sows) selling at saleyards and abattoirs (SS-C); and (3) small-scale producers selling informally (SS-I). Exposure and consequence assessments were conducted using stochastic quantitative simulation modelling and sensitivity analysis, assuming the virus was introduced into Australia through illegal importation of infected meat. Input data were obtained from data-gathering exercises with pig producers, industry statistics and literature. Our findings suggest the likelihood of exposure to FMD is very low and similar for the three sectors of the pig industry; with swill feeding being the most likely exposure pathway. Spread of FMD from the index farm is most likely to occur through movement of contaminated fomites followed by movement of pigs and ruminants. The probability of FMD spread from SS-C (moderate) was higher than that from LS and SS-I (low), due to the lower disease knowledge and biosecurity practices, the high proportion of producers keeping ruminants and the multiple destinations of pigs off farm, among SS-C. However, trade of pigs through informal pathways could jeopardize animal traceability and control strategies. The probability of farmer detection and reporting and the presence of ruminants are the most influential input values in the models. This assessment provides insight into the relative magnitude of the biosecurity risks among the three sectors of the pig industry, which can support decisions on resource allocation for improving biosecurity in the pig industry.

Quantitative risk assessment of formal pig movements in eastern Indonesia and transmission of classical swine fever

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A quantitative risk assessment was conducted on formal pig movements across Nusa Tenggara Timur Province in eastern Indonesia to assess the likelihood of classical swine fever virus (CSFV) transmission between pigs. Pigs in this region have high cultural and economic importance with most held in smallholder herds of 1-2 sows. Classical swine fever, a highly contagious viral disease, was first confirmed in the province in 1998. Since its introduction, substantial losses have been reported with infection spreading to uninfected islands as recently as 2011. This risk assessment sought to identify pathways in the live pig market chain with the greatest risk of CSFV transmission and to assess the effect of mitigation measures to reduce CSFV transmission. A modular risk model approach was used considering only live pig to pig transmission. Data obtained from market and farmer surveys on West Timor, Flores and Sumba islands, published literature and expert opinion were utilised. A Monte Carlo simulation was performed with @Risk (Palisade) with 10,000 iterations. Modules were divided based on market chain movement processes from village to market. Outputs included the number of infected and clinical pigs at market and the probability a market was infected with CSF. Mitigation strategies assessed were vaccination and pre-entry market inspection. The baseline model demonstrated that markets in West Timor and Sumba had the highest number of infected pigs. For market inspection to be effective, it needed to be strict with sensitivity >75% required to reduce the probability a market was infected. With increased vaccination coverage, there was a reduction in the number of infected and clinical pigs arriving at market. However, CSFV was not eliminated from the market environment. This work in combination with other analyses such as Social Network Analysis will be used to guide policy on CSF control in eastern Indonesia.

A qualitative assessment of the risk for Rift Valley fever virus introduction into Spain

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Rift Valley fever (RVF) is a vector-borne disease that may produce an important impact on the public and animal health in affected regions. In last decade, it has been considered a re-emerging disease with an increase on the number of outbreaks in the African continent, Madagascar, Saudi Arabia and Yemen. This situation has increased the concerns regarding the potential introduction in countries of the Mediterranean Basin such as Spain, where prevailing favourable climatic conditions may contribute to the spread of the disease and may challenge its rapid control. The aim of this study was to assess the risk for RVF virus (RVFV) introduction into Spain through different risk pathways and to identify the Spanish areas at highest risk for disease introduction. In order to achieve this goal, a qualitative risk assessment model was developed with data obtained from scientific literature, governmental and public sources and expert opinion. Pathways assessed were legal trade of ruminants and their products, entry of people and mechanical and wind-borne transport of RVFV or vectors. Several potential scenarios were evaluated to assess the impact that changes on the RVF epidemiological situation might have on the risk of entry into Spain. Model revealed that wind-borne transport of RVFV-infected vectors is the route that poses the highest risk for RVF introduction into Spain. Specifically, there was a moderate risk for RVF introduction into Canary Islands from Mauritania by this pathway. Moreover, it has been estimated that, if RVF affects the Maghreb, especially Morocco, the risk for RVF introduction into Spain would increase, being particularly high in the Spanish provinces of Cadiz and Malaga, which hold high ruminant densities. The methods and results presented here may be useful to support the design of risk-based surveillance programs of RVF in Spain and, ultimately, to prevent and rapid control potential RVF outbreaks in the country.

The risk of wild animals exposing domestic pigs to pathogens in Australia

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The objective of this project was to quantify the likelihood of pathogen transmission occurring from wild animals to domestic pigs in Australian piggeries. Specific pig pathogens of importance to the Australian pig industry were detected in European starlings (*Sturnus vulgaris*), rats (black rat *Rattus rattus*; brown rat *Rattus norvegicus*) and feral pigs (*Sus scrofa*) on or in close proximity to piggeries. These pathogens were *Salmonella* spp., *Escherichia coli* and *Campylobacter* spp. in European starlings; *Brachyspira hyodysenteriae*, *Salmonella* spp. and *Lawsonia intracellularis* in rats; and *Leptospira* spp., *Brucella suis*, *Lawsonia intracellularis* and *Mycoplasma hyopneumoniae* in feral pigs. Prevalence estimates for each pathogen were obtained and combined with additional information from a nation-wide survey of all commercial pig producing members of Australian Pork Limited, literature and expert opinion to assess the risk of exposure of these pathogens to domestic pigs. The exposure risk was quantitatively assessed using the OIE framework for import risk analysis and scenario trees, and described the pathways required for domestic pigs to become exposed to the relevant pathogens. The exposure assessment identified that rats posed the highest probability of pathogen transmission to domestic pigs on Australian piggeries and the pathogen most likely to be transmitted was *L. intracellularis* (median probability of 0.13). The sensitivity analysis identified the presence and high number of the wild animals on piggeries, as well as the wild animal access to pig environment, food and water as the most influential input parameters affecting the exposure risk for all three animal species. This study identifies the risk of disease transmission from wild animals to domestic pigs and those areas where mitigations strategies could be applied to reduce the risk.

Profiling of MRSA positive dogs arriving at a veterinary teaching hospital

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Risk factors and the molecular profiles of Methicillin Resistant *Staphylococcus aureus* (MRSA) strains circulating in humans are well known. However, this information in canines is lacking even though MRSA has emerged as an important zoonotic and nosocomial pathogen in dogs. The objectives of this study were to identify risk factors associated with MRSA carrier dogs on their arrival at a veterinary teaching hospital, and to characterize any MRSA isolates recovered to create an epidemiological and molecular profile. A total of 435 dogs were enrolled in the MRSA active surveillance program upon arrival at the OSU Veterinary Medical Center over one-year period. Each enrolled dog was screened in multiple anatomical locations for the presence of MRSA and an epidemiological survey/medical history was obtained to identify potential risk factors up to 12 months previous to their admission. All isolates were characterized by antimicrobial susceptibility testing, SCCmec typing, PFGE typing and dendrographic analysis. Of 435 dogs, 25 (5.7%) were MRSA positive, with the nostril the most commonly colonized location (18/25, 72%). Little molecular diversity was observed with 80% of the dogs (20/25) carrying MRSA strains classified as HA-MRSA (SCCmec type II/USA100). In addition, all MRSA strains were multiclass antimicrobial resistant. Dogs owned by veterinary students were 20.5 times more likely to be MRSA carriers ($P < 0.01$). No other epidemiological variables related to the medical history, dog's management, home environment, or other potential exposures were associated with MRSA carrier status. Interestingly, 4/25 MRSA carrier dogs were classified as clinically healthy. The presence of this pathogen in incoming patients without a specific epidemiological profile represents a risk to students, hospital staff, and other patients, and may result in contamination of the hospital environment.

Longitudinal study for the presence of livestock-associated MRSA in piglets

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On 4 closed pig farms, a longitudinal study was performed to determine the piglet colonization age and the effect of the sow status on the piglet status. Molecular typing was performed to detect the colonization origin and changes over time. The generated knowledge may help to develop intervention strategies to reduce the MRSA colonization in pigs. On farms A and B, MRSA was detected only occasionally in sows. The colonization rate in piglets increased remarkably at the end of the stay in the growing unit. On farms C and D, the MRSA colonization rate of sows and piglets was high from farrowing on. On all farms, a decrease in colonization was observed towards slaughter age. The overall colonization age of the piglets was 17.8 days [11.5-25.6]. There was a significant effect of the sow MRSA status at farrowing on the piglet MRSA status ($P < 0.001$). Molecular typing revealed the presence of one dominant type on farms A and B, whereas two or more on farms C and D. Sows did not always carry the same types as their offspring. In conclusion, the present study indicates that the sow status is of importance for the colonization of the piglets and should be included in remediating measures. However, the observed differences in colonization rates between the different farms complicate implementation of remediating measures on the farm. Molecular typing revealed that there is a certain dominance of MRSA strains within the animals and within a group of animals over time.

Epidemiological factors associated with FMDV serotype O genetic variability in Pakistan

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Most of the foot-and-mouth disease virus (FMDV) antigenic variation occurs within the P1 sequence, encoding the four capsid proteins VP1-4. Many of the emergent FMDV strains that caused recent epidemics in FMD-free regions emerged from the Indian sub-continent. Here, we quantified the extent to which epidemiological factors contributed to accumulated nucleotide (nt) variation of serotype O FMDV in Pakistan. We analyzed 82 FMDV O VP1 sequences from samples collected from 2005 through 2011; for 27/82 samples, the VP2, VP3 and VP4 (VP2-4) sequences were also available. A Pearson's coefficient correlation (r) of the changes in the VP1 and VP2-4 was computed to assess the hypothesis that VP1 sequencing is sufficiently informative to quantify FMDV nt variation. Genetic (nt) changes in the VP1 were strongly ($r=0.99$) associated with changes in the rest of the P1. Consequently, we used the 82 VP1 sequences to construct a neighbor-joining tree and identify FMDV genetic clusters. A hierarchical linear model, using the nt distance to the earliest isolate in the cluster as the independent variable; time difference, spatial distance and species as fixed effects; and phylogenetic cluster as hierarchy was fitted to the data. Time and distance were significantly ($P<0.01$) associated with nt variation, whereas no significant association was estimated for species of isolation. Results suggest that the genetic variation observed in FMDV O in Pakistan is spatially-clustered and time-dependent, but it is not specific for species, which is consistent with the frequent multi-species outbreaks observed in Pakistan. These results will have impact on the implementation of vaccination campaigns in the region.

Epidemiological factors associated with variation of the HA, NA, and NS genes of H5N1 highly pathogenic avian influenza viruses isolated from birds in Romania in 2005-2007

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Molecular characterization studies of a diverse collection of avian influenza viruses (AIVs) have demonstrated that AIVs' greatest genetic variability lies in the HA, NA and NS1 genes. The objective here was to quantify the association between epidemiological factors and pairwise nucleotide variation in the HA, NA, and NS1 genes of 70 isolates of highly pathogenic avian influenza (HPAI) H5N1 collected from October 2005 to December 2007 from birds in Romania. A mixed binomial Bayesian regression model was used to quantify the probability of nucleotide variation between isolates and its association with epidemiological factors. As expected for the three target genes, a higher probability of nucleotide differences ($ORs>1$) was found between: those viruses sampled from places at greater geographical distances from each other; viruses sampled over greater periods of time; and viruses derived from different species. However, a lower probability of nucleotide differences ($OR<1$) was detected in comparison of isolates from birds of different orders for the NA gene, compared to the HA and NS1 genes. The study quantifies the dynamics of evolution of H5N1 HPAI virus in bird populations, and will be useful in predicting the most likely genetic distance for any of the three gene segments of viruses that have not yet been isolated or sequenced based on space, time, and host species during the course of an epidemic

Presence of different-origin Israeli acute paralysis virus not related with Colony collapse disorder in Spanish honey bees

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Depopulation and collapse of honey bee colonies continue being one of the most concerning challenges in worldwide apiculture and agriculture, since honey bees are the main pollinator of crops in USA and Europe. Since the appearance of this multifactorial phenomenon known as Colony Collapse Disorder (CCD) many possible causes have been evaluated, including viruses such as Israeli acute paralysis virus (IAPV). IAPV is a Dicotivirus which was first described in 2004 affecting Israel colonies with heavy losses and whose importance derives from its association with CCD in the USA in 2007. However, this association has not been confirmed in other countries. The aim of this study is to assess the possible association between IAPV presence and CCD and to describe the origin of IAPV in Spain, the first honey producer in the EU. We sampled three important Spanish regions due to honey production (Valencia and Andalucía) and ecological relevance and situation (Navarra). An epidemiological survey was conducted to collect handling and sanitary data. Samples were analyzed for IAPV presence by RT-PCR. Positive IAPV samples were sequenced and a phylogenetic analysis was carried out using MEGA4®. In terms of results, absence of CCD in IAPV positive colonies dismisses possible associations between IAPV and CCD in Spain. Moreover, phylogenetic analysis showed two main lineages which suggest at least two differentiated origins of IAPV in this country. Navarra and Andalucía isolates were similar mainly to French isolates, which could be explained by proximity between regions, whereas the Valencia isolate was similar mainly to USA isolates, which is possibly explained by commercial trades. As conclusions, this study has confirmed the unlikely association of IAPV with CCD and the phylogenetic relationships of Spanish IAPV with specimens from other countries, which could serve to implement surveillance measures in the future.

Session 07**Theatre 1****Transmission of highly pathogenic H5N1 avian influenza in vaccinated and vaccinated poultry**

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Vaccination against H5N1 highly pathogenic avian influenza is a potentially attractive option for prevention and control in regions where the disease is endemically present. Unfortunately, the effectiveness of vaccination is difficult to assess in the field, while vaccine potency studies have the inherent disadvantage that extrapolation of the results to protection against infection is problematic. Here we report results from experimental transmission studies with native Indonesian layer and broiler chickens. The analyses are based on a Bayesian inferential framework, enabling precise estimation of the parameters of interest (latent period, infectious period, transmissibility). Earlier results with the experimental transmission model showed that vaccination can effectively halt transmission, and that maternal antibodies may interfere with vaccination if chickens are vaccinated early in life. Here we add that seroconversion (determined by a fourfold or more increase in log HI titers) occurs frequently upon exposure in vaccinated chickens, but that virus shedding is rare or grossly suppressed. We discuss the implications for vaccination strategies in endemically affected areas.

HPAI H5N1 virus from suboptimally vaccinated chickens was not transmitted to unvaccinated pen mates and not detected in environmental dust

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Suboptimal vaccination is considered a risk for the control of Highly pathogenic Avian Influenza (HPAI), because it may result in birds protected against clinical disease that are still able to transmit the virus to birds in the same flock, or even to birds in other flocks (e.g. by dust). In this study we examined virus transmission among suboptimally vaccinated chickens and determined the amount of virus in dust originating from these birds. Groups of 10 chickens were formed and per group 5 chickens were vaccinated with either 1/3, 2/3, or none of the recommended dose. Two weeks post vaccination the vaccinated birds were challenged with HPAI H5N1 virus, and thereafter placed with the 5 unvaccinated birds. Tracheal and cloacal swabs were collected daily to monitor virus transmission, and the amount of virus in dust was determined. None of the vaccinated birds showed clinical signs post inoculation, whereas all birds in the non-vaccinated groups did and died. Vaccinated birds only shed virus via trachea, as cloacal swabs remained negative. The amount of virus detected in tracheal swabs was $10^{4.5}$, $10^{3.7}$ and $10^{6.4}$ EID₅₀ for the 1/3, 2/3 and non-vaccinated group, respectively. None of the contact birds in the vaccinated groups became infected, whereas all contacts to the non-vaccinated birds did. All dust samples collected in the vaccinated groups appeared negative in RT-qPCR; dust samples in the non-vaccinated group showed on average $10^{2.8}$ EID₅₀ per m². This study showed that birds vaccinated with only 1/3 dose could be infected, but were unable to infect unvaccinated cage mates. Moreover, no virus was detected in dust collected around the cages. Possibly, the absence of cloacal shedding reduced deposition of viral particles via faeces and therefore reduced the amount of virus into the environment and transmission of virus to cage mates.

An ecological niche model of highly pathogenic avian influenza virus H5N1 occurrence in domestic poultry in Asia

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The control of highly pathogenic avian influenza virus (HPAIV) H5N1 in Asia – a region of widely diverse agro-ecological and socio-economic systems – continues to present formidable challenges to health practitioners. However, the use of an ecological niche-based spatial modeling method – maximum entropy (Maxent) – may help to extend our understanding, and thus control, of the disease. The objective of this study was to model the risk of HPAIV H5N1 occurrence in domestic poultry in Asia. Maxent was used to assess the correlation between five variables and the occurrence of HPAIV H5N1 outbreak data. The contribution of each variable to the model was determined together with the general trend of disease risk across the values of each variable. A risk map delineated areas of high and low risk, each of which were in turn characterized with respect to the individual variables. The predictive accuracy of the model was excellent (area under the curve (AUC) 0.903). Two of the five variables together accounted for just under 85% of the variation in HPAIV H5N1 occurrence – densities of domestic waterfowl (50%) and humans (33%) – with proximity to areas suitable for rice-growing (7%), proximity to roads (7%) and chicken density (3%) accounting for the remainder. Areas with the highest predicted risk included Bangladesh, parts of Vietnam and central Thailand and most of Java. High-risk areas were characterized by high densities of domestic waterfowl and humans, medium-to-high chicken density and were close to roads and areas suitable for rice-growing. Conversely, low risk areas were generally characterized as having no domestic waterfowl, low human and chicken densities and were far from areas suitable for rice-growing. By allowing regions of different risk to be characterized with respect to predictor variables, Maxent can extend our understanding of HPAIV H5N1 and enables the optimization of finite resources in designing risk-based disease surveillance systems.

Increase in low pathogenic avian influenza infections on poultry farms in the Netherlands

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Since Low Pathogenic Avian Influenza (LPAI) viruses have the potential to mutate to Highly Pathogenic Avian Influenza (HPAI) viruses, efforts are made to detect LPAI infections in poultry as early as possible. For this reason, a serological surveillance is in place in the Netherlands, testing all poultry farms 1-4 times a year, depending on farm type. In the last years the number of LPAI detections has dramatically increased: 2 primary LPAI introductions were detected in 2006, 23 in 2011. Most infections were detected by the serological surveillance (56/69), and no obvious causes could be found for this increase: the surveillance was not intensified, the number of poultry farms did not change. Because wild birds are considered as the main reservoir of LPAI viruses, the number of wild birds and the LPAI virus prevalence in wild birds were also taken into account, but both were not increased. A publication based on part of these data shows that free range layer farms have a 11x higher change of becoming infected than indoor layer farms. Also turkey farms and duck farms have a higher risk of infection. Considering control measures we did a spatial analysis and a time analysis. The spatial cluster analysis on the LPAI positive layer farms identified two small regions in the Netherlands with a higher risk of LPAI introductions and one large region with a lower risk. There is an obvious peak in the detections in May and June (25/69). To make a link between the moment of detection and the introduction Monte Carlo simulations were performed using transmission parameters from LPAI virus infections in the field and in experiments. In this way it was estimated that an infection is detected 7.8-41 (minimal 3; maximal 70) days after introduction.

The role of domestic ducks in the endemicity of highly pathogenic avian influenza H5N1 virus in Indonesia

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In some countries domestic ducks play an important role in endemicity of highly pathogenic avian influenza (HPAI), however, for Indonesia the role of domestic ducks in HPAI is not yet well understood. A cross-sectional survey was conducted to determine the prevalence of HPAI H5 in unvaccinated duck flocks in two H5N1-endemic provinces in western Java. Samples were obtained from 194 farms and were tested using hemagglutination inhibition and PCR. The flock seroprevalence was 31.4% (95% CI 24.9-38.5%). Within positive flocks the prevalence was 7% (95% CI 3.3-23.3%). The overall bird-level seroprevalence was 2.2%. Out of 194 farms surveyed, 29 farms (14.9%) tested PCR positive for influenza type A but only 4 farms (2.1%) tested PCR positive for H5 subtype influenza. The within-farm virus prevalence in positive farms was low for both influenza A and H5 PCR. The flock prevalence for influenza A tended to be higher in nomadic flocks compared to stationary flocks. Farmers of positive duck flocks did not report any illness in the past indicating that apparently healthy ducks do seroconvert and shed virus. The survey shows that ducks can be a reservoir for H5 virus but shedding seems to be low. Low prevalence of HPAI in the ducks showed by this study was consistent with recent study in other part in Indonesia. Although the role of the ducks is not yet clear, it could be that they are rather indicators for the virus pressure in the area than that they play an active role in driving the endemicity of the disease in Indonesia.

Porcine Reproductive and Respiratory Syndrome virus (PRRSV) transmission rate is not constant with time-since infection: a serial transmission experiment

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The objective of this study was to estimate the time-dependent transmission rate of Porcine Reproductive and Respiratory Syndrome Virus (PRRSV) in experimental conditions. Relationships between this time-dependent infectiousness and the evolution of virological parameters and antibody response were also assessed. Seven successive transmission trials involving a total of 77 specific pathogen-free piglets were carried out from 7 to 63 days post inoculation (DPI). PRRSV inoculated pigs were mingled successively with susceptible pigs at 7, 14, 21, 28, 42, 56 and 63 days post infection. Once mingled, they remained for 2 days with the seeders and were then returned to their original room to be monitored for PRRSV infection. The transmission rate defined as a function of time-since infection was modelled by maximizing the likelihood of the observed number of infections in each contact group. The PRRSV statuses of the inoculated and contact pigs were monitored until 63 days post-inoculation (DPI) using an in-house real-time RT-PCR in blood or nasal swabs to assess the PRRSV genome load. The infectiousness of inoculated pigs increased from 7 to 14 DPI and then decreased slowly until 42 days post infection (3, 7, 2, 1 and 0 pigs infected at 7, 14, 21, 28 and 42 DPI, respectively). Using those data, the time-dependent infectiousness was modelled by a lognormal-like function with a latency period of 1 day and led to an estimated basic reproduction ratio, R0 of 2.6 [1.8, 3.3]. Virus genome in blood was detectable in inoculated pigs from 7 to 77 DPI, whereas the viral shedding was detectable from nasal swabs from 2 to 48 DPI. Infectiousness was mainly correlated with the evolution of the viral genome load in blood and the decrease of infectiousness corresponded to seroconversion time.

Understanding foot-and-mouth disease virus transmission biology: identification of the indicators of infectiousness

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Foot-and-mouth disease virus (FMDV) causes one of the world's most important infectious vesicular diseases of domesticated and wild cloven-hoofed animals. In ruminants, a common route of transmission is by direct contact between infected and naïve animals. Using quantitative data on the transmission biology of FMDV between cattle we previously reported on the relationship between the onset of clinical signs (any visible lesions or body temperature above 39.5 °C) and the transmission of FMDV. Animals are unlikely to transmit virus unless they show clinical signs, which is a period of time when virus is readily detectable in pharyngeal and nasal secretions and in aerosols. We therefore re-examined the data from our experimental transmission study using Nonmetric Multidimensional Scaling and Nonparametric Multiplicative Models in an attempt to determine predictors of the onset of clinical signs. Identification of the predictors of the onset of clinical signs should enable refinement of epidemiological models/methods to combat outbreaks.

The association between transmission rate and disease severity for *Actinobacillus pleuropneumoniae* infection in pigs

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Infections can lead to variable course of disease between individuals, with subsequent variable consequences for the infectivity. In general, improved understanding of the variation in infectivity helps to understand the behaviour of outbreaks of disease and design effective control measures. In pigs *Actinobacillus pleuropneumoniae* causes respiratory disease and infectivity is highly variable. While subclinical infections are most prevalent, outbreaks of clinical disease occur occasionally. Knowledge of the association between clinical disease severity and infectivity could aid to better means of control. Pairwise transmission experiments were performed to investigate the role of disease severity on the transmission of *A. pleuropneumoniae*. Ten Caesarean-derived, colostrum-deprived pigs were inoculated intranasally with 5×10^6 cfu of *A. pleuropneumoniae* strain 1536 and housed together with a contact pig. Clinical disease was scored and the course of infection was observed by selective bacterial examination of tonsillar brush and nasal swab samples. In 6 of 10 pairs transmission was observed. While variable clinical disease scores (CS) was observed in all inoculated pigs, CS in contact exposed piglets were low. CS was significantly associated with bacterial load in *A. pleuropneumoniae* positive pigs. Results showed that transmission rate was positively associated with the bacterial quantity in nasal samples, but negatively associated to CS. Finally CS in contact pigs was not associated to CS in the inoculated pigs. With respect to the evolution of outbreaks of *A. pleuropneumoniae*, we conclude that clinical outbreaks are not due to increased transmission of *A. pleuropneumoniae*.

A model for introduction & ensuing spread of a duck origin H5N3 low pathogenic avian influenza virus in chickens

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Avian Influenza Virus (AIV) is found in numerous bird species throughout the world. Circulation of the virus within a susceptible population may lead to further adaptation to this host species. When different bird species come into contact, interspecific transmission of AIV may occur. In this study, a duck-origin H5N3 LPAIV was used in inter- and intraspecies transmission experiments, performed in isolation units. In a series of interspecies transmission experiments, experimentally infected Peking Ducks were brought into contact with SPF chickens in either a direct (housed in the same isolator) or indirect (contact with feces or drinking water from infected ducks) way. In intraspecies transmission experiments, experimentally infected SPF chickens were brought into direct contact with susceptible SPF chickens. In all experiments, virus shedding from animals was followed-up by RRT-PCR analysis of oropharyngeal & cloacal swabs and reproduction ratios were estimated using serological data. Direct interspecies transmission experiments showed virus transmission and following R values: 1.46 [95% CI: 0.55-4.14; infected/susceptible ratio=12/12] and 0.76 [95% CI: 0.10-5.49; infected/susceptible ratio=3/6]. Interestingly, indirect interspecies virus transmission was seen via infectious drinking water as 3 out of 6 SPF chickens were positive in AIV-specific antibodies, but was not seen via infectious duck feces. Conversely, intraspecies virus transmission between SPF chickens was not observed. This study demonstrates that direct or indirect contact between domestic poultry and infected wild birds is sufficient for the introduction of LPAIV in a domestic poultry holding. However, since it was not observed in this case, establishment of a wild bird-origin LPAIV that has been introduced in a domestic poultry holding may largely depend on the viral strain under consideration.

Quantification of the effect of physical separation of pigs on spread of *Streptococcus suis*

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Streptococcus suis infections are common in swine herds, resulting in abundant use of antibiotics and economic damage. Control of the disease might be achieved by reduction of spread of *S. suis* by physical separation of groups of pigs. The aim of this study was to quantify transmission of *S. suis* among pigs which had either direct or indirect contact with each other. In three replicate experiments, pigs were housed in boxes either pair-wise (direct transmission; n=50) or alone (indirect transmission; n=15). Stable units contained 2-4 pairs, and 1-3 single housed pigs. The distance between the boxes was ± 1 meter. At 7 weeks of age, one pig in each pair was inoculated intranasally with *S. suis* serotype 9. Colonization was monitored in all pigs for 4 weeks post inoculation by taking tonsillar brush and saliva swab samples that were cultured on selective media. All directly exposed pigs became colonized within 2 days after exposure. Thirteen indirectly exposed pigs became positive within 7-25 days after exposure. For direct transmission, a standard SIR model was used to estimate the transmission rate β_{dir} (3.58, 95% CI: 2.29-5.60). For indirect transmission, a model with linearly increasing infectivity of infectious animals (representing, for instance, accumulation of *S. suis* in the environment) fitted better than the standard model. The results show that physical separation of an infectious and a susceptible pig over ± 1 meter results in a mean time to infection of 39 days (95% CI: 30-51), compared to 0.28 days (95% CI: 0.18-0.44) when housed together. We conclude that keeping pigs separated might be an effective intervention measure to reduce horizontal transmission of *S. suis* within stables.

Comparison of transmission rates of *Salmonella enteritidis* between pair-housed and group-housed layer hens

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A major aim of transmission experiments is to estimate transmission rates, which can be used in mathematical models to evaluate surveillance or control programmes. Although animals are usually housed in groups, transmission experiments are often performed with pairs. This design increases the number of independent observations, but may reduce the accuracy of the estimate: the contact process in pairs or groups may be different, resulting in different transmission rates. The aim of this study was to compare results of transmission experiments in pairs and groups of laying hens. In 60 experimental groups of 2 hens (pairwise experiments), and 3 groups of 200 hens (group experiments), we inoculated 1 and 4 hens with *Salmonella Enteritidis*, respectively. The hens were housed at similar densities. Regular fecal samples were taken to test for the presence of *S. Enteritidis*, indicating excretion and colonization. Transmission parameters estimated from the pairwise experiments were used for simulations of the group experiments, which were compared to the actual experimental results. Although differences in dynamics (eg, prevalence in time) were observed, we can show that these differences were more likely due to differences in properties of diagnostic tests than to differences in transmission rates. This finding suggests that the transmission parameter estimates from small-scale experiments might indeed be extrapolated to the field situation.

Use of blood samples of aborting cows for early detection of (emerging) infectious diseases

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The objective of this study was to evaluate to what extent syndromic surveillance on the number of blood samples of aborting cows can contribute to early detection of (emerging) diseases in the Dutch cattle population. Elevations in time and/or space of the number of samples that were submitted for brucellosis monitoring (2007-2011) were investigated using linear regression and retrospective and prospective space-time cluster analysis. For the linear regression the number of samples per week was set as the dependent variable and seasonal differences in submissions were modelled with a sine/cosine function. The number of expected submissions was compared with the number of observed submissions. A threshold for an elevation of blood samples was set at 5% weeks with the highest difference between observed and expected submissions. In addition, a threshold for follow-up actions to determine the cause of the alert was set when two or more elevations occurred within four weeks. A retrospective cluster analysis was carried out to detect elevations of blood samples in time and space. Finally, a prospective cluster analysis was carried out for each week in 2010 to simulate a situation in which the syndromic surveillance would be operational. For the latter two analyses, the space-time permutation scan statistic was used. Data were aggregated per week and per 2-digit postal code. A result was considered significant at the 1% level. The sensitivity of the methodologies was determined for the bluetongue (2007) and schmallenberg (2011) virus epidemic. All methods detected these diseases that increased the number of abortions and thus the number of submitted blood samples. However, only prospective space-time analysis could contribute to early detection, relative to the other surveillance components that are in place.

Use of monthly collected milk yields for the detection of vector borne emerging diseases: a simulation based approach

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Two vector borne diseases, caused by the bluetongue and Schmallenberg viruses, have emerged in the European cattle population during the past 10 years resulting in high costs for the industry. The emergence of such diseases cannot be predicted, and the mitigation of their impact can rely on an early detection. A decrease of milk production is a non specific symptom associated with some diseases that can be incorporated in an early detection system. Cow milk yield is routinely collected on a monthly basis as part of the different milk recording schemes available throughout Europe. The aim of this project was to evaluate the ability of a space-time scan statistic to detect in real time the emergence of a vector borne disease through the simulation of its propagation and effects on milk production. Milk recording data collected in France between 2003 and 2006 were available. The years 2003 to 2005, before the bluetongue virus outbreak, were used to determine expected milk productions in the absence of disease. A range of plausible patterns of spread (speed of propagation, daily proportion of cows affected within a herd) and effects (rate and duration of decrease in milk production) were used to simulate the spatio-temporal propagation of a disease and its effects on the milk productions observed in 2006. Disease simulation was performed in R. Clusters of deviations from the expected yields were detected at the municipality-week level using SaTScan. The ability and timeliness of a space-time scan statistic to detect a disease emergence according to its propagation characteristics and impact on milk production will be presented.

A national risk assessment tool for emerging and re-emerging zoonoses

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The global economic and social impact of spread of emerging and re-emerging zoonoses has been enormous, and has not necessarily been closely correlated with the severity of disease effects. Part of this is the uncertainty about how severe the disease will be and how far and fast it will spread, which leads to widespread concern in the global community and inhibits balanced decision-making. A software tool is being developed to allow countries to make frequent assessments of novel disease threats and determine appropriate surveillance. The tool is called SARStrend – Surveillance And Response Strategy for Emerging Diseases. When a disease of potential concern to a country is identified elsewhere, available epidemiological information about the disease is collated and a list of putative risk factors prepared. The disease is then categorised into one of a limited number of ‘epitypes’ – diseases which are broadly similar in their epidemiological determinants. The list of factors to be used in subsequent steps is then refined. A risk map is prepared for the country using remotely sensed data combined with available demographic and other data of possible importance for this disease. This risk map is used to formulate potential surveillance strategies for the disease, and these strategies are compared for suitability and expected benefit by simulating an outbreak of the disease using the spatial model InterSpread-H, assessing the expected effects on human and animal health, and measuring the detection efficiency of different surveillance strategies to either confirm freedom from the disease, or to support control efforts. InterSpread-H models animal disease in a spatially defined population, estimates numbers of human cases, and assesses the economic benefit of different response strategies. This information can first be used to guide an initial response and dampen community concern, then the assessment can be conducted iteratively as new information becomes available.

The surveillance paradigm: ‘perceive an epidemiological reality through non reliable data’, the case of H5N1 wildfowl outbreaks in Europe

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Often, the only quantitative available data on the spread of a pathogen are those from surveillance. These data are diverse, sometime incomplete and biased. In this communication we describe a method to overcome the heterogeneity of cases of HPAIV H5N1 infection amongst wild bird population in Europe. This approach consists of grouping several cases according to a spatio-temporal criterion by smoothing the edges of the affected areas, thus forming a ‘case focus’. Using the concept of ‘case focus’, we described the spread of outbreak waves of HPAIV H5N1 in Europe between 2005 and 2010 and we studied the performance of the passive surveillance in wild birds in 2009 and 2010. Of the 628 reported cases (outbreaks) obtained from the World Animal Health Organisation information database (WAHID, OIE), we observed 300 ‘case foci’ in a first wave (01/10/2005 to 31/08/2006), 41 in a second wave, (01/09/2006 to 31/08/2007) and 10 ‘case foci’ for a third wave (01/09/2007 to 30/06/2010). The largest ‘case focus’ was observed during the second wave recorded in Germany, with a total of 101 cases; only sporadic cases were noted in a third wave. We discuss the power and representativeness of the data. As well as the descriptive study of the outbreak waves, the analysis of the surveillance performance showed distinct patterns for the successive waves and inform on the advantage or limitation of the current way of surveying wild bird infection by HPAIVs.

The monitoring and surveillance system (MoSS): external validation

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Because of the constant threat of emerging diseases, there is an increasing interest in animal surveillance systems. After the Bluetongue outbreak in 2006, the Monitoring and Surveillance System MoSS, an online multilingual web application for the early detection of (re)-emerging animal diseases, was designed and developed. Veterinary practitioners are encouraged to enter a clinical description of any atypical case they encounter into the MoSS-webpage. All records are compared with each other and are aggregated through a hierarchical clustering process when they show a similarity of at least 55%. As a focal point to share information between veterinary practitioners and experts, the MoSS should help to shorten the time between the onset of disease and the identification of the causative agent. To assess the functionalities of the MoSS, a crisis scenario was designed and simulated whereby two clusters of different diseases were expected to appear. Nine veterinarians recorded a total of ten cases of avian pox, ten 'Schmallenberg'-like cases in bovines and eight other atypical cases that served as background 'noise'. The two expected clusters were timely detected. For both clusters, the system selected the most appropriate experts by comparing their individual profiles with the information provided in each record of the cluster. This simulation exercise was also designed to test additional functionalities of the website: launching expertises with corresponding forums, text and electronic file exchange in the forum, management of leadership of expertises, challenging the Email procedure and stressing the specific website administrator's environment. No significant problems were reported during the simulation. Only the Email procedure was impeded by 'spam blockers'. Messages were released by whitelisting of the system's Email server. One can conclude that the MoSS is now fully operational and can be used at large scale.

Measuring association between location of human cases in a food borne outbreak and distribution of food products to identify potential sources of infection

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In 2006, Norway experienced an outbreak of hemolytic uremic syndrome caused by enterohemorrhagic *Escherichia coli* O103. A total of 17 patients from 16 households were identified from January to March. The outbreak investigation was complicated and it took 4 weeks from the alert was raised until cured sausage was identified as the source of the outbreak. The aim of this study was to develop a tool that analyze information on patient distribution and distribution of food products to give a quantitative measure for rating the food products according to their probability of being the source of the outbreak. The study used data from the HUS outbreak in 2006. A tool for calculating measures of association between the distribution of human cases in a food borne outbreak and the distribution pattern of food products being potential sources of the outbreak was developed. The tool uses the geographical location and time of the human cases and information on when and where the food products were delivered to retail shops as input data. All analysis was performed with municipality as the unit of concern. Two measures for association were applied, the first were based on Pearson's correlation, the second on the amount of product delivered to municipalities associated with HUS-cases. Thereafter an index value based on both measures was calculated. The model ranked the source product among the 5% most probable products. This type of analyses is useful in order to focus the outbreak investigation on the most probable products, and exclude products that are unlikely to be the source based on time and geographical distribution. Further work should be done in this area to refine the model and test on other outbreaks

Epidemiology of Shiga toxin-producing *Escherichia coli* (STEC) in finishing swine

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Every year, approximately 200,000 cases of illness are estimated to be associated with Shiga toxin-producing *Escherichia coli* (STEC) in the United States. STEC strains are one of the leading causes of hemorrhagic colitis (HC) and hemolytic uremic syndrome (HUS) in humans. Many STEC outbreaks are attributed to food contaminated by animal feces. Notably, some human cases of STEC O157:H7 and non-O157 infections have been associated with pork products. To this date, little is known about swine STEC. We have conducted a prospective cohort study to achieve our objectives: to provide the first longitudinal descriptive epidemiology of STEC shedding in US finishing swine and to characterize swine STEC isolates. Three cohorts of pigs from one production company were included. In each cohort, 50 pigs were randomly selected and individually identified. Fecal samples were collected from each pig once every two weeks throughout the 16 weeks of the finishing period (eight samples/pig). Fecal samples were assayed for STEC by enrichment (10 min in TSB, pH 3 followed by incubation for 15 h in TYTP at 41 °C) followed by DNA extraction and the polymerase chain reaction (PCR) targeting the Shiga toxin genes (*stx*) and the intimin protein gene (*eae*). Shiga toxin gene-positive enrichments were plated onto ChromAgar STEC. Presumptive STEC isolates were recovered, confirmed by PCR, and serotyped. At the time of submission, STEC isolates were recovered at least one time from 90% (45 out of 50) of the pigs in cohort one, 98% (48 out of 50) in cohort 2, and 86% (43 out of 50) in cohort 3. STEC were isolated from swine in this study at relatively high incidence rates with variability of shedding over time and between cohorts. These data will be critical to fill in current gaps in swine STEC epidemiology and determine the association between STEC in swine, pork, and humans.

An on-farm intervention for VTEC 0157 in cattle: the story so far

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Escherichia coli O157 infection of cattle is of considerable public health concern. Infection in humans, by either foodborne or environmental routes, can cause a range of clinical disease from diarrhoea and stomach cramps to potentially fatal complications. Children and the elderly are particularly at risk. In Scotland, one in five herds of cattle is estimated to be infected and over 200 human cases are reported each year. Hygiene measures have been put in place by food producers and suppliers with a subsequent reduction in the number of foodborne cases. The focus of attention has, therefore, moved to control of environmental contamination and measures that could be applied if a group of animals is identified as infected. A small percentage of cattle intermittently shed high levels of the bacteria in their faeces when an area in the rectum is infected by *E. coli* O157. Experimentally it has been shown that the bacteria can be effectively controlled by washing out the rectum with a disinfectant solution. Can this technique be practically translated to the field? After promising results from a pilot study on two farms in the winter of 2008-2009, a larger scale study is in progress. Selected beef finishing units are screened via faecal pat samples to establish the baseline levels of *E. coli* O157. Cattle are individually sampled and allocated to a treatment or control group. Follow-up consists of monthly collection of faecal pat samples from the pens until the animals are sold. Eleven farms have been involved in the project so far. The third season of sampling is in progress (11/12) with completion due in Spring 2012. We present the outcome so far.

Simulation model of vaccinating cattle against STEC O157 for pre-harvest food safety

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Pens of cattle with high *Escherichia coli* O157:H7 (STEC O157) prevalence at harvest may present greater risk to food safety than pens of lower prevalence. Vaccination against STEC O157 reduces STEC O157 prevalence in live cattle. Our objective was to create a stochastic simulation model (@Risk, V 5.7.1), to compare STEC O157 prevalence distributions for summer- and winter-fed cattle to summer-fed cattle immunized with a 3-dose regimen of Type III secreted protein (TTSP) vaccine. Model inputs were an estimate of vaccine efficacy, observed frequency distributions for number of animals within a pen, and pen-level fecal shedding prevalence for summer and winter. Uncertainty about vaccine efficacy was simulated using a log binomial distribution from a previous performed meta-analysis of four randomized controlled 3-dose regimen TTSP vaccine trials. The outcome was post-vaccination STEC O157 fecal pen prevalence. The simulation was performed 5,000 times. Summer fecal prevalence ranged from 0-80% and averaged 30% (std dev±0.24). Forty-one percent of summer-fed pens had STEC O157 prevalence greater than 30%. Winter fecal prevalence ranged from 0% to 60% and averaged 10% (std dev±0.13). Seven percent of winter-fed pens had STEC O157 prevalence greater than 30%. Fecal prevalence for vaccinated pens of summer-fed cattle ranged from 0-53% and averaged 16% (std dev±0.13). Sixteen percent of vaccinated pens had STEC O157 prevalence greater than 30%. The simulation outcome was most sensitive to shedding prevalence of control pens of cattle. In this simulation vaccination mitigated the risk STEC O157 fecal shedding to levels comparable to winter, with the major effect being reduced variability in shedding prevalence. Food safety decision-makers may find this model helpful for evaluating the usefulness of pre-harvest interventions.

Multilevel analysis to evaluate the association between environmental thermal parameters and *Salmonella* shedding in finishing pigs

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The objectives of this study were to evaluate the association between the thermal environment at the barn and *Salmonella* status in finishing pigs and estimate the proportion of total model variance attributable to cohort, pig and individual sample level effects. For these purposes, individual fecal samples from 800 finishing pigs (8 collections per pig) were collected from 16 cohorts (50 pigs per cohort) in 3 sites of a multi-site farrow-to-finish production system in a longitudinal study. Pen temperature and humidity were measured every 2 minutes during the study period. The thermal parameters of interest were: hourly average, highest lagged, hourly variation and lowest lagged temperatures at the pen level prior the sampling for 6 time periods (12 h, 24 h, 48 h, 72 h, 1 week and 1 month). Additional potential risk factors at the individual (e.g. gender, health events, mortality), cohort (e.g. production) and pen level were also evaluated. Multilevel logistic models using generalized linear models, with random intercepts at pig and cohort levels to account for clustering (individual samples nested within pigs, pigs nested within cohorts) were constructed. The outcome variable was *Salmonella* status of the individual sample. *Salmonella* was isolated from 431 (7.12%) of 6054 individual fecal samples. Overall incidence of *Salmonella* was 22% (176/800). Hourly average, high lagged and lowest lagged temperatures prior the sampling period, pig health status, pen category and age were associated with *Salmonella* pig status in the univariable analysis (P<0.25). The largest proportion of variance was associated with individual fecal sample (45.43%) followed by cohort (28.8%) and pig level (25.77%). Multivariable analyses are being conducted at this time. These preliminary results suggest thermal environment is associated with *Salmonella* shedding in finishing pigs.

Epidemiology and health policy for prevention of nosocomial *Salmonella* infections in hospitalized horses

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Despite implementation of biosecurity standard operating procedures, veterinary hospitals have experienced outbreaks of salmonellosis causing high mortality in equine inpatients and substantial financial losses. In the USA, surveillance systems in most hospitals target horses with colic or diarrhea for early detection of *Salmonella* shedding in feces during hospitalization. At the University of Florida: Large Animal Hospital, one issue of concern is the early detection of *Salmonella* shedding in horses without diarrhea. An examination of hospital surveillance data over the last five years showed that almost 8 of every 10 adult equine inpatients that tested positive to *Salmonella* shedding did not have diarrhea at admission or during hospitalization. Furthermore, *Salmonella* positive culture results of 7 of every 10 horses without diarrhea were completed and reported after discharge. This subpopulation of horses presents a threat because there is no opportunity to implement infection control measures during hospitalization and because other horses or humans in the community can become infected when the equine inpatient returns home. We are currently investigating exposure factors (ie, clinical signs, hematological and plasma chemical parameters) associated with *Salmonella* shedding in 46 case horses without diarrhea and 73 control horses. In addition, we are investigating the diagnostic performance of a RT-PCR test for early diagnosis of *Salmonella* in 70 horses that were sampled and tested 3 to 7 times during hospitalization. Preliminary results show that among horses without diarrhea, high plasma triglycerides at admission, abdominal surgery, and season can be predisposing factors for *Salmonella* shedding. Final research results (including diagnostic performance of RT-PCR and bacteriologic culture) and discussion of recommended health policies associated with this study will be presented at the Symposium.

Epidemiology of West Nile virus Lineage 2 as a cause of neurological disease in horses in South Africa: lessons for Europe

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West Nile virus (WNV), a mosquito-born flavivirus is an important emerging neuropathogen in horses in Europe, the USA and Africa. Two major genetic lineages exist: lineage 1, associated with encephalitis in humans and horses in the Americas and Europe, while lineage 2 is endemic in southern Africa, Madagascar, and has recently been associated with encephalitis in humans and horses in South Africa, central Europe, Greece and Italy. To define the epidemiology and significance in South Africa, a 3-year surveillance project for neurological disease in horses was used to identify cases and define the molecular epidemiology of WNV, and a lineage 1 vaccine currently licenced in the USA and Europe was evaluated for cross lineage protection in mice and horses. Screening of 300 horses with neurological disease identified WNV in 15% of cases with an estimated mortality rate of 42%. Cases occurred in late summer and autumn across the country. All strains identified by isolation and RTPCR were lineage 2 with the exception of a single lineage 1 strain identified in 2010. Mice were 100% protected by the inactivated vaccine Duvaxyn WNV following challenge with a highly neurovirulent lineage 2 strain. Horses vaccinated according to the same schedule had similar cross lineage neutralising antibodies. Conclusion: lineage 2 WNV is an important cause of neurological disease in horses in South Africa. Epidemiological data collected in this study will be used to inform vaccination policies for the South Africa and could be translated to regions in Europe where lineage 2 has recently emerged.

Evaluating the effectiveness of strategies for the control of equine influenza virus in the New Zealand equine population

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The New Zealand equine population has never experienced an equine influenza (EI) outbreak and, consequently, is naive to the EI virus. Due to the speed at which EI would spread in New Zealand, strategies for control and eradication will need to be implemented rapidly. A spatially explicit stochastic simulation model, InterSpread Plus, was used to evaluate EI control strategies for the New Zealand situation. The control strategies considered were movement restriction on the day the virus was detected and movement restriction in combination with vaccination that began on day 14. The vaccination strategies were protective, suppressive or targeted. A protective strategy involves vaccination in a radius around infected properties, while a suppressive strategy involves vaccination in a ring around infected properties. Targeted vaccination involves the vaccination of all breeding and racing properties within 20 kilometres of an infected property. Sensitivity analysis was conducted to determine the impact of timing of vaccination and earlier detection on the size of and duration of the outbreak and the number of vaccinated properties. All three vaccination strategies implemented at day 14 resulted, on average, in 62% fewer infected properties ($P < 0.001$) and an epidemic that was 70 days shorter ($P < 0.001$), compared to movement restriction alone. Any vaccination strategy implemented on day seven resulted fewer properties infected with EI and the epidemic had a shorter duration, compared to vaccination implemented on days 14 or 21. Overall, the suppressive vaccination strategy resulted in fewer infected properties and fewer vaccinated properties than the other two vaccination strategies. The findings suggest that any vaccination strategy, if combined with complete movement restriction, could be effective for the control and possible eradication of EI if an outbreak was to occur in New Zealand.

The effect of humidity, air temperature and wind on local spread during the 2007 equine influenza outbreak in Australia

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The influence of humidity and air temperature on aerosol transmission of influenza A viruses has recently been defined under laboratory conditions. Limited research has been conducted on how meteorological factors influence outbreaks in the field. We applied geostatistics and survival analysis to data from the 2007 outbreak of equine influenza in Australia to quantify the association between hazard of infection and air temperature, relative humidity, rainfall and wind velocity, whilst controlling for premises-level covariates. The pattern of disease spread in space and time was described using extraction mapping and instantaneous hazard curves. Meteorological conditions at 3,557 premises were estimated by kriging daily meteorological data, and included in Cox regression models as time-lagged time-varying covariates. Meteorological covariates time-lagged by 3 days were strongly associated with hazard of infection, corresponding to the incubation period of equine influenza. Hazard was higher when winds from the direction of nearby infected premises were >40 km/h (hazard ratio=2.10; 95% CI: 1.54, 2.86) whereas high relative humidity ($>60\%$) was protective (hazard ratio=0.29; 95% CI: 0.17, 0.50). A highly nonlinear relationship was observed with air temperature that was consistent with laboratory-based research into aerosol and contact transmission of influenza A viruses. Our findings support and extend those of studies into influenza A transmission conducted under controlled conditions. The relationships described will directly inform the modelling and management of disease risk during future equine influenza outbreaks and advance our understanding of the transmission of influenza A viruses under field conditions. This research was funded by the RIRDC and the ABCRC.

Evaluation of data sources for modelling of equine infectious disease in Britain

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There are currently no accurate data for the size and distribution of the British horse population that could assist with surveillance or planning for disease outbreaks. The National Equine Database (NED) may provide such data, but there has been no evaluation of its accuracy or utility. Objectives were to assess the extent of obsolete and missing data in NED, to evaluate the degree of spatial separation between owner and horse locations and to apply these data to developing a credible national distribution of horses suitable for use in future risk modelling of equine disease incursions. Separate questionnaires were used to assess the amount of data missing from NED using data collated from Local Authorities (LA's) and the amount of obsolete data retained in NED using a survey of 11,000 horse owners. A national distribution of horses was developed adjusting for overall population size, owner-horse spatial separation and land usage. According to LA data, 595 (3.5%) of passports inspected were missing. Of 1,400 owner questionnaires completed, 380 passports were obsolete (27.5%). Responses showed 53% of owners kept their horse at home, and 92% resided within 10 km. Inaccuracies exist in NED with both missing data and retention of obsolete records. Although missing and obsolete data act to cancel each other out to some extent, they would affect NED's efficiency to locate horses and horse owners rapidly in the event of a major disease outbreak. Taking these data into account, the UK horse population was calculated to be 1.1016 million (95% confidence limits: 1.0776-1.1256 million) horses. Appropriate adjustment for population size, owner-horse spatial separation and land usage would facilitate meaningful use of the national horse population derived from NED for risk modelling purposes.

Spatiotemporal epidemiology of H5N1 disease and infection in people and poultry: a continuing enigma

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Despite the large investment which has gone into investigating avian influenza H5N1, a number of aspects of the relationship between infection and disease remain enigmatic. Comparison of experience in Vietnam and China demonstrates the epidemiological conundrum posed by findings since the detection of H5N1 in Vietnam in 2003 and its progenitor viruses in China in 1996. The disease has shown marked seasonality, with epidemics occurring principally between December and March. This is the cool season when influenza viruses typically spread more readily, but is also the time of peak rice harvesting and major national festivals, resulting in increased poultry movements and production. In Vietnam smaller epidemics have also occurred in mid-year. Poultry and human cases have shown strong spatial and temporal association in Vietnam, but not in China. In Vietnam, infection has been tightly clustered in the two major river deltas, with differences in spatio-temporal patterns between the deltas which provide insights into spread mechanisms. Studies in the Mekong River delta have shown that at the smaller scale there is marked heterogeneity in frequency of disease outbreaks between spatial units, which cannot be fully explained by prevalence of H5N1 virus distribution. Studies have also shown that infection can be detected during periods when there is no evidence of disease. In China, it has similarly been found that infection with H5N1 is widespread, but there are few outbreaks of poultry disease reported, and when human cases occur they have typically not been associated with poultry disease outbreaks in the immediate vicinity. Both countries use mass vaccination but vaccination has not prevented persistence of infection in vaccinated populations. In this paper potential explanations for these apparently inconsistent epidemiological features will be discussed, and unanswered questions will be identified.

Determination of HPAI H5N1 spatio-temporal dynamics in Indonesian poultry

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Data collected by the Disease Surveillance and Response Programme (PDSR) programme between April 2008 and September 2010 for Java, Bali and Lampung Province of Sumatra were used to examine the spatial-temporal dynamics of HPAI H5N1 outbreaks in Indonesia. Ecological approaches were used to identify potential drivers of outbreak maintenance and spread. The study set out to determine: (1) the probability of a district becoming infected after a period of freedom (90 days), referred to as the 'colonization probability'; (2) the probability of an outbreak persisting in a district, referred to as the 'persistence probability'; (3) how a district's HPAI status in a previous period influenced the occurrence of outbreaks (colonization and persistence) in that district; and iv) the effect of risk factors such as human and poultry population densities on the probability of outbreaks (colonization and persistence) at a district. The analysis was conducted at the district level for nine 90-day rolling period. The analyses suggested that there were strong temporal and spatial differences in outbreak probabilities across the areas examined. The analyses also showed that the occurrence of outbreaks in each study district was affected by poultry and human densities and the number of villages in the district assigned to controlled status during a previous period. These findings provide an opportunity to guide future surveillance efforts in the Indonesian poultry sector.

Social network analysis of poultry trade movements in Sikasso county, Mali: implications for surveillance of avian influenza

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Social network analysis (SNA) is a set of tools increasingly used in veterinary epidemiology. It enables to better understand the structure of animal movements and its impact on disease spread. It also helps predicting the most efficient outbreak surveillance and mitigation measures, which is especially useful for developing countries with limited resources and for emerging diseases such as avian influenza (AI). Here we apply SNA to quantify and decipher the web of poultry movements in the Sikasso county, the main supplier for 43% of all live bird markets in Mali. A cross-sectional survey was conducted in May-July 2010 in all markets (n=21) of Sikasso county and in 6 markets of adjacent counties. 180 poultry traders (PT) were interviewed with tested questionnaires and led to identifying 604 PT working in 186 locations. A directed weighted network was built with locations (villages, farms, markets) as nodes, sale of poultry as link, and number of poultry sold/mo as weight. The network was highly hierarchical with overdispersed distributions of centrality measures which led to identifying 4 hubs. The main targets for AI surveillance were the markets of Medine and Wayerma, (which accounted for 59% of all in-degrees). Targets for AI control were the markets of Medine, Wayerma, Farakala and Lobougoula whose removal from the network decreased the size of the giant weak component by 57%. 70% of poultry traded in the Sikasso county was sold to markets in Bamako and Ivory Coast, representing respectively 32 081 and 3600 poultry/mo. Building networks can be challenging in developing countries with no compulsory recording of animal movements as in the North. Our network was probably not complete but influential nodes can nevertheless be identified by degree centrality measures without requiring assessment of entire networks. Further work will analyse the network with PT as nodes and will assess the relationship between the geographical distance and the proportion of linked nodes and the number of poultry traded.

Assessing the contributions of the various between farm contacts to the spread of highly pathogenic avian influenza (H7N7) virus during the 2003 epidemic in the Netherlands

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Estimates of the per-contact probability of transmission between farms of Highly Pathogenic Avian Influenza virus of H7N7 subtype during the 2003 epidemic in the Netherlands are important for the design of better control and biosecurity strategies. We used standardized data collected during the epidemic and a model to extract data for untraced contacts based on the daily number of infectious farms within a given distance of a susceptible farm. With these data, we used a maximum likelihood estimation approach to estimate the transmission probabilities by the individual contact types, both traced and untraced. We found that egg delivery contacts had the highest per contact chance of spreading infection while majority (93% of the new cases) were potentially caused by unknown contacts. Importantly, all the identified contacts made a substantial contribution to the risk of virus transmission between farms. Therefore, any measures to reduce on their frequency and to improve biosecurity during all these contacts are potentially worthwhile. The fact that the 'unknown' contacts contributed the most emphasizes the need for a better understanding of the mechanisms underlying virus transmission. These estimates can be used to inform further studies on the role that improved biosecurity between contacts and/or contact frequency reduction can play in eliminating between-farm spread of the virus during future epidemics. The findings also highlight the need to: (1) understand the routes underlying the infections without traced contacts; and (2) to review whether the contact-tracing protocol is exhaustive in relation to all the farm's day-to-day activities and practices.

HPAI risk perception of poultry keepers within the traditional poultry sector in Egypt

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Egypt has experienced one of the worst outbreaks of highly pathogenic avian influenza (HPAI) outside Asia. Since the first outbreak of HPAI in 2006, the government has adopted several mechanisms to limit the spread of HPAI and the risk of human infection. This study used a mixed method approach in investigating levels of risk perceptions and underlying beliefs and rationales. For this study 140 female poultry keepers within the traditional poultry sector in Egypt were interviewed. Levels of risk perceptions were collected by means of a three point Likert-scale. Scores for perceived likelihood of human infection, likelihood of flock infection, severity of flock infection and level of fear for flock infection were collected. Risk perception scores were tested against the following variables: flock size, number of household member, location, education and the number of self reported outbreaks during 2006-2010. Correlation tests were performed using SPSS version 18. The results showed no associations between perceived risk and flock size, number of household members, education and location. However, there was a correlation between high-risk scores and the number of outbreaks already experienced by the household. This is in line with current risk theory, which predicts a positive association between the memorability of an event and perceived risk scores. Further, qualitative data analyses revealed some interesting underlying beliefs. High-risk perceptions were associated among others with a believe that HPAI can be transmitted through air. Low-risk perceptions were associated with no previous human infections in the village and skepticism about human susceptibility to HPAI among others. Understanding and targeting these underlying beliefs and norms might be more effective in supporting behavior change than simply dictating behavior changes.

Spatio-temporal analysis of bovine tuberculosis in Spain (2006-2009)

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A Bayesian spatio-temporal Poisson model was applied to Bovine tuberculosis (bTB) data aggregated at county level, in order to analyze the space-time evolution of the bTB eradication campaign in Spain between 2006 and 2009. The results of the model showed that the risk of a herd being infected or new infected was higher in counties located in central and southern Spain. There were no significant changes in the risk of infection between years in Spain as a whole, indicating that there were no significant improvements in the bTB eradication campaign between 2006 and 2009. Even though, significant variations of the risk to become infected or new infected were detected at county level suggesting that, at this level, the evolution of bTB was more heterogeneous: some counties presented a significant improvement in the eradication process and in other counties the campaign not only failed to decrease the risk, but even ended up with a significant increase of the risk. The model enabled to assess the bTB evolution at a finer spatial scale i.e. at county level, which is more useful for disease management than the global temporal effect. In order to elucidate the cause of the differences between counties, the model will be extended to include covariates like density of potential wildlife reservoirs, mixed herds with other domestic ruminants, diagnostic protocols or animal movement network.

The impact of the national full herd depopulation policy during 2003 to 2005 on the recurrence of bovine tuberculosis in Irish herds

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This study evaluated the impact of the Irish herd bovine tuberculosis (bTB) depopulation policy (depopulation, disinfection, contiguous testing and local badger removal where implicated) on the recurrence of bTB infection, by comparing the future risk in restocked herds following depopulation for either bTB or bovine spongiform encephalopathy (BSE) during 2003 to 2005. Each herd was assigned a 'previous bTB risk', based on bTB history during the 5 years before depopulation. Future bTB risk was estimated, using a multivariable Cox proportional hazard model for time-to-breakdown for each study herd, to identify risk factors associated with bTB. Future bTB risk varied significantly by reason for depopulation and previous bTB risk. Herds depopulated for bTB (by definition, at high bTB risk) were not significantly different from BSE herds with no or a low previous bTB risk. BSE herds with a high previous bTB risk were found to be at significantly greater future bTB risk. Herd bTB depopulation measures, as currently applied in Ireland, are shown to be effective in enabling herds to attain and retain bTB freedom following restocking. Based on the data presented, and consistent with current knowledge of the bTB epidemiology, local badger removal contributes to efforts to limit recurrence of bTB in Ireland.

Bovine tuberculosis in badgers in France: prevalence and risk of transmission between cattle and badgers

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In France, surveillance programs were carried out to monitor the presence of bovine tuberculosis (bTB) in badgers in three areas where cattle or wildlife displayed high bTB prevalence (Seine-Maritime, Côte d'Or, Dordogne/Charente). Diagnostic methods included *post-mortem* examination, PCR and/or culture. *M. bovis* was detected by culture in 1 badger out of 103 (0.97%) in Seine-Maritime and in 49/878 (5.6%) in Côte d'Or. In Dordogne/Charente, the PCR prevalence reached 29/230 (12.6%). Spoligotyping and multiple locus variable number tandem repeat analysis showed that all *M. bovis* strains isolated from badgers were of the same genotype as those isolated from cattle in the vicinity, demonstrating an epidemiological link between the two species. To investigate how this transmission can occur between cattle and badgers, a specific study was undertaken in Côte d'Or. Ten badgers were fitted with GPS collars and tracked during 3 to 6 months. The contact rate between cattle and badgers was determined from the selection of cattle habitat, i.e. pastures and farm buildings, within the home range of each badger. The first results show that contact may occur in pastures and farm buildings, which are used in a variety of ways, depending on the landscape and season. These results, in addition to video surveillance data on selected places in cattle zones, should provide elements for the risk assessment of bTB transmission between the two species.

Influence of the distance on the testing for bovine tuberculosis and brucellosis in Brazil

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The aim of this study is to evaluate the distance between Private Veterinarians (PV) and farms as a determinant of the adhesion to a voluntary, privately funded national governmental program for control of bovine Tuberculosis and Brucellosis. All tests performed in 2008 in the state of Rio Grande do Sul were considered to calculate the total round-trip distance (km) traveled by the PV for perform diagnostic tests for the aforementioned diseases. The data comprised 5,012 tested farms (TF) located on 332 counties out of the existing 496. The starting point was the registered professional domicile of the Veterinarian (PDV). Since TF were not georeferenced the distance between the PDV and TF was estimated in a two steps process: the county-to-county distance (A), considering the shortest road linking their headquarters; and the intra-county distance (B), estimating the distance from the TF to its jurisdictional county headquarter. The calculation of (B) was the average straight line from the center to the perimeter of the half of the county area, considering three different shapes: square, circle and equilateral triangle. Finally, the total travelled distance per TF (TD) was estimated as $TD=(A+B)*2$. In the case the test was performed in the same county of PDV it was considered that $TD=B*2$. The data analysis showed that 49.66% of the TF (n=2,489) were performed in a TD up to 50 km, and 82.2% (n=4,120) were executed in a TD up to 100 km. It also demonstrated that 48.26% of the TF (n=2,429) were performed within the same county of PVD. Lastly, tested counties presented odds ratio 65 times higher of having a PDV. The presented analysis proposes a tool for decision makers on identifying areas where the allocation of PV should be stimulated, as well as where more effective public awareness campaigns should be developed in order to promote a more even development of the animal health status.

Patterns of cattle farm visitation by white-tailed deer in relation to bovine tuberculosis transmission risk in Minnesota, US

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The objective of this study was to characterize spatial patterns of white-tailed deer movement related to bovine tuberculosis (BTb) transmission risk to cattle in northwestern Minnesota. Sixteen adult deer (12 females and 4 males) were captured in January 2011 and fitted with GPS collars just outside the BTb Management Zone in a 140 mi² study site that represented transitional deer habitat interspersed with cattle operations (n≈30). This area was similar in habitat composition to the Minnesota BTb Core area, in that free-ranging deer could move east into the forest zone, west into the farmland zone, or remain in the transition zone. GPS collars were programmed to collect location information every 90 minutes. Ground-truthing was performed seasonally to assess the locations of fenced cattle, cattle feeding areas, and feed storage areas potentially visited by deer. Due to unexpected high winter mortality (38% between January and March 2011), mostly due to wolf predation (83%), a second capture was performed in March 2011 which added 5 deer (4 females and 1 male) to the study. The current analysis included ≈30% of data collected until January 2012 from all deer remaining in the study (n=9) and the complete data of deer removed from the study (n=10). Results show that 94% of deer visitations occurred on two cattle farms and 73% of deer visits occurred in areas with both cattle and feed. Five deer visited cattle and feed locations on farms, with four visiting only one farm and one visiting two farms. The months of October (29%) and May (27%) had the most deer farm visitations. A higher proportion of visits occurred from 12 am to 6 am (61%), followed from 6 pm to 12 am (26%). These study results provide baseline information regarding cattle-deer interactions critical to transmission of BTb in this region.

Farm animal contact is a risk factor for salmonellosis caused by bovine-associated subtypes

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Nontyphoidal salmonellosis remains a formidable public health challenge, causing approximately 93.8 million illnesses and 155,000 deaths annually throughout the world. It was recently estimated that 94% of *Salmonella* infections in the United States are foodborne. The objective of this study was to identify risk factors for salmonellosis caused by bovine-associated subtypes, using data collected in New York and Washington between March 1, 2008 and March 1, 2010. Exposures of case-patients infected with bovine-associated *Salmonella* subtypes (isolates that matched contemporary bovine isolates from the respective state by serovar and pulsed-field gel electrophoresis [PFGE] pattern) were compared to those of control-patients infected with non-bovine-associated *Salmonella* subtypes. Farm animal contact during the five days prior to illness was significantly associated with being a case (OR=3.1, P=0.0007), after accounting for the consumption of undercooked ground beef and unpasteurized milk. A specific history of bovine contact was also significantly associated with being a case (OR=5.7, P=0.0005), while controlling for those food exposures. This has important public health implications, particularly for dairy farm workers and their families, veterinarians and veterinary staff, and those who visit open farms, petting zoos, and animal exhibits at fairs. More human *Salmonella* infections originating from bovine sources may result from direct contact with cattle (vs. foods of bovine origin) than previously recognized. Thus, it is imperative that efforts to control salmonellosis include a focus on transmission routes other than foodborne.

Attributing human salmonellosis: a German approach towards source attribution

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Salmonellosis in humans is one of the major zoonotic diseases in Germany. Although a decrease in reported salmonellosis cases could be observed during the last years, still 24,500 human cases have been reported in Germany in 2011. To reduce the exposure for the consumer it is important to identify and quantify the contribution of the different zoonotic sources to human infections. Source attribution methods attribute cases of foodborne disease to the food vehicle or an other source responsible for illness. One of these methods is the microbial subtyping approach, whose principle is to compare the subtypes of isolates from different sources (e.g. animals, food) with the same subtypes isolated from humans. Following this approach a source attribution model based on a model described by Hald *et al.* was developed and adapted to *Salmonella* surveillance data from Germany. The German model allows for handling data sets with many subtypes that are unique for a specific source which was not possible with the original model by Hald *et al.*. Furthermore, the proposed framework analyzes the impact of each data component on the model outcome and so gives insight into the requirements regarding the quality of data necessary for microbiologic source attribution. For identifying important sources for *Salmonella* in Germany, two different data sets are considered: one aggregated set with national data from the baseline surveys for the years 2004-2007 and one set with data from the control programs and monitoring programs for 2010. The identified and quantified contribution of each source is compared and discussed for the different years. Additionally, the model outcomes will be put in context with source attribution outcomes in other European countries.

Session 14**Theatre 3****Estimation of the rate of egg contamination from *Salmonella* infected chickens**

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Salmonella enterica serovar Enteritidis is one of the most prevalent causes of human gastroenteritis, and is by far the predominant *Salmonella* serovar among people, followed by *S. Typhimurium*. Contaminated eggs produced by infected laying hens are thought to be the main source of human infection with *S. enterica* throughout the world. Although previous studies have looked at the proportion of infected eggs from infected flocks, there is still uncertainty over the rate at which infected birds produce contaminated eggs. The aim of this study was to estimate the rate at which infected birds produce contaminated egg shells and egg contents. Faecal and environmental sampling and testing of ovaries/caeca from spent hens was carried out in parallel with testing 4,000 eggs in pools of 6, with shells and contents tested separately, in a series of 20 flocks of commercial laying hens. Bayesian methods were used to estimate the within-flock prevalence of infection from the faecal and spent hen data, and this was related to the proportion of positive eggs. Results indicated a linear relationship between the rate of contamination of egg contents and the prevalence of infected chickens, but a non-linear (quadratic) relationship between infection prevalence and the rate of egg shell contamination, with egg shell contamination occurring at a much higher rate than that of egg contents. There was also a significant difference in the rate of egg contamination between serovars, with *S. enterica* causing a higher rate of contamination of egg contents and a lower rate of contamination of egg shells compared to non-*S. enterica* serovars. These results will be useful for risk assessments of human exposure to *Salmonella*-contaminated eggs.

Case study of *Salmonella* contamination in a category 3 fat rendering facility

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Producing safe food and feed is the constant objective of pet food manufacturers. Pet foods and treats are often found in the home kitchen, in food preparation areas and are often handled by children, the elderly and others with immune system deficiencies. Food safety issues involving direct human contact with processed pet foods and animal feeds is becoming a major regulatory focus. This case study focuses on a Category 3 animal fat rendering facility that produces tallow for the oleochemical industry and greaves for pet-food manufacture via a HACCP system. The facility is overseen by the Competent Authority. Over a protracted period 10.8% (n=305) of official greaves samples intermittently revealed the presence of *Salmonella anatum*, *S. newington* and *S. kentucky*. Audit of CCPs did not reveal loss of control. The source of contamination was believed to be post rendering contamination. *Salmonella* was not isolated from the environment. Analysis of pre-requisites showed deficiencies in door management, sanitation, zoning, operator practices and structure fabrication. Deep cleaning and corrections to operational pre-requisites resulted in temporary improvement. The establishment closed for 10 months. Prior to re-opening, facility fabrication was improved by laying a smooth floor, removing roughened welded seams on equipment, smooth plastering the walls and properly sealing and ducting cables and hoses. Post improvement, none of the 120 official samples indicated *Salmonella* presence. We conclude that the source of contamination was from intermittent shedding from nidi located in the deep recesses of blemishes in the fabric. The case demonstrates the key role of sound pre-requisites that cannot be compensated for by maintaining control at CCPs.

Evaluation of the impact of *Salmonella* control programmes in fowl (*Gallus gallus*) on public health in the EU

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The European Union Directive 2003/99/EC obligates the European Union (EU) Member States to collect data on zoonoses and zoonotic agents every year, and requests the European Food Safety Authority to analyse these data and publish an annual European Union Summary Report. Human data is collected and analysed by the European Centre for Disease Prevention and Control. Based on *Salmonella* data collected annually according to the EU monitoring programmes, eggs are considered to be the most important source of human salmonellosis cases in the EU, particularly of those caused by *Salmonella Enteritidis*. In order to evaluate the impact of *Salmonella* control programmes in fowl (*Gallus gallus*) on public health in the EU, the reported human *S. Enteritidis*-cases per 100 000 population, the numbers of *Salmonella* food-borne outbreaks caused by eggs, the prevalence of *S. Enteritidis* in laying hen flocks and the proportion of table eggs positive for *Salmonella* spp. were examined. In EU, during 2007-2010, a 54.3% drop in the notification rate of human *S. Enteritidis* cases per 100,000 population was observed (from 21.0 to 9.6). In parallel, a 39.9% reduction in outbreaks caused by eggs and egg products was reported from 2007 to 2010 (248 to 149 outbreaks). The proportion of productive laying hens flocks infected with *S. Enteritidis* decreased from 3.9% (23,994 tested flocks) in 2007 to 1.6% (29,506 tested flocks) in 2010. During the same period the proportion of table eggs positive for *Salmonella* spp. decreased from 0.8% (16,626 sampling units tested) in 2007 to 0.3% (19,142 sampling units tested) in 2010. The results indicate that the reduction of *S. Enteritidis* in productive laying hen flocks is likely to have contributed to the decline of *S. Enteritidis* cases in humans.

A cross-sectional study of horse-owners approaches to the management and prevention of colic

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Equine colic is reported as a high priority health concern among horse owners and occurs frequently. A postal questionnaire was distributed to 1000 randomly selected horse owners from Northern UK. The questionnaire design was based upon hypotheses emerging from in-depth interviews with horse-owners analysed using Grounded Theory methodology. The questionnaire aimed to explore horse-owners' knowledge and approaches to the management and prevention of colic, whether owners could be categorised by type dependent on the human-horse relationship and the role of the horse and, to collect socio-demographic data. A total of 722 questionnaires were received with a useable response rate of 70.8%. Cluster analysis based on Euclidean distance and Ward's agglomeration method was used to explore owner typologies based upon their relationship with horses. The associations between; owner typology and management of colic and, owner experience of colic and attitudes to colic prevention were examined using chi-square statistics. Owners' perceptions of equine health priorities were also examined. Our analysis found 5 meaningful groups of horse owners representing 2 professional and 3 amateur typologies. The top three health priorities were laminitis, colic and weight gain. The owner groups differed with regard to their management of colic and health conditions they had experience of and attempted to prevent. Colic experience had a significant effect on attitudes towards prevention strategies used by horse-owners. This is the first study to quantify owner management and prevention strategies for colic among a large population. Owners understanding of the causes of colic and their experience appears to play a role in promoting prevention activities and seeking veterinary advice, and these are moderated by owner typology. These findings should be considered when designing appropriately targeted colic prevention advice aimed at reducing colic incidence.

Findings from a case control study of equine laminitis in Great Britain, 2009-2011

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There are few high quality studies investigating risk factors for equine laminitis, with most including only a limited number of risk factors and invariably not involving information on management practices. This study aimed to identify risk factors for veterinary-diagnosed active laminitis in British horses and ponies attended by practitioners 2009-2011. A prospective case control study of equine laminitis was conducted nested within a cohort of British equine veterinary practices. Laminitis cases were practitioner-diagnosed and controls were non-affected animals attended by the same practices. Owner-derived questionnaire data on signalment, management and health status during the preceding week. Multivariable mixed-effects logistic regression methods were used to assess risk factors associated with laminitis. A final multivariable model for equine laminitis was derived with odds ratios adjusted for other variables and random clustering of cases and controls within veterinary practices. Factors associated with an increased risk of laminitis were increasing bodyweight in the previous 3 months, summer and winter season compared to spring, new access to grass in the previous 4 weeks, box rest in the previous week, owner-reported history of laminitis, lameness or soreness after farriery, existing endocrinopathic disease and increasing time since last anthelmintic treatment. Factors associated with a decreased risk of laminitis were increasing animal height and feeding of additional supplements and transportation, both in the previous week. This study identified novel factors associated with laminitis among veterinary-attended horses and ponies in Great Britain between 2009 and 2011. With further targeted studies, these findings may improve knowledge on the aetio-pathophysiological mechanisms underlying laminitis and thereby provide opportunities for improving prevention and control of the disease.

Health care and disease prevalence in British horses, 2009-2011

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Equine preventive health care is intended to reduce disease and improve welfare but owners may fail to employ adequate preventive measures. Knowledge of common diseases in the general equine population is important in evaluation of risk factors for these diseases. This study aimed to describe preventive health care and owner-reported disease prevalence in British horses and ponies. A cross-sectional survey collected data via postal questionnaire from a random sample of veterinary-registered horse owners in Britain (n=797). The majority of animals received regular preventive health care: 96% received farrier visits at regular intervals; median time since last anthelmintic administration was 8.7 weeks and only 8% were unvaccinated, although fewer ponies were vaccinated compared to horses (P=0.008). Animals >25 years old received less frequent hoof care and lower proportions of retired animals were shod or vaccinated. Thirty-one percent of animals were overweight; a greater proportion of ponies were overweight compared to horses. In the previous 7 days, lameness affected 11% of animals and 7% developed a new health problem, of which 59% were veterinary-diagnosed. The most prevalent conditions were musculoskeletal (2%), skin (2%) and respiratory disorders (1%). Thirty-one percent had a long-term/recurrent condition, of which osteoarthritis (14%), sweet itch (8%) and recurrent airway obstruction (6%) were the most prevalent. Fifteen percent had a history of laminitis, of which 46% had suffered more than one episode. Greater proportions of animals with a history of laminitis and of recurrent cases were ponies (P<0.001). There was evidence of reduced provision health care in retired animals and in ponies compared to horses. Description of the most prevalent conditions affecting British veterinary-registered horses/ponies will aid improvements in their health care and inform future research to identify risk factors for disease.

Session 15**Theatre 4****Horse demography and movements within mainland Great Britain (GB)**

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Recent outbreaks of diseases such as Equine Infectious Anaemia & Dourine in the EU & the threat of African Horse Sickness, mandate the need for data to improve horse disease preparedness within GB. At a national level, this depends on knowledge of the risk of disease introduction & disease spread (through population demographics & movements). The objective of this study was to obtain data on the geographical distribution & patterns of movements of horses within mainland GB (which are not routinely recorded). These data were obtained from horse owners via an online questionnaire. After exclusions, there were 4481 respondents included in the study. All data obtained were anonymous & summarized at the resolution of postcode area & geographical region within GB. On average, respondents owned 4 horses (range 1-150, median 2). The majority of owners kept horses on their own premises, although owners in London tended to keep their horses between 10-50 miles away. The South West, South East & the Midlands (England) appeared to have higher numbers of horses than other regions. The recorded destination for imports of foreign horses was highest for the South of England & East Anglia. Wales & the South of England reported approximately twice as much international travel as other regions. There were also regional differences in the maximum number of road hours for the purpose of horse care as well as for local & national events. Horse owners were more likely to travel for competition than for leisure activities such as hacking & spent on average, a maximum of 4 nights/year away from the home premise. These data provide valuable insights into previously unknown attributes of the horse population of GB. These data will parameterize mathematical models that will be used to predict the impact of disease incursion into different regions of GB. Acknowledgements: Defra & the Institute for Animal Health for funding this study.

Risk factors for hind limb and pelvis fractures in Thoroughbred horses undertaking jump racing in the UK

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There have been multiple studies examining risk factors for the more common fracture types affecting the forelimbs of Thoroughbred horses. There have been fewer studies focussing on fractures affecting the hind limbs or the pelvis. The aim of this study was to identify risk factors associated with sustaining a hind limb fracture (HLF) or a pelvic fracture (PF) and to evaluate differences in these risk factors. A retrospective analysis of records from horses running in all National Hunt (NH) races in the U.K. between 2001 and 2009 identified cases diagnosed with a HLF or PF whilst still at the racecourse. Because a significant difference in risk of HLF was identified between hurdle and steeplechase racing, these were considered separately. Univariable and multivariable logistic regression were used to identify risk factors at any one start. There were 99 HLF case starts and 169,569 control starts in hurdle; 90 HLF case starts and 102,804 control starts in steeplechase; and 86 PF case starts and 298,209 control starts in NH. In the final multivariable models several significant risk factors were identified. Risk factors associated with HLF included: weight carried and age in hurdle racing; and season, number of runners and first race type in steeplechase racing. Risk factors associated with PF included: season, going, race distance, jockey and trainer success and previous racing history. The only risk factor shared between injury and discipline types was previous flat racing history. There is variation in the risk factors for similar injuries between racing disciplines. The results of this study will direct future research and shape the development of interventions to minimise the risk of hind limb fractures in NH starts in the future.

Session 15**Theatre 6****Who should take the blame: multi-level modelling and horse racing injuries in National Hunt racing in GB**

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Over the past 20 years many studies have investigated risk factors for a number of injuries in horse racing. However, the incidence of injury has not reduced significantly over the same period. The aim of this work was to identify which sectors of the racing industry should be the focus of renewed efforts to minimise the risk of equine injury. The structure of the data associated with racing is complex and highly clustered. For example, several horses are trained by the same trainer and races are clustered within course. We created multi-level multivariable logistic regression models for a number of injury outcomes. For each outcome several models were produced that accounted for different hierarchies. Known risk factors were included in models where there was a significant degree of higher-level of clustering to identify how much of that variance can already be explained. Variance was estimated at the level of the horse, sire, dam, trainer, jockey, course, race and race day. More than 200,000 race starts were included in the data set representing all National Hunt starts in GB between 2001 and 2009. The largest unexplained variance estimates were associated with the horse (56% when modelling hind-limb fracture in steeplechasing; 42% – epistaxis in hurdling; 33% – tendon injury in steeplechasing). Higher variance estimates were calculated at the level of the race than race day. For example, when modelling hind-limb fracture in steeplechasing: at the level of the race there was 24% unexplained variance compared to <0.1% at the level of the race day. No single hierarchical level was significant across all outcomes but race and horse were significant in most models. These analyses enable prioritisation of future research funding to target the sectors of the racing industry that are most likely to produce significant reductions in the incidence of injury in the Thoroughbred.

Framework for risk assessment of vector-borne infections

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Since the epidemic of bluetongue virus serotype 8 (BTV-8) in Northwestern Europe, the awareness of emerging vector-borne infections in livestock has increased. As a result, risk assessments of these exotic infections became a frequent request from policymakers. While risk assessments of directly transmitted infectious diseases are a commonly applied tool, vector-borne diseases have specific characteristics which make risk assessment more complicated. To solve this, we developed a framework which guides the user through the process of a risk assessment of vector-borne diseases. It uses a stepwise approach which is guided by a questionnaire and a checklist enabling a risk assessor to include all relevant steps into the assessment. The framework can be completed as a whole, or in separate modules, depending on the specific risk question being addressed. The modules comprise (1) entry of the pathogen; (2) transmission dynamics (transmission, establishment, spread, and persistence); and (3) impact of disease. The framework can also be applied at various levels of detail, and is specifically useful for a first quick evaluation of the overall risk.. The framework will speed up and increase the completeness of both qualitative and (semi-)quantitative assessments by guiding and structuring the process. Finally, the framework is also useful to complete an existing risk assessment. We tested the tool on Rift valley fever (RVF) because RVF incorporates many of the complexities of vector-borne infections in one infection. It affects multiple host species, is transmitted by multiple vector species and is a zoonosis. The framework was tested in a workshop with an international group of experts where the completeness of the framework was proven. It also showed to be practical for both quick and more detailed assessments.

Session 16**Theatre 2****Working towards a risk-based surveillance system for *Culicoides*-borne diseases in Southern Alberta (Canada) and Montana (USA)**

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Bluetongue (BT) and Epizootic Hemorrhagic Disease (EDH) are vector-borne diseases that affect wild and domestic ruminants. The main arthropod vector for these diseases in North America is considered to be *Culicoides sonorensis*. BT and EHD have important trade and socio-economic implications, especially when they occur in immunologically naive populations. Both diseases are endemic in the United States and have occasionally reached Canada. An effective surveillance system is therefore needed to ensure early detection and response to disease incursions. The purpose of this study is to develop probability distribution maps for *C. sonorensis* to help inform Canadian risk assessment. *Culicoides* spp. were trapped in 82 locations throughout Southern Alberta and Montana over a ten year period (2002-2011). Remotely sensed variables and Digital Elevation Models attributes were obtained and derived for the whole study area. A species distribution model was then developed combining trap sites where *C. sonorensis* was detected and environmental layers using a maximum entropy algorithm (MaxEnt) which has been shown to be robust in modelling species distribution from presence-only data. The *C. sonorensis* probability map generated can be used to develop a risk-based surveillance program for the region.

The dynamics of livestock ownership, asset ownership and human health in rural households and the role of animal based product consumption: a cross sectional study in Western Province Kenya
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Ascertaining relative socio-economic position of households has become of recent focus in an attempt to identify those at greatest risk to adverse health or to guide allocation of resources in interventions. Asset ownership has become a proxy measure of the gold standard of the measurement of wealth, expenditure. However, due to the intricacy of livelihood strategies in rural areas, recent methods have been criticised for their urban bias. Frameworks by Carney (1998) and Dorward (2001) describe the complexity of rural livelihoods and demonstrate how the role of livestock, non – productive assets, and human wellbeing are interlinked. Whilst it is commonly stated that there is a collinear accumulation of multiple asset types and improved wellbeing there is little statistical evidence to support this theory. Indices of asset wealth, as a proxy measure of purchasing power, were created using principal component analysis and mixed effect linear regression models were used to assess the association with livestock ownership of homesteads – as measured by total livestock value. Univariate and multivariate methods analysed the association of both primary exposures with the nutritional health of household members and the role of animal based product consumption. The evidence suggests that livestock and expenditure are closely linked but that livestock ownership plays a neutral role in the provision of foodstuffs and health to individuals. However, more information is needed to explore the influence of non-livestock agricultural activities and alternative income sources. Livestock are likely to be more important at a community level demonstrating the social importance of livestock species and dependency upon them in a wider setting.

Simulating *Salmonella dublin* epidemiology within Danish dairy herds in the Dublin-Simherd model
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An age-structured dynamic, stochastic and mechanistic Monte-Carlo simulation model of *S. Dublin* ('Dublin-Simherd') was developed based on an existing model that incorporates complex feedback mechanisms between reproduction and culling in addition to the main effects of *S. Dublin* in dairy herds. The aim was to use this model to investigate the effect of hygiene, management and herd size on the population and infection dynamics of *S. Dublin* in neonatal calves, pre-weaned calves, weaned calves, growing heifers, breeding heifers and adult cows. Five infection states were simulated: susceptible, acutely infected, carrier, super shedder and resistant. The model simulated population and infection dynamics in each of the six age groups over a period of 10 years in weekly time steps. The effects of introducing one infectious heifer on the probability of spread of *S. Dublin* within the herd, duration of infection and epidemic size were estimated through 1000 iterations for 48 scenarios covering all combinations of three herd sizes (70, 200 and 400 cows), four hygiene levels and four management levels. Poor hygiene increased the probability that the infection spread within the herd, duration of infection and epidemic size. Low herd susceptibility was influential, but not sufficient to control infection on its own. Probability of spread of infection upon exposure was independent of herd size. With increasing herd size good management and hygiene became more and more important to shorten durations of infection and increase the probability of extinction in the herd. In general, disease and mortality patterns followed epidemic waves in the herds. Sensitivity analyses of 24 alternative scenarios showed that a persistent carrier state was required in the model to mimic real life *S. Dublin* infections, while a super shedder state was not necessary.

Modeling the economic consequences of indicator based treatment strategies against subclinical and clinical mastitis

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Mastitis is costly for the dairy herd. Dairy farmers are adopting new technologies for dynamic monitoring of the mastitis status of the individual cow. As these systems provide routinely and more detailed information about subclinical infections it becomes a management issue, how to optimize mastitis treatment strategies accordingly. The aim of the study was to develop a model for simulating the economic consequences of indicator based treatment strategies against subclinical and clinical mastitis. Recent contributions in simulation of mastitis in a dairy herd include differentiation of pathogens, modeling the pathogen specific transmission dynamics, differentiation of clinical and subclinical mastitis, differentiation of the infection and the treatment and differentiation of types of treatment. The contribution of this study was to combine these characteristics in one model and to model detailed treatment criteria according to cow characteristics and alarms for infections. The model was implemented in the mechanistic, dynamic and stochastic SimHerd model. The treatments criteria included clinical signs, result from bacteriology or PCR, somatic cell count in the milk, lactation stage and the milk yield level of the cow. The different types of treatment included intramammary and intramuscular antibiotics and no treatment. The model was parameterized according to the literature and new experiments. A recent Danish study showed penicillin treatment of subclinical *S. aureus* mastitis had a beneficial effect on infection load (bacteriological cure), inflammatory status (somatic cell count and lactate dehydrogenase) and milk yield (MSc thesis of Duse and Albrechtsen, 2011). The new mastitis model was implemented in the SimHerd model and scenarios were simulated for combinations of treatment criteria and treatment types. Results for the technical and economic consequences of these scenarios in different dairy herds will be presented.

Epidemiologic and economic simulation model for BVDV eradication scenarios in dairy herds

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Bovine Viral Diarrhoea Virus (BVDV) is highly prevalent worldwide and has a detrimental effect on the performance of dairy herds. The goal of this study was to determine what the costs and benefits are of reducing the BVDV prevalence in the Netherlands. An S (susceptible) I (infected) R (recovered) model on herd level was built. In this model BVDV prevalence and economic consequences were modelled from 2010 up to 2020 (10 years). In total, eight potential eradication scenarios were simulated to evaluate the effects on prevalence of BVDV and the economic consequences, given either the presence or absence of the risk of BVDV from other types of cattle herds. The three most effective scenarios were: (1) All dairy herds will trace and cull BVDV carriers and their BVDV status will be monitored for 10 years. In addition, in the first three years all herds will be vaccinated. (2) Throughout the study period, an ear notch sample is taken from each newborn dairy calf, tested for BVDV, and culled if the calf appears to be a carrier. (3) All dairy herds will be screened for BVDV in the first year based on individual serum and bulk milk samples. In herds where BVDV is detected, an ear notch sample is taken from each newborn calf, carriers are culled and their dams are tested and culled if carrier as well. Herds without BVDV are monitored. After three years, all herds will enter the monitoring scheme and when BVDV is re-introduced carriers are traced and culled. Scenario 3 showed the largest decrease in the BVDV prevalence against the lowest costs. Scenario 1 and 2 were slightly more expensive but were also very effective in decreasing the prevalence. However, when non-dairy herds will not control BVDV at the same time, BVDV may not completely be eradicated from the Netherlands in these three scenarios. Vaccination scenarios are very effective in eradicating BVDV, even if the non-dairy herds do not control BVDV, but are costly.

Helminth infections: do they affect the productive efficiency of specialised dairy farms?

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Subclinical infections with gastrointestinal (GI) nematodes and liver fluke are an important cause of production losses in grazing dairy cattle. Attempts to evaluate the economic impact of these production losses were mainly based on partial analysis techniques, and few studies have looked more integrally at the impact on productive efficiency at farm level. The objective of this research is to analyse the effect of GI nematode and liver fluke infections on the technical efficiency in dairy farms. Farm-specific results from a parasitic monitoring campaign, expressed as an optical density ratio (ODR), are linked with individual farm data from the Belgian Farm Accountancy Data Network (FADN). As a result, a dataset of about 70 specialised dairy farms is obtained, combining economic and epidemiologic information. Their technical efficiency (TE) is calculated with non-parametric data envelopment (DEA) analysis. Multiple variants of the DEA approach are used, differing in the way they incorporate infection in the production model. Rank correlation, regression models, and cluster analysis are used to analyse the relationship between TE and the level of helminth infection. Preliminary data analysis shows an ODR mean and standard deviation of 0.82 ± 0.21 and 0.79 ± 0.34 , for GI nematode and liver fluke infections, respectively. More than 80% of the farms have an ODR above 0.5, suggestive for a negative effect of helminth infections on milk production. The TE scores, which range between 0 (totally inefficient) and 1 (fully efficient), show a mean technical efficiency of 0.708. More than 90% of the farms are shown to produce at an inefficient level.

Evaluation of alternative testing strategies for estimating likelihood of infection with Johne's disease in Irish cattle herds

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Animal Health Ireland is facilitating national discussion and action on a range of non-regulatory animal health issues in Ireland, including Johne's disease (JD). A technical working group is developing the framework for a voluntary national JD control programme, which will involve herd classification. A simulation model was developed in the programming language R, to allow evaluation of testing strategies for initial herd screening and subsequent testing for JD in suckler and dairy herds in Ireland. Key model inputs included sensitivity and specificity estimates for the individual serum ELISA, the individual milk ELISA and the faecal culture, the design prevalence and testing options. Key model outputs include SeH (the probability that infection will be detected, if present at the design prevalence or greater) and ProbF (the probability that infection in the herd is either absent or at very low prevalence (less than the design prevalence)). ProbF can be updated periodically as additional herd testing is undertaken and will form the basis for herd classification. Testing strategies evaluated include whole-herd testing, compared to testing of half the herd, for design prevalence values of both a single animal and 5% of the herd and using serum or milk ELISA with faecal culture follow-up, or faecal culture alone. Whole herd individual faecal culture provided the highest SeH and ProbF but was nearly four times the cost of serum ELISA plus faecal culture follow-up. ProbF declines over time unless producers significantly change their purchasing patterns to maintain closed herds or purchase only low-risk cattle.

Modelling the net benefits of alternative management strategies for bacterial kidney disease in Scottish salmonid aquaculture

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Bacterial kidney disease (BKD) of farmed salmonid fish is caused by the pathogen *Renibacterium salmoninarum* which is often sub-clinical and might go undetected if diagnostic methods have low sensitivity. The observed prevalence of infected farms is low for salmon production relative to trout. Management measures such as movement controls constitute a regulatory burden, in financial terms, for both the Industry and Government. The awareness of the potential cost of disease in fish farming is increasing, but there has been little economic assessment of the costs of disease and benefits of intervention. This presentation describes a decision analysis model of the impact of BKD under different policy options. It uses event trees to assess the risks and then evaluate the net benefits of changing statutory controls, either strengthening or weakening them. In the tree, decision nodes depict policy options for which subsequent events have a probability of being uninfected or infected; this splits into diseased or sub clinically infected which in turn divides between those known or unknown to the authorities. These are states determined by a separate Susceptible-Infected (SI) model. These outcomes lead to consequent costs associated with on the one hand disease and on the other surveillance and movement restrictions. Total probabilities and costs can then be established at the end of each node; this however assumes that events are dependent. For each node the expected impact in any year as a result of changes in surveillance and intervention is the sum of the change in value from disease-related losses and the change in disease management costs to both business and the regulator. The model has helped the team to collectively structure the analysis and identify data sources from inspectorate, laboratory, and questionnaire, etc. The approach can be used for other diseases.

Detection of Schmallenberg virus in the Dutch surveillance system

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In the Netherlands, a surveillance system is in place for detection of (emerging) infectious diseases at the Animal Health Service. This system consists, amongst others, of a telephone service that provides advice to veterinarians and farmers about animal health related problems that they encounter. The signals that are obtained from the field are discussed weekly in a multidisciplinary team of veterinarians, epidemiologists and pathologists. At the end of August 2011, several reports were made of a severe drop in milk production, watery diarrhea and sometimes fever in dairy cattle. Initially, the reports seemed to be clustered in the eastern part of the Netherlands. After two weeks reports were also received from other regions, including some adjacent regions in Germany reporting similar clinical problems in dairy cattle, except for diarrhea. The reports ceased in October. Blood and manure samples of clinical cases were obtained and tested, but no definite causal agent was found. On November 18th, FLI reported the isolation of Schmallenberg virus (SBV). In the last week of November, an increased number of congenital malformations in newborn lambs on sheep farms throughout the country were reported. In this case many flocks and many lambs were affected throughout the country. A real-time PCR for SBV was carried out on brain tissue of 54 deformed lambs, on 50 serum samples of dairy cows, which had shown clinical signs in August, and on 115 healthy cows sampled in November. In 22 lambs and 18 cows the virus was detected. The healthy cows all tested negative. In December, the first clinical cases in calves were reported and on January 23rd the first two calves were tested SBV positive. Based on the initial reports of clinical signs in dairy cows, the following case reports of lambs and calves, and census data on production, fertility and mortality of Dutch cattle and sheep herds, the sensitivity of the surveillance system for SBV and emerging diseases in general is discussed.

Culling of livestock: not for vector-borne infections!

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Removal of selected livestock (i.e. culling) is an important measure in the control of an infectious disease outbreak. However, the impact of culling for a vector-borne disease is not straightforward. Culling reduces the infectious period of hosts, but due to an increase in vector-host rate the speed of spread within a host population can increase. Furthermore, increased migration of vector, due to a local lack of hosts, might increase the spread between host populations. The reproduction number, the magnitude of a local outbreak and the spread between host populations of a vector-borne disease are investigated with a mathematical model. Several culling strategies were assessed on the effect on the development of the outbreak, number of livestock lost, and spread to other populations for different culling rates, values of R_0 and time until detection of the infection. Preventive culling of susceptible hosts is counter-productive, unless all possible susceptible hosts are removed from the target area. Culling of susceptible and seropositive hosts during an outbreak increases the size and duration of an outbreak, and the number of lost livestock for a large range of R_0 and culling rates. In contrast, culling of viremic hosts is a strategy that reduces the size and duration of an outbreak and minimizes its damage in livestock lost. The spread of vector-borne infection between host populations might be prevented by culling. However, if started too late culling decreases the time until spread to another host population, and increases the number of infectious bites in other host populations. Important factors, such as R_0 and the time since introduction, are unknown during an outbreak of a new non-endemic vector-borne disease. If these factors are judged incorrectly culling might worsen the outbreak. Hence, culling is a dangerous policy in the control of a new vector-borne disease.

Transmission of FMDV within and between species: quantification and comparisons

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Data on experimental transmission of FMDV between animals have been collected for a long time. In the previous century several countries have built special facilities to study transmission and other aspects of FMDV infection. The latter experiments sometimes also allowed observation of transmission events. More recently techniques have been developed for statistical inference on experimental data on transmission in small groups of animals. Therefore, we have undertaken to collect and statistically analyse existing data on transmission of FMDV. We focussed first of all the transmission of the virus in unvaccinated animals and on both within species and between species transmission. As far as this was in the same datasets we also looked at the consequences of vaccination on transmission. The species that were studied were cattle, pigs and sheep as these are the major livestock species. The results of our data collection can be summarised in a 3×3 matrix where either transmission rate parameters or transmission ratios are the matrix elements. Not all different combinations are studied equally well but by assuming separability between infectivity and susceptibility of each of the species we could for example infer that transmission from cattle to pigs has a low transmission rate whereas it was observed that transmission from pigs to cattle has a high transmission rate. The data apply to transmission between individual animals but for the control of FMDV quantitative data for the transmission rates between farms with the same or different species is even more important. We will discuss possibility of extrapolating from the between individual rates to those between farm rates. In addition we will discuss the data gaps and how we could attempt to fill them.

Association of antimicrobial use and resistance in bovine mastitis coliforms

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Concurrent data on antimicrobial use (AMU) and resistance are needed to contain antimicrobial resistance (AMR) in bacteria. The present study examined the association between herd-level AMU and AMR in *Escherichia coli* (n=394) and *Klebsiella* species (n=139) isolated from (sub)clinical mastitis cases on 89 dairy farms in 6 Canadian provinces. Antimicrobial use data were collected using inventory of empty antimicrobial containers and antimicrobial drug use rate was calculated to quantify herd-level AMU. MIC were determined using Sensititre NARMS Gram-negative MIC plate containing antimicrobials commonly used in a clinical setting. Multivariable logistic regression models were built to determine an association between herd-level AMU and AMR in bovine mastitis coliforms. Herd-level use of systemically administered tetracycline was associated with tetracycline resistance in *Klebsiella* species isolates (Odds ratio [OR]: 2.59). The use of systemically administered tetracycline was associated with tetracycline resistance in *E. coli* isolates on dairy farms using tetracycline and penicillin (OR: 3.61). Herds with tie-stall barns had higher odds of ceftiofur, ampicillin and kanamycin resistance in *E. coli* and sulfisoxazole resistance in *Klebsiella* species isolates than herds with free-stall barns (OR: 10.06, 14.15, 3.41, 3.96, respectively). Alberta dairy herds had lower odds of having ceftiofur-resistant *E. coli* isolates than dairy herds in Ontario (OR: 0.13); however, dairy herds in Alberta had higher odds of TMPs, tetracycline, kanamycin, ampicillin, and chloramphenicol resistance in *E. coli* isolates than dairy herds in Québec (OR: 1.89, 2.54, 4.94, 5.48, 20.27, respectively). In conclusion, herd-level use of certain antimicrobials was positively associated with AMR in bovine mastitis coliforms. Barn type was positively associated with AMR for many antimicrobials. Geographical variation in AMR was also observed.

Using mixed treatment comparison meta-analysis to compare antibiotic treatments for bovine respiratory disease

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The principle behind mixed treatment comparison meta-analysis (MTC) is to use evidence from the full network of trials to make inferences about comparative efficacy. Mixed treatment comparison meta-analysis combines direct and indirect estimates of efficacy using a network of information from trials, while accounting for lack of randomization at the study level. The rationale for conducting MTC meta-analysis have been summarized as follows: to quantify differences between interventions where no direct comparisons exist, to rank treatments when multiple options exist, to borrow evidence from indirect comparison when few direct comparisons exist and to assess sources of bias in a network of trials. We use treatment for bovine respiratory disease to illustrate the application of MTC to therapeutic interventions in veterinary science. The network of evidence contained 13 active therapy arms and a non-active control arm. The analysis used data from 88 trials from 36 manuscripts and FDA reports. 36 trials were identified in the peer-reviewed literature and the remaining trials were identified in the FDA drug summaries. The model was a random effects model to accommodate multi-arm trials. This approach incorporates a covariance structure that accounts for multiple non-independent study arms, a factor that cannot be accommodated in standard meta-analysis. The model was fitted by calling WinBUGS through R using the R2WinBUGS package. The output of the model were estimates of the log odds of failure in the treatment arm, the odds ratio/risk ratio for all possible pairwise comparisons, a distribution of the ranking for each arm and an estimate of the 'worst' treatment arm. The output from the MTC analysis for BRD antibiotics treatments provide examples of all four uses of MTC analysis including a ranking of best and worst treatments.

Modeling within-host and on-farm dynamics of plasmid-mediated resistance to cephalosporin ceftiofur in commensal *Escherichia coli* in cattle

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Enteric bacteria of food animals are a reservoir of antimicrobial-resistance genes. Antimicrobial pressure on these bacteria from enteric drug metabolites is poorly understood. Ceftiofur resistance in *Escherichia coli* in cattle is primarily mediated by a plasmidic blaCMY-2 gene. We built deterministic compartmental mathematical models to evaluate how the parameters of pharmacodynamics of ceftiofur enteric metabolites against *E. coli*, and the bacterial ecology impact on the frequency of resistance in enteric *E. coli*, and overall in the meta-population of commensal *E. coli* on a beef farm. The models showed that a low fraction of resistant enteric *E. coli* could persist without ceftiofur pressure, being influenced by ecological parameters: frequency of blaCMY-2 horizontal transfer, rate of replacement of enteric *E. coli* by ingested *E. coli*, and frequency of resistance in the latter. During therapy, irrespective of whether drug formulation was sustained-release or not, resistant *E. coli* expanded in absolute number and relative frequency; this was determined by pharmacodynamics (e.g. MIC values). However 4 weeks after therapy and beyond, the ecological parameters were again most important. There was a substantial uncertainty in the outcome during and post therapy. On-farm dynamics of ceftiofur resistance in commensal *E. coli* depended on housing system (feedlot vs pasture), and other factors.

The effect of cephalosporin usage on the occurrence of ESCs producing *E. coli* in pig herds

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An increased occurrence of bacterial strains producing extended-spectrum cephalosporinases (ESCs) has been observed and it is now the fastest emerging antimicrobial resistance problems worldwide. The usage of 3rd- and 4th-generation cephalosporins (ceph.) in livestock is believed to be significant for the development and spread of ESCs resistance. Generic antimicrobials usage is assumed to have an impact on the spread of ESCs resistance as well. The objective of this study was to assess the effect of prescribed ceph. in pig herds on the occurrence of ESCs producing *Escherichia coli*. The study was conducted in 19 pig herds which have had five to fourteen prescriptions of ceph. and 20 pig herds without prescribed ceph. in a previous 12 month period. The 39 herds were all integrated and represent typical Danish pig farms. The occurrence of ESCs producing *E. coli* in the herds were tested in a total of 9 pooled samples per herd. A pig herd was considered positive if one or more of the nine samples contained ESCs producing *E. coli*. Initially, the association between usages of ceph. and occurrence of ESCs producing *E. coli* in the pig herds was analyzed using logistic regression, and the effect was adjusted for potential confounding effect due to purchase of pigs, number of sows, and use of disinfectant. The change of OR for ceph. usages, when the potential confounders were added were less than 20%, which indicated no confounding effect of these risk factors. Therefore, the effect of ceph. usage on occurrence of ESCs producing *E. coli* was estimated as risk ratio (RR). The results showed that consumption of ceph. increased the risk of occurrence of ESCs producing *E. coli* significantly with a RR of 5 (95% CI: 2-11). This demonstrates that ceph. usage significantly affect the occurrence of ESCs resistance, and in order to limit further emerging and spread, considerations of ceph. use in livestock should be taken into account. The next phase will be to consider occurrence of ESCs due to co-selection from generic antimicrobial usage.

Dairy goat demography and Q fever infection dynamics in the Netherlands

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Between 2007 and 2009, the largest human Q fever epidemic ever described occurred in the Netherlands. One of the putative causes was the intensified goat production system with associated abortion waves on infected farms. In the Netherlands, dairy goats are commonly kept in larger herds (600-1000 animals) than elsewhere in the world. However, the influence of herd size and other demographic characteristics typical for goat herds such as seasonality of kidding on the within-herd infection dynamics of Q fever were never studied. We adapted an existing, fully parameterized model for Q fever transmission in French dairy cattle herds, to represent dairy goat herds in the Netherlands. The original model represents the infection dynamics in a herd of 50 dairy cows after introduction of a single infected animal; the adapted model has 770 dairy goats. For a full comparison, also herds of 770 cows and 50 goats were modeled. The effects of herd size and demographic (goat versus cattle) characteristics on the probability of and time to extinction of the infection, environmental bacterial load and abortion rate were studied. Extinction after introduction of infection into the herd was more common in small herds versus large herds and in goat herds versus cattle herds. In the non-extinct simulations, a steady-state environmental bacterial load was reached faster in small herds than in large herds. In goat herds seasonal peaks of abortions and environmental contamination were observed. Abortion waves in goat herds behaved differently in the model than observed in the sparse field data.

A deterministic mathematical model for the within-herd transmission of Q fever in Dutch dairy goats to evaluate control measures

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In the Netherlands in the period 2007-2011 *Coxiella burnetii* led to four thousand detected human infections with Q fever and 24 confirmed deaths. The magnitude of the disease incidence was unprecedented. This public health problem is thought to be associated mainly with infected goat herds by exposure via air to dust particles formed from dung and birth products. The human case incidence declined substantially after vaccination of goat herds followed by culling of pregnant goats in positive tested herds. We developed a within-herd transmission model for Q fever in commercial Dutch dairy goat herds to evaluate the effect of control measures. Using knowledge from literature and from (yet) unpublished experiments, we developed and parameterised a flow-chart of a suitable transmission model, which optimally represents current knowledge on the biology, transmission and pathogenicity of *C. burnetii*. Based on this model, we calculate the expected *C. burnetii* emission of a randomly infected goat during its full infectious period, including the effect of persistent infection in the reproductive organs. Subsequently, we formulated the basic reproduction ratio of the infection, using the information regarding excretion. We found basic management methods can influence transmission and reproduction ratio of the infection, e.g. the birthing cycle frequency strongly affects transmission. Applied at the right age and moment vaccination as a control measure is effective, while dung treatment has little impact on within-herd transmission but does affect risks for public health and neighbouring farms. Measures to control within-herd transmission were ranked based on the reproduction ratio. Transmission to humans and other farms was ranked via total herd excretion of infectious material.

Vaccination of small ruminants to prevent Q fever in humans: what is the evidence?

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A major Q fever epidemic started to occur in the general population in 2007 in the southern part of the Netherlands. An explanation was found in dairy goats farms, where abortion storms due to *Coxiella burnetii* had been observed since 2005. In Australia, persons at risk are vaccinated against Q fever. In contrast, in the Netherlands, dairy goats and dairy sheep were vaccinated in a specific geographic area with the aim to reduce abortions and bacterial shedding levels, thereby reducing the exposure of humans. We did an observational study to quantify the effect of vaccination on bacterial load in excreta of pregnant animals, and thereby indirectly on human exposure. At the time of the epidemic, only limited data on the vaccine efficacy was available. When despite control measures the number of human cases kept rising, politicians applied the precautionary principle and decided at the end of 2009 to cull all pregnant dairy goats and dairy sheep. On the day of culling, 957 dairy goats and dairy sheep from 7 vaccinated and 6 unvaccinated herds were sampled. Vaginal swabs, milk samples and uterine fluid were collected. In vaccinated animals, prevalence and bacterial load were reduced compared with unvaccinated animals. This indicates that vaccination may reduce bacterial load in the environment and probably human exposure to *C. burnetii*. The number of human cases was low in 2010 (~504) compared to 2009 (~2000), and was even lower in 2011 without additional culling (~82), suggesting a beneficial effect of the (combined) intervention measures. However, dose-effect relation for human disease and the role of environmental contamination or wildlife are still unknown. In conclusion, observational evidence suggests that vaccination of small ruminants helped to reduce the incidence of human Q fever to low levels.

Session 21**Theatre 4****Reduction of *Coxiella burnetii* load in bulk tank milk using vaccination in Q fever affected dairy cattle herds**

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Coxiella burnetii is the infectious agent responsible for Q fever, a world wide spread zoonosis. Infection mainly occurs after inhalation of contaminated aerosols generated in the environment by domestic ruminants. Vaccination using a phase 1 vaccine has been shown as an effective tool to prevent shedding in ruminants at the animal level especially when applied on dairy heifers. Antibiotics (mainly tetracycline) are also used by practitioners as a medical measure to limit shedding especially around parturition, but their effectiveness has not been quantified yet. The aim of this study was to assess the impact of medical strategies applied on dairy cows, combining vaccination using a phase 1 vaccine and/or antibiotics at drying off on the evolution over time of the *C. burnetii* load that may be released by cows in the environment. As milk was reported as the main shedding route in cattle, the Cb load in Bulk Tank Milk (BTM) was here the criterion under study. In 74 Q fever clinically affected dairy cattle herds, BTM was sampled 3 months apart over one year. In each herd, all dairy cows were assigned to one of the 4 following strategies: (1) vaccination; (2) tetracycline; (3) vaccination and tetracycline; or (4) no intervention. The *C. burnetii* load in each BTM sample was quantified using qPCR (LSI, Lissieu, France). The likelihood for a given herd to show a reduction in *C. burnetii* load was quantified function of the implemented strategy using logistic regression. Herds implementing vaccination had a significantly higher probability to exhibit a reduction in *C. burnetii* load over time (OR=6.25; CI: 1.4-33.3) than herds with no vaccination. The reduction was the highest when at least the vaccinal coverage was >80% of dairy cows. Implementation of antibiotics had no significant effect on reducing the *C. burnetii* load in BTM. These findings confirm the effectiveness of vaccination on limiting *C. burnetii* shedding and provide some evidence for a rational use of antibiotics.

The efficacy and effectiveness of Q fever vaccines in small ruminants: a systematic review and meta-analysis

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The European Food Safety Authority Scientific Opinion on Q fever (*Coxiella burnetii*) recommends vaccination of sheep and goats to prevent zoonotic transmission and reduce livestock production losses. To assess the quality of evidence and derive a pooled estimate of vaccine efficacy/effectiveness (VE), a comprehensive and replicable scoping study, systematic review and meta-analysis was undertaken. Primary research criteria of VE of inactivated whole-cell phase I vaccines to prevent Q fever shedding in small ruminants were identified, appraised, summarized or synthesized when appropriate. Sixteen electronic databases and grey literature were searched for potentially relevant publications. Abstract-level initial classification relevance screening, full-paper primary and secondary review, data extraction and assessment of study methodological risk of bias (RoB), were performed by two independent reviewers on included control trials (CT) and cohort studies (CS). From thirteen potentially relevant publications, four were excluded for non-relevant vaccine strains (n=1), lack of comparison group (n=1) and non-relevant (antibody assay) outcomes were reported (n=2). Extracted data of *C. burnetii* shedding in CT (n=5) and CS (n=4) contained sheep (n=8) and goat (n=8) data sets. Risk ratios (RR) were calculated from published raw data. A meta-analysis will be performed for studies reporting phase I vaccines to observe visual trends, assess heterogeneity for meta-regression, and present pooled estimates of VE. RoB of studies revealed unclear to high risk of bias across most design categories. Available evidence of Q fever VE in small ruminants needs to be interpreted with caution due to the low number of studies and observations, and limited methodological reporting that could potentially bias the outcome.

Risk factors for porcine reproductive and respiratory syndrome virus (PRRSV) infection on pig farms in England

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The objectives of this study were to: (1) evaluate the prevalence of porcine reproductive and respiratory syndrome (PRRS) infection in English pig herds; (2) identify the risk factors for active PRRS infection at herd level; (3) estimate the probability that an infected PRRS farm would be detected through passive disease surveillance. Data came from a cross-sectional study carried out in England in 2008/2009. Information on farm characteristics was collected through interview with farmers. Twelve blood samples from pigs aged >10 weeks were collected from each herd and tested for antibodies against PRRSV and, on farms where sows/gilts were vaccinated, also for virus using PRRSV specific RT-PCR. Risk factors for active infection were identified in multivariable logistic regression. The probability of detection of PRRS infected farm through passive disease surveillance was estimated using stochastic scenario tree model. Thirty percent of farms showed evidence of active PRRS infection. Live vaccine was more likely used on those farms. They were located in high pig density areas or had dead pigs collected. Weaning piglets at the age ≥ 28 days was found to be a protective factor compared to weaning slightly earlier. The overall probability of detecting an infected farm through passive disease surveillance was 1.21%. The lowest probabilities obtained were for infected farms located in high pig density areas and using live PRRS vaccine. This study indicates high prevalence of active PRRSV infection amongst English pig farms often in the face of vaccination to control the disease. The absence of significant clinical signs in endemically infected herds or vaccination may explain the low probability of passive disease surveillance detecting infected herds. The results support a combined approach of strengthened surveillance, vaccination and improved biosecurity to control PRRS infection in a region.

A simulation method to reconstruct the longitudinal animal and herd level infection status based on repeated screening tests with no gold standard: application to paratuberculosis modeling

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As gold-standard tests are not always available, evaluating the performance of imperfect tests is important to determine the infection status of animals regularly screened for disease. Although methods to evaluate performance of tests with binary outcomes exist, no methods are available to determine multiple infection states from longitudinal data such as fecal culture and ELISA tests for *Mycobacterium avium* subsp. *paratuberculosis* (MAP). The parameters from infectious disease models (IDM) are often estimated from such test results. Yet, the joint uncertainty in the test results is rarely considered. The objective of this study was to develop a method to estimate the confidence on the animal level infection progression using longitudinal screening test results, and use the results to estimate IDM parameters. Test results from a paratuberculosis control program were used to demonstrate the method. The results of 12,957 parallel fecal culture (HEY media) and serum ELISA (IDEXX) from 8 Minnesota dairy herds over 9 years, and 970 fecal culture (TREK) from 3 Wisconsin dairy herds for 4 years were used to build a stochastic Markov Chain model for the within-herd spread of MAP and estimate its parameters. The infection/disease states were Susceptible, Latent, Low Shedder, Heavy Shedder and Clinical. Test parameters estimated with a latent-class Bayesian model were used to simulate a longitudinal disease trajectory for each tested animal. The uncertainty distributions of the IDM parameters were estimated iteratively using the animal-level trajectories. The parameter means were similar to those obtained using traditional MLE methods (at 95% confidence level) but the new method also produced joint uncertainty distributions unavailable elsewhere. Functional box-plots were used to validate the predicted animal trajectories via simulation studies.

Modelling changes to the delivery of early warning surveillance

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Early warning surveillance has successfully identified several new, re-emerging and exotic diseases in the British cattle population in recent years, including Bluetongue, Bovine Neonatal Pancytopenia and Psoroptic mange. It is expected that the benefits provided by early warning surveillance greatly outweigh the costs of implementation but there is a need to understand better the economic value of surveillance. Crucial to this is understanding the impact of alternative approaches to the delivery of surveillance on the time to detection of emerging disease. The aim of this project was to develop a simulation model to explore alternative allocations of resources for early warning surveillance in England and Wales, and to provide inputs into an economic assessment model. An individual animal-level model was built incorporating disease transmission, surveillance and control systems. A hypothetical disease with BSE-like characteristics was used and surveillance systems were represented by approximating the key decision making processes of farmers and vets, including factors such as farm history and distance from regional laboratory. Multiple streams of simulated surveillance data were used to trigger surveillance alerts. A baseline surveillance scenario was compared to scenarios incorporating free carcase collection and a dedicated telephone advice service. From the model output, the telephone advice service shifted the detection mechanism from *post-mortem* to telephone data but had little effect on mean epidemic size or time to detection; whereas the carcase collection scheme was more costly to implement but resulted in quicker detection and fewer affected holdings.

An introduction of African Horse Sickness in the Netherlands; what to expect?

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African horse sickness (AHS) is a non-contagious, vector-borne disease of equines. The effects of the disease can be devastating and mortality rates may exceed 90%. AHS is endemic in sub-Saharan territories and East Africa. As a consequence of its severity and its ability to expand rapidly out of its endemic areas AHS is an OIE listed and regulated disease. Intervention measures are mainly based on the use of emergency vaccination and the installation of movement restriction zones. AHS virus is closely related to the Bluetongue (BT) virus and is spread principally by midges of the same species that transmit BT virus in ruminants. Following the expansion in 2006 of BT virus infection to the more temperate regions of Europe, concerns regarding the risk of AHS outbreaks transmitted by these midges into Europe are increased. With an estimated number of 450,000 horses (or 11 horses/km²), the Netherlands is one of the most densely horse-populated countries in Europe. Main motivation for keeping horses is a passion for equestrianism as the majority of the Dutch horse population is kept for non-profit, recreational purposes. Only a minority (10%) of the horse premises is commercially managed, housing more than 60% of the horses. An outbreak of AHS is expected to result in large financial impacts and substantial social disruptions within the Dutch society. The aim of this research is to assess the potential socio-economic impact of an AHS epidemic and its control by quantifying the financial consequences of the primary stakeholders. Depending on the severity of the outbreak (0.5-2% of premises infected) and time needed to regain the AHS free status (27-38 months), total direct control costs ranged from €101 million till €232 million. Consequential losses exceeded the direct costs (ranging from €171 million to €284 million) and were mainly a consequence of applied movement restrictions, affecting primarily commercial stables. Training/sports stables were affected most, facing losses of more than €76,000 per stable.

Session 22**Theatre 5****Assessing the sensitivity of serial testing for equine influenza in quarantined horses**

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In 2007 equine influenza (EI) was diagnosed in Australia's horse population following its introduction with imported horses. The outbreak was eradicated following the single largest animal disease emergency response in Australia's history. Subsequently, additional risk management measures for EI were introduced for horses in quarantine, including collection of nasopharyngeal swabs and testing by PCR, prior to release. A review of the effectiveness of the testing regimes for detecting EI in the absence of clinical signs was undertaken. This study examined the value of multiple tests for EI in horses during pre-border and post-arrival quarantine, and in particular looked at the sensitivity of testing when the number and timing of tests is varied. A stochastic simulation model was developed to represent EI transmission within consignments of vaccinated horses in quarantine using a susceptible-exposed-infectious-recovered (SEIR) approach. The model was used to examine the effectiveness of multiple rounds of testing to detect EI virus in consignments over a 21 day period, taking into account that sample collection and test procedures are imperfect. The model uses conditional probabilities and parallel testing to determine the likelihood of failing to detect at least one infected horse following each test round and a cumulative probability that a consignment containing infected horses is not detected at the end of the quarantine period. This study provides a decision support tool for animal health authorities to assess testing protocols for detecting disease in animals whilst in quarantine. Key findings from the study show that transmission rates and the timing of testing influence the likelihood of detecting EI. The outcomes of this study will be useful to policy makers to reduce disease risks associated with international movement of horses.

Risk factors and control of FIV and FeLV infections in Danish cats

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The objective was to identify risk factors and trends in prevalences as related to control of infections with Feline Immunodeficiency Virus (FIV) and Feline Leukemia Virus (FeLV) in Danish cats from 1994 to 2010. Three datasets were used for the study: Set I: inclusion of 2890 unowned free-roaming cats from Society for the Protection of Cats tested during 2000-2010 in a catch-neuter-release program with focus on FIV/FeLV testing, neutering, ear tattooing and release into the same area where they were caught. Set II: inclusion of 968 mainly unowned free-roaming cats from Inges Cat Home tested during 1994-2008 in a similar catch-neuter-release program. Set III: inclusion of 7,255 stray cats or client-owned cats found in distress partly tested by The Danish Animal Welfare Society at 16 animal homes during 2006-2009. The first two datasets were analysed separately in logistic regression and trends in prevalences were compared to the third dataset which was only available in tabulated form. The average prevalences of FIV in the three sets were 7.5%, 15.4% and 0.3-1.7%, and the average prevalences of FeLV were 0.8%, 3.6% and 0-0.9% respectively. The prevalence in Set II increased from 1994 to 2002 followed by a general decrease for both diseases. Prevalences in Set I also showed a general decrease for both diseases from 2002. Significant FIV risk factors included male gender, increasing age, solitary lifestyle and being tested during the breeding season February-August. Significant FeLV risk factors included male gender and certain geographical regions. The reduced prevalences during the period 2002-2010 are possibly an effect of the voluntary control program for both diseases. The low prevalence of FeLV may be an effect of vaccination against this disease. Differences in FIV and FeLV prevalences between the three animal welfare organizations are presumably due to different criteria and consistency in testing cats. Thus, such data shall be used with caution.

Session 23**Theatre 2****Characterisation of the size, origin and fate of un-owned pets in the United Kingdom: results of a 2010 census**

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The pet population is in a constant state of flux, with estimates suggesting that 14-25% of pets are removed from their home every year, and only one third remain in their original home throughout their lives. Many of these animals are either abandoned or relinquished to the care of charitable organisations. Little data exists regarding these animals. The aim of this study was to characterise this population, and to document its origin and fate. A sampling frame was formed by searching the databases of registered charities for England, Scotland and Wales, registers of breed rescues and internet searches of animal welfare websites. Overall, 2,556 contacts for 1,420 organisations were identified. All were sent a questionnaire asking for data on the number of dogs and cats housed, their origins and fates, and details of husbandry during 2010. For those which were registered charities (582), their financial records for this period were also obtained. A total of 739 questionnaire responses were obtained, representing 502/1,420 (35.4%) of the organisations identified. These respondents cared for a total of 89,516 dogs in 2010. Most dogs (39%) were relinquished by their owner, or found straying (27.4%). Data were available for the eventual fate of 83404 dogs (93.2% of the total). The majority were rehomed (74.5%) or reunited with their owner (7.2%); however, 10.5% (8,864) dogs were euthanased. Respondents cared for a total of 157,163 cats, of which a similar proportion (9.4%, 14,800), were euthanased. Financial records were available for 525/582 (90.2%) of the registered charities. Their total expenditure in 2010 was £205,877,158. This study shows the scale of the un-owned pet problem, with considerable implications for the welfare of this population. The substantial numbers euthanased, despite the resources expended, suggests that further understanding of how and why pets become un-owned is essential.

Using metrics in animal shelters in the US

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The new veterinary discipline, ‘Shelter Medicine’, has grown tremendously during the past 13 years. As shelter software evolves to enable the collection and retrieval of health-related data, shelter veterinarians have the growing capability of using metrics in their shelter health programs. While similarities to livestock population health metrics are apparent, differences also exist. We have been working to identify the metrics most pivotal to achieving and maintaining population health in animal shelters. These include capacity measures (e.g. physical and staffing), monitoring daily census and length of stay estimates, as well as traditional incidence measures of disease frequency. Shelters not using these metrics are limited in their ability to monitor the status of the health of their populations and assess the effectiveness of new protocols aimed at continuously improving the health and welfare of their animals. Most staff and many veterinarians are unfamiliar with using metrics to manage the health of dog and cat populations. Veterinarians have been exposed to herd health concepts during their training, but many companion animal-oriented practitioners have never needed to utilize these concepts in the care of individual patients. Teaching staff and veterinarians how to calculate and interpret basic metrics to assist them in the management of their health programs has been an important goal of the Maddie’s Shelter Medicine Program at Cornell. We have been identifying and working with pivotal management measures (e.g. length of stay) and evaluating their impact on disease rates to help train shelter personnel. Not surprisingly, exceeding shelter capacity and increasing length of residence in the shelter are two highly influential metrics. Demonstrating these relationships, graphing disease rates and demonstrating how personnel can evaluate the effectiveness of changes in protocols is beginning to make metrics monitoring a routine tool for shelter veterinarians.

Preliminary epidemiological and spatial investigations into an emerging seasonal canine illness in Great Britain

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Seasonal canine illness (SCI) is a recently emerged disorder of unknown aetiology in Great Britain that manifests with gastrointestinal signs in dogs, occasionally fatally, soon after walking in woodland areas in late summer and autumn. SCI was investigated using a case control study based at one affected site in Norfolk. Questions were based on routine health and management of the dog and management and behaviour of the dog during the visit to the site and included a detailed map for owners to indicate routes of walks taken. Cases were dogs that walked at the site and developed two or more clinical signs of vomiting, diarrhoea, abdominal pain, fever, lethargy, anorexia and muscular tremors. Control dogs were walked at the site but did not become ill. Data from 2010 and 2011 were collated on 80 cases and 192 controls and analysed using logistic regression and spatial analyses. Controlling for year of study, multivariable analysis revealed distance travelled was a significant risk factor, with dogs travelling further than 100 km being more than 3 times more likely to become affected with SCI compared to those travelling from less than 10 km away (OR=3.24, P=0.013) and dogs were at a decreased risk if walking more than one route (OR=0.51, P=0.042) whilst at the site. Spatial analysis of 2010 data highlighted areas of the site with a higher ratio of cases compared to controls and these areas, deemed at higher risk for SCI, were indeed where cases subsequently occurred in 2011 when they were investigated during site visits by a naturalist. Although the specific aetiology of SCI remains unknown, the study provided insights into specific features of populations at risk and geographical sites worthy of further investigation. Site visits conducted soon after cases recurred in September 2011 strongly suggested that toxins from blue-green algae, poisonous plants and fungi were unlikely to be causes of SCI. Investigations into alternative theories and pathogenic mechanisms for the disease are continuing.

Exploring the epidemiology of canine and feline overweight/obesity in United Kingdom using a national database of veterinary practices

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Most studies investigating companion animal obesity have been restricted to small geographical areas, which is a major constraint to understanding the epidemiology of companion animal obesity. The aim of this study was to describe canine and feline obesity prevalence, geographical distribution and demographic risk factors from a UK wide first opinion veterinary practice database. Body condition scores were available for 7,821 dogs and 3,227 cats from 46 practices collected between 2008 and 2010. The prevalence of overweight/obesity was 11.5% in cats and 25% in dogs. Using both SatScan and GLMMs, we found a higher prevalence of overweight/obesity in dogs within Scotland compared to England & Wales. No significant spatial differences in overweight/obesity were found in the cat population. The canine GLMM (with random effects being practices nested within regions) showed that males were less likely than females to be overweight, neutering increased the likelihood of being overweight and animals were more likely to be overweight with middle age. Certain breeds appeared at greater risk. A fixed effects-only model provided a better fit to the feline data. Sex, neutering and age remained in the final model with the main difference being that male cats were at increased risk. No breed effects were evident from the feline dataset. Further exploration between the relationship of canine age and breed was carried out using GAMs. This study has confirmed that neutering, age and sex are important risk factors associated with overweight/obesity for both species. There were important differences in the epidemiology of canine and feline obesity: namely the spatial distribution and impact of breed. Understanding these differences may help to unravel the complex pathogenesis of obesity in cats and dogs.

Disease surveillance in dogs and cats: a practitioner-based system

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In 2010, a prospective national disease surveillance project was launched in Australia to capture data on diseases in dogs and cats. This system – called Disease Watchdog – is based on the reporting of disease cases by veterinary practitioners. Since its launch, approximately 40% of Australian practitioners have registered and participated in Disease Watchdog, attracted by the information generated from this system (including real-time disease mapping). Practitioners can report a range of diseases, including canine parvovirus, distemper and hepatitis; feline calicivirus, herpesvirus, infectious peritonitis and leukaemia virus; and tick paralysis. Ancillary data recorded include practitioner information, case occurrence date and location, species, breed, age, gender, neuter status, disease, case diagnosis method, case outcome, vaccination status, vaccine given and vaccination date. In addition, there is an optional field to record litters infected. During 2010 and 2011, 8,443 disease reports were submitted to Disease Watchdog. The conditions most commonly reported were tick paralysis (n=4,499, 53.3%) and canine parvovirus (n=3,372, 39.9%). Estimated case fatality rates were 58% (canine hepatitis), 23% (canine parvovirus), 7.4% (tick paralysis), 1.6% (feline calicivirus), 1.3% (feline herpesvirus). To date, information generated by Disease Watchdog has been used to investigate risk factors for canine parvovirus mortality and disease clustering. The risk of death was significantly associated with season of diagnosis (summer) and pedigree type (hounds and non-sporting dogs). Clusters were found to occur in postcode areas with a greater level of relative socioeconomic disadvantage and a lower rank in education and occupation (P<0.05). Although the project is still in its infancy, already new information on the distribution and risk factors for diseases of dogs and cats has been produced. This system is continuing to evolve to include new diseases and additional information.

Mining free-text companion animal medical records for surveillance

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The lack of an efficient systematic and standardized means for collecting and analyzing pet animal data is a significant obstacle to evidence-based companion animal medicine, the appropriate assessment of the role of pets in the epidemic of antimicrobial resistance and the application of pets as sentinels of emerging public health risks. Approximately 30% of the pet practices in the city and the surrounding rural areas of Calgary, Canada used electronic medical records in 2009. A data extraction program was developed and installed on the computers at 12 sentinel companion animal practices. Data were collected from January 1, 2007 to December 31, 2010. The extracted data were integrated and stored in a data warehouse for subsequent analyses. Infectious enteric diseases of pets were used as the case study. As there were a limited number of confirmed diagnoses, we used syndromic surveillance of 'diarrhea' to classify the patients. The data were in a free-text format without any structure such as pick lists, codes or fixed vocabulary. A linguistics-based text mining program was used to automatically encode and extract cases of diarrhea. The data extraction, text-mining and space-time epidemiology software were applied to a one year simulated prospective surveillance system and they were evaluated for their ability to provide an early warning with effective and efficient surveillance. The ability of the text-miner to accurately identify cases was determined by comparing its results to a manual review of the records. The sources of false positive and false negative cases will be presented and an assessment of the capacity for the electronic medical record and informatics to assess for spatial and temporal clusters will be discussed.

Extracting the evidence: veterinary practice-based research

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The principle of Evidence-based Veterinary Medicine (EVM) is to employ high quality research from population samples to enhance clinical decision making for the optimal treatment of individual patients. In order to identify areas in which research is needed, it is necessary to understand which conditions present most commonly, and determine perceived gaps in information. The aim of this pilot study was to investigate the feasibility of extracting data, from a practice management software (PMS) system used in a first opinion veterinary practice, and to assess the value of the data extracted. The Centre for Evidence-based Veterinary Medicine (CEVM) in collaboration with Vet-One and the Vet XML Consortium, designed a PMS extraction method to access information from the Electronic Patient Records (EPRs) of one first opinion veterinary practice. An XML schema was used to select and extract data of interest. Over a three week period all practice based consultations were extracted. A veterinary database of small animal EPRs containing case histories and consultation details was created. Three hundred and fifty eight animal records were extracted and downloaded to the database. The predominant species examined were dogs (57.3%), cats (26.8%) and rabbits (2.2%). A total of 862 records were extracted including animal demographic fields (e.g. species, age, breed), consultation information (e.g. condition history, examination findings, and consultation outcome) and any treatments given. Validation confirmed 100% accuracy for extraction. The results of this pilot study suggest the extraction of clinical data from veterinary PMS systems is a viable method for the capture and analysis of small animal health data, and for practice-based research. The aggregation of patient data and analysis of this type can provide information that is suitable for longitudinal and observational studies, and offers a unique method for practice-based research.

Primary practice clinical data for companion animal surveillance

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Introduction Companion animal health data derived from referral caseloads, pet insurance, cancer registries and surveys are limited by constrained disorder lists and inherent selection bias. Primary practice-based systems address these limitations by including all disorders diagnosed and all clinic-attending animals. This paper describes the implementation of the VetCompass project (<http://www.rvc.ac.uk/VetCompass>), sharing clinical data from UK first-opinion veterinary practices for epidemiological research. Method Practices, recruited via notices in the press, agreed to record summary diagnoses using VeNom Code terms (<http://www.venomcoding.org>) following episodes of clinical care. Clinical data fields extracted from practice management systems included patient ID, species, breed, sex, neuter status, insured status, microchip number, age, clinical notes, treatment and diagnosis. A secure structured query language (SQL) database was developed to store data and facilitate queries. A pilot project validated data management and research utility prior to extended project roll-out. Results A pilot project (2007-2009) with 7 clinics efficiently captured clinical data for 9,872 cats and 10,007 dogs within 129,387 unique episodes of clinical care. Summary diagnosis terms were recorded for 22,111 of 38,872 (56.88%) episodes of care with pharmacotherapy. Subsequent project expansion collaborated with 92 clinics with data on 101,000 cats and 111,000 dogs and over 2 million episodes of care (Feb. 2012). Breed and sex data were available for 99% of cats and dogs. Future applications will evaluate pyoderma in dogs, cancer in dogs and also the role of breed in predisposition to disorders of dogs and cats. Conclusion The VetCompass project demonstrates that veterinary first-opinion clinical data can be successfully captured and will be a useful epidemiological research tool.

Differences between samples of vet-registered and vet-visiting cats

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Case-control studies of companion animals often recruit controls from veterinary practices. Animals attending for veterinary appointments ('vet-visiting' (VV) animals) are sometimes used as animals/owners are readily available for examination and/or questionnaire completion; however this sample is anecdotally thought to be biased towards young animals presenting for vaccination/neutering or older animals with age-related signs of ill health. An alternative strategy of sampling animals from practice registers ('vet-registered' (VR) animals) that may/may not have attended an appointment recently, is sometimes used to try to reduce selection bias, despite problems such as out-of-date records. This study aimed to compare characteristics of cats selected by these two sampling methods. A convenience sample of 20 UK veterinary practices was used. A questionnaire was issued to the first 30 compliant cat-owning clients attending an appointment on a specific week at each practice (VV sample). Practice staff mailed a questionnaire, and a reminder to non-responders, to 20 randomly selected cats from their practice register (VR sample). A multivariable logistic regression model was based on 232 VV and 101 VR cats. No significant differences existed for age, pedigree or neuter status; however, VV cats were significantly more likely than VR cats to be restricted to indoor-only access (OR=3.5, 95% CI 1.6-7.5), to have not been vaccinated as a kitten (OR=4.0, 95% CI 1.4-11.3), to have been vaccinated within the last three years (OR=2.5, 95% CI 1.2-5.3), to have had an appointment at the practice within the last year (OR=2.5, 95% CI 1.2-5.3) and to be taking antibiotics (OR=4.9, 95% CI 1.6-14.5). Therefore, indoor/outdoor lifestyle and history of vaccination risk factors for diseases such as feline idiopathic cystitis and injection-related sarcomas need to be interpreted with caution as the strength of associations with identified risk factors may be influenced by control selection methodology.

Antimicrobial resistance surveillance: bacterial prevalence estimates are not enough

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Surveillance programs for monitoring antimicrobial resistance in foodborne (enteric) bacteria largely focus on estimating and comparing phenotypic prevalence among different livestock species, their farm environments and food products, and assessing trends over many years. Often, these monitoring systems have a high threshold for detection of rare resistance geno- and pheno-types owing to: (1) relatively small sample sizes that are further diluted by multiple species/strain/antimicrobial combination endpoints; and (2) the use of non-selective media that, while assuring unbiased resistance prevalence estimates at the bacterial population level, provide little confidence in freedom from the presence of bacterial resistance at the sample / animal / pen / farm / industry / country level, particularly for commensal (indicator) organisms. Much of the latter problem lies with the enormous size of the bacterial population in a single gram of feces, and therefore the relatively small probability of culturing a strain unless it is present in relatively high numbers. Very few surveillance programs specifically target early detection and characterization of emergent strains of resistant bacteria, particularly in the years immediately following the introduction of new classes, variants or formulations of antimicrobial. This has serious implications for the utility of these surveillance programs in ensuring food safety and protecting public health. Using the relatively recently introduced 3rd generation cephalosporin class of antimicrobial and the more longstanding tetracycline class as contrasting examples, we illustrate an alternative approach to monitoring and surveillance that blends elements of more traditional resistance prevalence estimation with targeted detection and strain characterization; this, in order to better understand novel threats to food safety and potentially mitigate emerging problems before it is too late.

Antimicrobial resistance trends among *Salmonella* isolates obtained from dairy cattle and dairy farms in the northeastern USA, 2004-2010

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Monitoring antimicrobial resistance trends among bacteria isolated from food animals and people is necessary to inform public policy regarding appropriate antimicrobial use. Our objectives were to describe the antimicrobial resistance status of *Salmonella* isolates from dairy cattle and dairy farms in the northeastern USA and to identify trends in resistance to various antimicrobial agents over time. Data were collected retrospectively for all bovine *Salmonella* isolates that were obtained from samples submitted to Cornell University's Animal Health Diagnostic Center between January 1, 2004 and December 31, 2010. Temporal trends in the prevalence of resistant *Salmonella* were investigated for each antimicrobial agent using the Cochran-Armitage trend test. Antimicrobial susceptibility testing was performed on 4,589 bovine *Salmonella* isolates during the study period. Resistance to each antimicrobial agent ranged from 0% (amikacin) to 73.9% (sulfadimethoxine). There was evidence of a significantly decreasing trend in prevalence of resistance to most agents: amoxicillin/clavulanic acid (AUG), ampicillin (AMP), ceftiofur (FOX), ceftiofur (TIO), ceftiofur (TIO), ceftriaxone (AXO), chloramphenicol (CHL), florfenicol (FFN), chlortetracycline (CTET), oxytetracycline (OXY), tetracycline (TET), kanamycin (KAN), neomycin (NEO), spectinomycin (SPE), streptomycin (STR), and sulfisoxazole (FIS). Among the 1,727 isolates that were tested using the National Antimicrobial Resistance Monitoring System (NARMS) panel, the most common resistance patterns were pan-susceptible (51.5%), AUG-AMP-FOX-TIO-AXO-CHL-KAN-STR-FIS-TET (10.3%), AMP-KAN-STR-FIS-TET (7.9%), and AUG-AMP-FOX-TIO-AXO-CHL-STR-FIS-TET (7.9%). These results do not support the notion that the current level of antimicrobial use in dairy cattle is driving an increase in the emergence and dissemination of drug-resistant *Salmonella* in the region served by the laboratory.

Screening bulk tank milk for methicillin resistant *Staphylococcus aureus* in Ohio dairy farms

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Initially a problem in human hospitals, Methicillin resistant *Staphylococcus aureus* (MRSA) has emerged as a concern in veterinary medicine as well in the last few years. A large range of animals, including companion animals, livestock and exotic species has been diagnosed with MRSA infections or identified as healthy MRSA carriers. The origin of MRSA in livestock is different from that in companion animals: In food animals, a distinct strain (ST 398 LA-MRSA) seems to have developed separately, with subsequent interspecies transmission. Recently, a novel variant of *mecA* gene (*mecA*_{LGA251}) which shows 70% DNA identity with the classical *mecA* was discovered in Europe from both human and bovine populations. In the USA, low prevalence of MRSA in dairy herds has been reported in a limited number of studies. The objective of the present study was to estimate MRSA prevalence in Ohio dairies. Bulk tank milk (BTM) samples from 307 OH dairy herds were cultured. Isolation and identification of *S. aureus* was based on growth in selective Baird Parker media, Gram stain, and positive catalase and coagulase tests. Over two-thirds (69%) of the herds were found positive for *S. aureus*. For species confirmation and methicillin resistance, a duplex PCR was performed following the modified version of Jonas *et al.* using *femB* and *mecA* genes. To date, 169 randomly selected *S. aureus* isolates, from different herds distributed across the state, have been screened. The *mecA* gene has been detected and amplified in only one (0.6%) of the samples. This finding supports the evidence that *mecA* MRSA is present in dairy herds, but in a very low prevalence. The epidemiology of MRSA in dairy herds needs further investigation.

Antimicrobial resistance profile in faecal *Escherichia coli* of sows and their offspring in the farrowing unit and their interaction

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Sows and their respective piglets from 3 pig herds were sampled to determine the antimicrobial resistance profile of faecal *Escherichia coli* for 7 different antimicrobials. On each farm, fecal samples were taken from twenty sows before parturition, at birth and at time of weaning of the piglets. From each sow, three piglets were sampled at birth (before any antimicrobial administration), at 14 days of age and at weaning. In each herd, antimicrobial usage data were collected for the sows and piglets during the suckling period and quantified as treatment incidences or the number of days during which an animal was administered one dose of an antimicrobial agent. The percentage of resistant *E. coli* isolates was compared between samples from piglets taken at the various sampling times and between sows and their respective piglets. Antimicrobial resistance to all tested antimicrobials was found in *E. coli* obtained from newborn piglets independent of a direct antimicrobial selection pressure. However, the administration of antimicrobials around birth to their dam can result in an indirect selection pressure for the microbiota of the piglets. After birth, resistance in *E. coli* from piglets increased for ampicillin, ceftiofur, enrofloxacin and trimethoprim/sulfadiazine after the administration of antimicrobials and decreased again swiftly for ceftiofur, enrofloxacin and trimethoprim/sulfadiazine after 14 days of age and before weaning. Resistance in *E. coli* from sows at birth and weaning was seen as a risk factor for resistance in their respective piglets at 14 days of age and weaning respectively. This confirms the commensal gut flora of the sows as a reservoir for antimicrobial resistant *E. coli* isolates in their litter. These data indicate that the level of antibiotic resistance in piglets is not stable in the early stage of life and is dependent on the level of antibiotic used in the piglets and the degree of resistance in the dam.

Knowledge, attitude and practices of livestock workers on antimicrobial resistance and detection of antibiotic residues in slaughtered cattle in a tropical cattle market in Ibadan, southwestern Nigeria
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Antimicrobial resistance (AM) represent a major public health problem globally. However, antibiotics are indiscriminately used by livestock marketers (LM) on trade animals meant for immediate or eventual slaughter in a Tropical Cattle Market in south-western Nigeria. We conducted a study to evaluate the level of knowledge, attitudes and practices of 216 randomly selected LM on issues relating to AM through the methods of questionnaire and the data analyzed using the SPSS version 12.0. We also assessed 90 randomly selected tissue samples from their slaughtered cattle for the presence of tetracycline and penicillin residues, being the two most frequently used by these LM using high power liquid chromatography. Our findings reveal that about half (50.37%) of LM had poor knowledge on issues relating to AM with 81.02% unaware of drug withdrawal period. Almost two-third (64%) had poor attitudes towards AM issues and only 11.11% indicated the need to observe withdrawal period in animals under treatment before sale or milking. Poor practices by these LM for possible AM in humans include milking and drinking milk from animals under treatment. Significantly higher proportion (91.67%) of the LM has never been advised by the Veterinary doctors on site regarding withdrawal period while 95.37% have never observed it. All the tissue samples screened contained residues of tetracycline and penicillin, although below the maximum residual limits. The need for adequate awareness campaigns among these LM towards stemming the problem of antimicrobial resistance acquired through the food chains in humans is thereby stressed.

It depends on which outcome: a plea for truly multivariate analyses in epidemiologic research
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For far too long, the terms multivariable and multivariate analysis have been interchangeably used by many in epidemiology and its allied fields. While purists shudder, the naïve may be led into the false illusion that most of what matters in our explorations lies to the right side of a regression equation. Admittedly, our discipline has been limited in accessible methods for dealing with multivariate responses; that is, to those coded as continuous and distributed normally. When the choice of outcomes is limited to live versus dead, health versus disease, or even mild, moderate, or severe, then a simple multivariable approach is justified. However, in many situations encountered in veterinary epidemiology, the outcomes reflect a suite of variables that may reasonably be expected to depend upon each other as well as to a given set of predictors. One obvious set of multiple dependent outcomes arises when measuring and analyzing factors that affect utilization rates of prophylactic, metaphylactic, and therapeutic antibiotics to prevent, control, and treat infectious diseases, respectively. In such cases, the factors that increase one use may well be expected to reduce another use of another, and vice versa. Likewise, this can be expected to result in changes in levels of bacterial resistance as an endpoint when different products are used in different ways. Using data arising from a multi-state U.S. survey of antibiotic use practices among veterinarians and cattle producers, examples of several multivariate techniques useful for a variety of dependent variable coding schemes will be illustrated. In addition, applications of such approaches to multivariate antibiotic resistance data in binary, ordinal, and continuously coded forms will be explored.

Dissemination of CTX-M cephalosporinase-bearing *Escherichia coli* in US finishing swine populations
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Conveying resistance to penicillins and critically important cephalosporins, the extended-spectrum β -lactamase bacterial resistance gene $\text{bla}_{\text{CTX-M}}$ was first described in US livestock in 2010 and characterized in dairy cattle populations in 2011. It has been hypothesized that the dissemination of $\text{bla}_{\text{CTX-M}}$ is a product of selection pressure from the veterinary use of 3rd and 4th generation cephalosporins in food animals. Our objectives were to estimate the frequency and distribution of coliform bacteria harboring $\text{bla}_{\text{CTX-M}}$ in fecal flora of finishing swine populations in the US, and to characterize the CTX-M alleles, their plasmidic contexts, and the genetic diversity of the bacterial isolates. We also evaluated the association between barn-level ceftiofur use and the likelihood of recovering extended-spectrum cephalosporin resistant bacteria in these populations. We collected 30 fecal samples from each of 50 finishing barns located in 5 US states. We recovered *Escherichia coli* containing $\text{bla}_{\text{CTX-M}}$ from 22 of 1,495 (1.5%) fecal samples in 6 of 50 (12%) barns. Twelve of 30 (40%) samples from a single barn in MI produced *E. coli* containing $\text{bla}_{\text{CTX-M-1}}$ on IncN ST1 plasmids. The remaining 5 positive barns were in OH and yielded between 1 (3.3%) and 3 (10%) *E. coli* containing $\text{bla}_{\text{CTX-M-1}}$ or $\text{bla}_{\text{CTX-M-15}}$ on IncF plasmids. Five of the 10 OH isolates from 2 barns also transferred fluoroquinolone resistance to MG1655 *E. coli* transconjugants. Pigs in most (82%) barns received prophylactic ceftiofur treatment as piglets in either the farrowing or nursery facilities prior to the finishing phase of production. In addition, up to 8.7% of individual pigs in approximately half (48%) of finishing barns received therapeutic ceftiofur to treat acute disease. We were unable to detect an association between ceftiofur use and the probability of recovering $\text{bla}_{\text{CTX-M}}$ *E. coli*.

Determinants of ceftiofur resistance in human *Salmonella Heidelberg* infections in Canada: drug selection pressure or foodborne origin?

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Third-generation cephalosporins are an important class of antimicrobials used to treat serious *Salmonella* infections in humans. The zoonotic pathogen *Salmonella* serovar Heidelberg is commonly found in poultry in Canada. The Canadian Integrated Program for Antimicrobial Resistance Surveillance (CIPARS) described a strong correlation between ceftiofur resistance in *S. Heidelberg* isolated from retail chicken and incidence of ceftiofur resistance in *S. Heidelberg* infections in humans. Thus, ceftiofur resistance in Heidelberg strains causing human disease could have developed due to antimicrobial consumption (AMC) in the community or to its presence in chickens, identified as the main source for *S. Heidelberg* in Canada. We explored these hypotheses by applying time series methods to monthly data gathered from 2003 to 2010 by CIPARS or MAPAQ for Ontario and Québec on ceftiofur resistance in human *S. Heidelberg* cases and ceftiofur resistance in *Escherichia coli* in chicken at the retail, abattoir and farm level (Québec only) and on community AMC. The provinces were studied separately. No significant link was assessed for AMC in the community for both provinces. In Québec, ceftiofur resistance in chicken at retail level was significant in the same month (regression parameter: 0.29 [0.04;0.53]) and, at the abattoir level, with one month lag (regression parameter: 0.44 [0.11;0.78]). In Ontario, the approach didn't provide similar results. This is the first time that time series were used to assess the potential link between resistance in *Salmonella* cases and community AMC or resistance in food sources in Canada.

ESBL and quinolone resistant enterobacteriaceae in livestock husbandry: a cross sectional study

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In the course of the research consortium RESET the occurrence of ESBL and (fluoro)quinolone resistant Enterobacteriaceae (*Escherichia coli* and *Salmonella enterica*) in humans, animals and the environment are investigated. Epidemiological studies are accompanied by molecular characterisation of the isolated bacteria. All generated data will result in a risk analysis in order to assess the situation of resistant bacteria in Germany. In a cross sectional study 200 agricultural farms in 4 regions in Germany are investigated. 10 samples (collective faeces, dust, boot socks) per farm are analysed culturally for ESBL and (fluoro)quinolone resistant *E. coli* and *S. enterica*. The laboratory investigations are completed by informations in a questionnaire. Questions regarding the general farm structure, feeding and hygiene management as well as the antibiotic use are included. To date, 54 farms (fattening pigs, dairy cows, fattening cattle, broilers) in two regions were visited. In 88% of 25 pig farms, 67% of 12 dairy cattle farms, 67% 9 of fattening cattle farms and all of 6 broiler farms ESBL-suspected *E. coli* were found. Statistical analyses will focus on correlations between the antibiotic use and the occurrence of resistant bacteria. Furthermore, the farms' management data will be screened in order to identify possible risk factors.

A comparison of antimicrobial resistance in faecal *E. coli* from cattle and sheep in the Scottish Highlands

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Any quantitative risk assessment of the likelihood of transfer of antimicrobial resistant bacteria from animals to humans is likely to take into account the level of resistance within the animals. Using data from random surveys we compared the prevalence of faecal samples containing antimicrobial resistant *Escherichia coli* from calves, adult cattle and sheep. The antimicrobials tested were ampicillin, apramycin and nalidixic acid. We found a higher prevalence in calves than adult cattle, and higher in adult cattle than in sheep and these prevalences are presented. There were also large differences in prevalence between the three different antibiotics. Using a simple measure of bacterial density, the density of *E. coli* was highest in sheep and calves and lowest in adult cattle. The *E. coli* density score predicted less of the variation in prevalence than was predicted by the class of animal (sheep, calf or adult cattle). This implies that something other than bacterial density may account for the difference in antimicrobial resistance prevalence between sheep, adult cattle and calves. Recorded antibiotic usage was generally low and it was different in calves, adult cattle and sheep. We found no relationship between antibiotic usage and prevalence of resistance.

Possible consequences of changes in livestock production structure on cross-border contagious livestock disease control

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Frequency and impact of contagious livestock diseases (CLD) are mainly determined by features of the production structure of livestock, e.g. number of farms, farm size, specialisation of production and reliance on cross-border production markets. Changes in these features result in altered CLD risks and veterinary and financial-economic impacts. Particularly countries with increasing specialisation of production, e.g. piglet production, and increasing dependency on demand of specialised cross-border producers, e.g. fattening pig farms, will be affected in case of CLD. Insight in changes in production structure is thus important for veterinary policy, e.g. contingency plans and cross-border collaboration agreements. The aims of this study were: (1) to explore changes in the livestock production structure of the cross-border region of the Netherlands (NL), North Rhine Westphalia (NRW) and Lower Saxony (LS) during 2011-2020; and (2) to assess consequences for CLD introduction, spread and control. Experts constructed and quantitatively assessed various scenarios that describe major driving forces that influence future livestock production features of the pig, poultry and dairy sectors. Results indicate a +58% farm size and -37% number of farms until 2020. In the pig sector, major shifts were expected: -0.4 million NL and -4.7 million NRW/LS piglets produced, and +1.1 million NL and -2.4 million NRW/LS fattening pig places (FPP). The NL export of piglets to NRW/LS is likely to increase because of the potential surplus of 2.3 million NRW/LS FPP, resulting in increased piglet movements and increased risks of CLD introduction and spread. Consequently, the expected increase in cross-border trade intensifies the cross-border production dependency, resulting in an increased need for collaboration between NL-NRW-LS. It is concluded that veterinary policy makers should proactively anticipate to these future changes in livestock production structure.

Session 25**Theatre 2****Livestock disease control in frontier regions: problems and prospects, challenges and limitations for cross-border collaboration**

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Frontier regions have specific features that make them more vulnerable for introduction and spread of livestock diseases compared to 'backland areas', e.g. more intensive livestock trade and transport. This holds for traditional diseases such as Classical Swine Fever (CSF), but even more for vector-borne Emerging Infectious Diseases such as Blue Tongue. On the other hand, the cross-border inter-dependency offers quite some possibilities for collaboration and mitigation of particularly the economic impact of livestock diseases. Currently these possibilities are not fully recognized and hence under-utilized. This paper aims to review the development of cross-border collaboration in livestock disease control from two perspectives: (1) specific veterinary aspects; and (2) mitigation of economic impacts. Specific attention will be given to the following issues: (1) communication and data exchange; (2) capacity building; (3) routine versus crisis time measures and practices; (4) collaboration in prevention and control; (5) cross-border exercises; and (6) harmonization of disease control. The frontier region Germany-Netherlands is a very prominent example of cross-border economic inter-dependency and veterinary risks, and steps towards harmonization have been taken in the last decade. Therefore, particularly examples from this area will be presented and put in a wider perspective. One such an example shows the contradictory effect that might occur: cross-border harmonization of CSF can reduce the overall impact, however, because of differences in institutional aspects (i.e. compensation schemes), for some German stakeholders the impact can increase. This emphasizes the need for an integrated beyond-veterinary approach. It is concluded that in frontier regions specific veterinary and economic risks can be mitigated provided an integrated veterinary-economic approach.

IT support for German-Dutch crisis communication: needs analysis, guidelines and requirements on the example of classical swine fever

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Being prepared for an outbreak of animal diseases like Classical Swine Fever is a key issue in an area of intensive pig production like the Dutch-German border area. The border is no obstacle to the trade of pigs and meat but to instruments of disease control. Today disease control is exercised by national veterinary administration using their own national official systems for communication and decision making. In case of cross-border disease outbreaks information gaps and communication breaks occur that hamper efficient decision making. In general this causes avoidable delays in disease control and avoidable direct and indirect damages. The aim of this study was to develop a model for an IT support system which enhances cross-border crisis communication in case of animal disease and related crises. The system shall combine existing official and private information systems along the chain and extend them to a communication tool for official and private actors along the supply chain. Based on findings of preceding research projects in the fields of food safety, traceability in meat production and cross-border animal disease control and examined for issues of quality, information and crisis management as a cross-cutting topic, we conducted interviews with experts of Dutch and German livestock production and veterinary authorities. The interviews were prepared and added by literature. Result of the study is the Engage-Exchange-Model (EEM). The EEM bases on a two-level approach. At first level an information transfer between chain members (whether German or Dutch) takes place. During an outbreak the second level supports a quick and effective communication with and between Dutch and German authorities by temporal and mutual exchange of relevant information and the engage of specific additional information.

Session 25**Theatre 4****Veterinary ethnography: new shoes for 'shoe leather' epidemiology?**

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National disease control programmes involving government veterinary services often begin with ambitious targets and optimism in achieving disease eradication. There have been many successes over the years, but for some endemic diseases and in certain countries eradication seems a distant dream. Whilst there can undoubtedly be epidemiological and technical reasons for the failure to eradicate, socioeconomic reasons (human factors) may often be overlooked. My contention is that government veterinary services and policymakers need to pay more attention to the humans who control the animals, rather than focussing all their attention on the diseased animals themselves. Gaining the confidence and co-operation of farmers and veterinarians at the frontline involves a more in-depth understanding of their attitudes and behaviours with respect to disease control, which may in turn provide explanations as to why a programme has failed to meet its objectives. Using a suite of qualitative techniques from the social sciences offers a complementary approach to quantitative veterinary epidemiology, and provides a full-orbed approach to improving disease control policy. This presentation will introduce ethnography, a methodology commonly used in the social sciences to investigate human phenomena. As a case study, I will describe my intended PhD research talking to farmers, vets and policymakers involved in the bovine tuberculosis eradication programme in Northern Ireland. I speak as someone who has worked in bovine TB control in the role of private veterinary practitioner, government veterinary officer and veterinary epidemiologist, and I am also a cattle farmer's son. I will suggest that ethnographic techniques provide different shoes to complement 'shoe leather' epidemiology on the farm, at the vet clinic, and in the government office.

Reducing surpluses of piglets due to movement restrictions in case of Aujeszky's disease

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In the Netherlands, outbreaks of Aujeszky's Disease (AD) are controlled by vaccination and movement restriction zones (MRZ) for all pigs around infected farms. Although this strategy avoids the socio-ethical concerns associated with pre-emptive slaughter, it can easily result in animal welfare problems and negative economic consequences. These occur because movement restrictions result in surpluses of live (vaccinated) piglets on farms. The aim of this research is to provide insight into the development of these surpluses and its impact, and to describe how measures that allow early transportation of pigs under certain conditions and to specific destinations (channeling) could help to reduce these problems. For the analysis a deterministic simulation model was developed, which calculates surpluses of piglets of 10 weeks or older at multiplier farms in MRZs on a weekly basis for AD outbreaks. The results show that in case of complete movement restrictions surpluses of piglets varying in age and vaccination status will quickly arise in the MRZ. These surpluses become larger if the epidemic lasts longer and can become as large as 180 to 340 thousand piglets (45-75% of weekly domestic production) for medium and long epidemics, respectively. Implementation of channeling strategies that allow earlier transportation within the MRZ can reduce surpluses by about 50% to 100-150 thousand piglets maximum. Strategies that also allow transportation outside the MRZ can reduce surpluses even further to below 100 thousand piglets. It was concluded that allowing transports of piglets at an earlier time result in a drastic reduction of problems with accommodating ready-for-transport piglets. Moreover, it reduces shortages during movement restrictions and peak supply immediately after removing the restrictions. The impact will be considerable fewer problems with animal welfare and smaller changes in prices.

Update on the participatory epidemiology network for animal and public health (PENAPH)

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Public and animal health communities are working globally to better predict and respond to health threats. This is leading to growing demand for better information on the health status of people, domestic animals and wildlife. In many countries, the ability to collect quantitative animal health data is challenged by lack of infrastructure and resources to maintain systems. Participatory epidemiology (PE) is the application of participatory approaches to the collection of epidemiological knowledge. The application of PE to surveillance (participatory disease surveillance, PDS) recognises the knowledge that people who rely on livestock and wildlife have about animal health. The integration of PDS with conventional epidemiological methods increases the flexibility, timeliness and sensitivity of surveillance systems. Examples include enhanced surveillance of foot and mouth disease, highly pathogenic avian influenza, classical swine fever, as well as the contributions to the eradication of rinderpest. In 2007, the Participatory Epidemiology Network for Animal and Public Health (PENAPH) was established. It promotes institutional capacity development for surveillance and epidemiological services, PE practice and training standards, evidence-based policy analysis and advocacy, and research and exchange of information. PENAPH and its' partners have conducted training programs and piloted one health activities. PEANAPH advocates for institutional analysis of surveillance systems leading to defined social and technical objectives and an integrated mix of surveillance activities suited to those objectives. The current activities of PENAPH focus on empowerment of regional stakeholders in the network and on increasing the participation of all stakeholders in the development of national and international policy related to health.

Classical epidemiological approach versus participatory methods: a comparison of two research methods applied to identification of key health issues for working horses in Lesotho

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Few reported studies have simultaneously applied quantitative and qualitative methodologies for the purpose of direct comparison of their findings. To compare issues identified via classical epidemiological field survey methods with those identified and prioritised by animal owners using a participatory approach. A cross-sectional field survey of individual horses and their owners, using structured pre-tested face-to-face owner questionnaires, clinical examination and a standardised tack examination was undertaken in August-October 2009. In March 2010, owner workshops were convened at which participatory resource mapping and matrix ranking techniques were employed to facilitate owner identification and prioritisation of horse-related issues. The main issues identified in the survey were sharp enamel points on teeth, endo- and ectoparasites, suboptimal nutrition, tack-associated wounds, overgrown and poorly balanced feet and poor owner knowledge and practice of key husbandry tasks. In the participatory workshops, all owner groups defined priority issues based on perception of their adverse impact on horse health and work ability rather than frequency of occurrence. Overall their ordered priority issues were mouth health, nutrition, disease management, husbandry including wound management and foot- and limb-associated issues. Whilst classical epidemiological approaches provide objective estimates of frequency, without the vital components of developing community ownership of the process and grounded researcher appreciation of local circumstances, interventions based solely on epidemiological measures of frequency are less likely to succeed. Acknowledgements: World Horse Welfare; Lesotho Department of Livestock.

Rinderpest surveillance in South Sudan: developing a system for a region with limited veterinary services

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In the 1980s and 1990s the southern region of Sudan, now the Republic of South Sudan, was considered to be an endemic focus of rinderpest and a source of infection for neighbouring countries. During the 1990s, the community-based animal health programme, supported by indigenous and international organisations, conducted rinderpest vaccination using thermostable vaccine. The subsequent reduction in rinderpest incidence allowed Sudan to enter the final stages of rinderpest eradication: vaccination ceased in 2002 and a surveillance system was established. The objectives of the rinderpest surveillance system were to detect any remaining foci of rinderpest and provide evidence of freedom from infection. Methods were developed that, in the absence of conventional veterinary services, could be implemented by the community-based animal health programme. The results are described. The data contributed to the Republic of Sudan's successful application to the World Organisation for Animal Health (OIE) for recognition of freedom from rinderpest. International guidelines and regulations for disease control and eradication should be sufficiently flexible for adaptation to diverse environments. Characteristics of livestock systems should be understood so that appropriate and effective surveillance methods can be designed. Where veterinary services are limited, basic surveillance can be carried out by community-based animal health workers and animal health auxiliaries, with veterinarian support, and participatory disease surveillance can be used for risk-based purposive disease surveillance.

Understanding the perception of surveillance system stakeholders, through lexical analysis and sample surveys: an example of FMD in Mato Grosso do Sul, Brazil

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The state of Mato Grosso do Sul, in central Brazil, is a major beef exporter and is recognized by the OIE as free from foot-and-mouth disease (FMD) with vaccination. However, the number of notifications in the state is low, making it difficult to assess the sensitivity of the surveillance system. This study aimed at identifying factors that influence the quality and quantity of reports of vesicular diseases in the state, focusing on the perception of stakeholders. The first stage of the methodology included 19 interviews with open questions, targeted at employees of slaughterhouses, state veterinary officers, staff of veterinary retail shops, farmers, small-scale farmers and private veterinarians. The interviews were transcribed and processed through lexical analysis, using the software Alceste. These results guided the development of a questionnaire that was the basis of a sample survey involving four important and representative counties. The lexical analysis revealed that the respondents know the clinical signs of the disease, but tend to ask assistance from third parties before notifying any suspicious event to the veterinary administration. Most of them understand the rapid spread and economic impact of FMD. The sample survey results showed that knowledge about the disease increases with education and training level. There's insufficient knowledge about differential diagnosis. Private veterinarians may have a key role in a reporting a suspect case and should be better integrated into the system. Farmers do not fully recognize their important role as sensors of the surveillance system, as they tend to perceive the process as a pure public good. The use of lexical analysis made it possible to undertake a more focused survey based on preliminary data on stakeholder perceptions. Its application in animal health is novel and should be further explored.

Comparing prevalence estimates from participatory epidemiology to conventional surveys, Kenya

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There is a need to find locally and globally relevant surveillance tools to measure disease prevalence and inform control programs. Traditional veterinary knowledge has a contested role in surveillance systems. We examined participatory epidemiology (PE) surveys for agreement between community perceptions of prevalence of cattle conditions compared to clinical and laboratory results. Community meetings to understand traditional knowledge of endemic disease were convened in randomly selected communities in Western Province, Kenya. Community perceived prevalence for common cattle diseases and five focus conditions (anemia, helminthosis, fascioliasis, trypanosomiasis and theileriosis) was determined using PE tools. Within selected communities, all cattle (>1 month old) were clinically examined and blood and stool specimens collected. Definitive diagnosis was made by clinical findings, microscopy and molecular techniques. Agreement was determined for prevalence obtained from community perceptions compared to laboratory and clinical analysis. To assess the ability of individual farmers to identify ill animals and accurately diagnose disease, the perceived health status from animals on randomly selected farms was obtained by owner interview. A clinical examination was then performed with blood and stool specimens analyzed for a battery of other endemic diseases. Agreement between farmer assessment of health status and diagnosis for selected conditions against results from laboratory and clinical examination was determined. This study highlights the accuracy and limitations of traditional knowledge. The usefulness of PE for preliminary prevalence estimation was demonstrated by the ability of non-pastoralist farmers to estimate herd level prevalence and individual animal health status. The study shows that PE can serve to combine local knowledge inquiry with scientific study at a cost lower than laboratory and clinical surveys.

Evaluation of the social impact of HPAI surveillance network at the community level in Vietnam

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The need to set up efficient and sustainable surveillance networks is a major concern which must be continually placed at the heart of the overall issue of development. In developing countries, the political priority to reduce poverty means that it is vital to include social aspects in public decision making on health management in general. This focus on social aspects can be considered all the more important regarding surveillance as it is deeply embedded in agents' everyday life. The flow of information about animal health involves different non-monetary costs, ensuing from stigmatization or from social pressure to withhold or disclose information. Understanding, measuring and alleviating these social costs of information is required to ensure the effectiveness and viability of surveillance. The present study considers the case of highly pathogenic avian influenza surveillance in Vietnam. It aims at establishing a protocol allowing for understanding and quantifying social costs incurred by surveillance agents at the community level. In this prospect, tools and concepts from anthropology, participative epidemiology and experimental economics were combined. More particularly, social network analysis, participatory observation, companion modeling and stated preference surveys were applied for the thorough examination of constraints and costs of health information flows. The opportunity for the scaling-up of such methodologies and for the inclusion of the so-elicited quantitative values in socio-economic evaluation of surveillance systems are discussed.

Collaborative response to 2010 foot-and-mouth disease outbreak in Miyazaki, Japan between veterinary and psychiatry experts: analyses into mental health of veterinarians, farmers and citizens and barriers against restarting farming

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In April 2010, Foot-and-mouth disease (FMD) outbreak occurred in Miyazaki, Japan. Culling on infected farms could not stop the outbreak and vaccination-to-kill policy was implemented. In total, 290 thousand animals were culled. Miyazaki Prefecture Center for Mental Health and Welfare (MPCMH) conducted mental health monitoring of 1300 FMD-affected farmers using telephone in June 2010 during outbreak. Questionnaires were sent to local citizens and those who participated in culling. In 2011, in order to describe livestock related stress, participatory appraisals were conducted with field veterinarians and farmers. MPCMH conducted the second survey using the questionnaires designed based on the appraisals. The first survey found 20% of farmers had mental health problems and high K6 score was associated with having problems before outbreak. Low public mental health was associated with stagnant local economy. Mental stress for veterinarians was greater than physical stress and the tension and contents of mental stress changed dynamically with outbreak situation. The second survey found that mental stress of farmers was associated with economic problems and physical illness. Local economy and public mental health had not been improved since previous year. Sixty percent of farmers restarted and the obstacle factors against restarting were physical illness, being aged and living in the center of outbreak, and encouraging factors were having participated in helping culling, larger household and being a full-time livestock farmer.

Integration of cattle Fallen Stock data with diagnostic laboratory data to enhance early warning surveillance

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Supplementary datasets can be used to enhance the efficacy and efficiency of early warning surveillance. This work explores the potential to integrate data from cattle (Fallen Stock) with diagnostic laboratory data (FarmFile) to increase the power of detecting emerging disease threats to the livestock industry at little additional cost. The list of diseases/syndromes were harmonised between the datasets by the application of text mining to the reason for death field in Fallen Stock data and then matching the reason for death to diagnoses in FarmFile. The statistical method of Capture-Recapture (CRC) was then applied to the combined dataset to estimate the true prevalence of selected diseases. Over the study period 358,268 deaths were recorded in the Fallen Stock dataset of which 299,099 (83.5%) had a reason for death recorded. There were 2,931 unique reasons for death recorded. Data mining and manual review identified 19 reasons to categorise 239,557 (66.9%) of records. Some Fallen Stock reasons for death could be linked to a specific condition recorded in FarmFile (e.g. hypomagnesaemia). Other reasons for death had to be linked to a syndrome (e.g. lung disease, fog fever, breathing problems, husk and IBR were all allocated to the respiratory syndrome). The use of CRC suggested that the sensitivity of FarmFile to identify infected holdings varies according to the condition. The estimated true prevalence of Johnes was 4-fold higher than the observed FarmFile prevalence and the estimated true prevalence of hypomagnesaemia was 300-fold higher than was observed in FarmFile. The integration of supplementary data greatly increased the number of holdings identified with each condition in the combined dataset compared with FarmFile alone. The importance of considering the quality of available data and the methods to match the datasets will be discussed.

Session 27**Theatre 2****Comparing analytical methods to classify pathogens or bacteria by the analysis of headspace metabolites in milk**

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In this research project the possibilities to predict the presence of pathogens or bacteria in milk samples by using headspace GC-MS are investigated. The purpose is to develop an analytical method by which the presence of the pathogens or bacteria can be accurately predicted by their measured volatile metabolites. A classification method that is commonly used is multinomial logistic regression (MLR). The performance of a probabilistic neural network (PNN) is compared with MLR using two experimental datasets. The first dataset contained 120 samples (40 bacteria, 6 metabolites), the second dataset contained 59 samples (5 pathogens, 19 metabolites). Both datasets were divided in two parts: 2/3 of the data were used to train the method (training set). The remaining 1/3 of the data was used to test how well both methods can classify the presence of specific microorganisms (test set). The MLR-analysis was done in R using the multinom program. The algorithm of the PNN is quite simple to implement, so it was programmed directly in Stata. In the first test set, the MLR-method was able to predict correctly 17 of the 40 samples (43%), the PNN method predicted 23 of the 40 samples correctly (57%). In the second test set, MLR predicted 15 of the 18 (83%) samples correctly, whereas PNN predicted 17 of the 18 (94%) samples correctly. For these two datasets the PNN method proved to be better in predicting pathogens or bacteria by their measured volatile metabolites. Its main drawback is that it is probably more sensitive than other methods for new information that was not contained in the training data. Future work will allow further validation of the PNN method.

Building a model of spread of HPAIV H5N1 in aquatic wild bird populations as a tool for an early warning system

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The spread of HPAIV H5N1 was investigated using an agent-based, stochastic epidemiological model assuming a three-species scenario with intra- and interspecies transmissions in Mallards, Mute Swans and Common Pochards at fixed geographic localities and during migration. Starting with a single-location scenario, each modelling step simulates randomized contacts between individuals of different model compartments (SEIR). Differences in feeding habits and seasonal gregariousness of the three species, environmental factors mediating or facilitating virus spread and all year-round LPAI prevalence with focus on homo- and hetero-subtypic immunity were taken into account. Development and parameterization of the model was only possible by integrating data obtained by ornithologists, virologists and epidemiologists within the frame of the NewFluBird project. The onset of migration was modelled to start in September and involved three locations: a starting, a staging, and a wintering site. Basic assumptions regarding migratory behavior were as follows: Mute Swans were present at all three sites as purely resident/sedentary populations; Mallards undertook a simplified 'stepping-stone' migration with a prolonged stay at a staging site, whereas Pochards reached the wintering grounds in a single movement. Burn-in runs had highlighted parameters to which the model reacted sensitively. Changes in the overall length of the epidemic course, as well as amplitude and time point of maximally infected birds were used as readouts. If scenarios were related to the onset of migration, the chance of migration-capable birds propagating virus and spreading it over larger distances was examined. The results were evaluated to come up with proposals for optimized surveillance strategies.

Systematic review on the existence of integrative information systems for zoonotic disease surveillance

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Introduction Even though 65% of recent major disease outbreaks have zoonotic origins, there is still a sharp division of the disciplines in human and veterinary health. In the last decade, a global integrative concept, often referred to as 'One Health', has been strongly endorsed. In the course of its adoption in Germany, claims were raised to enable a cross-sectoral data interpretation of zoonotic disease information in different epidemiological databases, applying the requirements of secondary data analysis. It is assumed that this will improve the prevention, prediction and control of zoonoses. In this paper the current state of research knowledge and existing projects throughout the world will be identified, appraised and synthesized regarding the integration of data to monitor zoonotic diseases from a One Health perspective. Material and methods A systematic review of existing projects throughout the world was conducted by means of a search in scientific publications and on related websites. Projects found were categorized and described regarding their concepts and realization. Results 107 projects were identified at all. However, only 17 of them combine human and animal health information. These projects either analyse syndromic surveillance information (n=5) or condensed information from experts of different health sectors (n=7) or retrieve information to enable a cross-sectoral data integration with raw or less aggregated data from official sources to describe level and distribution or changes in disease occurrence (n=5). Conclusion There are few examples for integrated disease surveillance projects that connect animal and human health data and allow for the investigation of more than one zoonosis. Their approaches are diverse, so the feasibility of the stated claims in Germany has to be conducted on an individual level and closely fitted to the demands of the different stakeholders.

Syndromic Surveillance based on laboratory test requests in the province of Ontario, Canada

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Modern biosurveillance systems, focusing on early detection, make use of low-specificity disease data aggregated in syndromes, hence the coined term 'syndromic surveillance'. The potential for developing a syndromic surveillance system based on diagnostic test requests to a veterinary laboratory was explored through the Animal Health Laboratory (AHL) in the province of Ontario (Canada), using data from laboratory test orders for diagnoses in cattle. Three years of historical data were analysed and grouped into 16 syndromes. One year of data was evaluated prospectively, in order to determine the best combinations of algorithms to deal with a strong day-of-week effect and detect temporal aberrations. Weekly differencing was the most efficient method for removing the day-of-week effect. Control charts were applied to residuals, and exponentially weighted moving averages (EWMA) and Shewhart charts showed potential to perform well if used complementarily. Holt-Winter smoothing using weekly periods showed high sensitivity. Detection using this method is based on modelling the data, making a 5-day-ahead prediction, and using the confidence interval of the prediction as the threshold of detection. Sensitivity, specificity and detection day values are needed in order to identify the settings for each algorithm that provide the optimum sensitivity while avoiding a large number of false alarms. Additionally, the use of these detection algorithms in series or parallel should be investigated. In order to achieve this, 100 years of synthetic data with controlled injection of outbreaks of different shapes and magnitudes have been simulated. Results will be presented and discussed at the conference.

Modelling the spread of avian influenza A (H5N1) virus through the network of northern Vietnamese live bird markets: implications for surveillance and control

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Highly pathogenic avian influenza virus subtype H5N1 (HPAIV H5N1) is endemic in South-East Asia, with live bird trade as a major pathway for disease transmission. A cross-sectional survey was undertaken in northern Vietnam to investigate the structure of the live bird market (LBM) contact network, and the implications on the spread of HPAIV H5N1. A total of 567 traders were interviewed. Based on the movement of those traders between LBMs, weighted and directed static networks were constructed. The northern Vietnamese network incorporated 162 LBMs, of which 83% were encompassed in a giant strong component. Two provincial-level networks were also constructed. The removal of a small number of hubs (1-3 hubs, depending on the network) dramatically disconnected each network. A stochastic individual-based model was used to simulate the spread of HPAIV H5N1 through one of the provincial-level LBM networks. Degree appeared to be a good predictor of LBM infectiousness and susceptibility. LBMs exhibiting high susceptibility or infectiousness were always the same, regardless of transmission rate. This suggests that LBMs suitable for surveillance and control interventions could be effectively targeted without prior knowledge of the force of infection, which requires laboratory-confirmed surveillance. By targeting thorough, daily disinfection of LBMs and traders' vehicles and equipment to only the small number of markets acting as network hubs, the epidemic size was reduced by 80%. Disease spread within the network could therefore be effectively contained. These findings are of particular relevance to resource-scarce settings with extensively developed LBM systems, commonly found in South-East Asia.

Alternative scan-based approaches to identify clusters of HPAI H5N1 cases among Tufted Ducks and other wild bird species found dead in Denmark and Sweden in 2006

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The objective of this study was to demonstrate the effects of alternative model choice and parameterizations in the detection of space-time clusters of HPAIV H5N1 cases reported among wild birds in Denmark and Sweden in 2006. Data included 1,469 records (109 cases/1,360 controls) collected between February and June by passive surveillance of dead wild birds. Laboratory diagnoses were obtained by PCR methods and/or virus isolation. Tufted Ducks were particularly frequent among the wild bird species affected in Denmark and Sweden during this epidemic, and Tufted Duck species (62 cases/57 controls) vs. other wild bird species (47 cases/1,303 controls) was considered in the analysis as a potential risk indicator. Bernoulli and permutation scan statistics models were performed to compare the impact of the probability model choice on the cluster detection. Bernoulli and permutation scan analyses detected significant ($P < 0.01$) multiple clusters with similar locations, but with certain differences in their number and size. The observed-to-expected case ratios in the clusters detected by the Bernoulli scan model after stratification by species, were substantially heterogeneous, suggesting effect modification. However, the permutation model didn't detect the effect modification of species on clustering of cases. Bernoulli model results suggest that the clustering was partly related to the heterogeneous collection of samples and the uneven distribution of the bird species in space and time. Scan-based models are commonly used for the identification of clusters of disease, and this study provided useful insights into the impact of analytical model choice and parameterizations for the identification of high-risk areas for infectious animal disease surveillance.

Informal pig movements across eastern Indonesia: risk for classical swine fever transmission

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Classical swine fever (CSF), a highly contagious Pestivirus has caused substantial socio-economic loss for pig farmers in Indonesia since introduction in 1994. Live pig movements are believed to have facilitated CSF introduction into Nusa Tenggara Timur province (NTT), in eastern Indonesia. This province has the largest pig population with 85% of households owning at least one pig. Pigs have high cultural and economic importance being used for financial security and traditional ceremonies. The number of reported CSF cases in NTT is still increasing with newly infected islands as recent as 2011. To investigate informal movement of pigs, a survey of smallholder pig farmers was conducted on West Timor, Flores and Sumba islands from March to April 2010. Using multi-stage sampling, 18 villages were selected across the three islands and 289 pig farmers interviewed. Information on trading practices, source and destination locations and pig volumes being moved was obtained to conduct a Social Network Analysis (SNA). Over half of farmers (55%) moved pigs informally, most commonly during August to October. Inter and intra island movement was detected. West Timor had a highly connected network with pigs moving across Timor Island reaching the border with East Timor. Flores and Sumba islands had fragmented networks with localised movement influenced by terrain. Rindi Village in Sumba represented a high risk location for CSF spread with the greatest exiting pig volume (78 pigs) from 2009-2010. Nanbaun Delha Village in West Timor was a high risk location for CSF introduction with external contact from 13 other villages. SNA was used to identify high risk movement pathways and locations to inform decision making for policy development to control CSF in eastern Indonesia.

A Bayesian approach to evaluate effectiveness of Gudair™ vaccine by combining information from multiple diagnostic tests

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Vaccination has been used as a major component of the control program since the registration of Gudair™ vaccine in 2002. This study was conducted to evaluate the effectiveness of vaccine in decreasing the prevalence of shedding of Mycobacteria in flocks of varying initial prevalence. We enrolled 38 flocks in the study that had been tested prior to or at commencement of vaccination with either pooled faecal culture test (PFC), agar gel immunodiffusion test (AGID), or both. These pre-vaccination test results were used to estimate pre-vaccination prevalence. Post-vaccination prevalence was estimated from culture of pooled faecal samples (usually 7 pools of 50 sheep from each flock) collected from the enrolled flocks in 2008-2009, approximately five or more years after commencement of vaccination. A Bayesian approach was used to estimate and compare the pre- and post-vaccination true prevalences. Apparent prevalences for flocks were modelled as functions of the true prevalences and the sensitivities and specificities of the respective diagnostic tests used. The modelling resulted in a likelihood function contribution that tied together the contributions from flocks tested with different tests. Of the 38 flocks enrolled in the study, 7 were apparently not shedding post-vaccination suggesting that 31/38 (81%) flocks were still shedding five or more years after commencement of vaccination. Bayesian modelling estimated a significant decline in OJD prevalence from a pre-vaccination median prevalence of 2.99% (95% Probability Intervals (PI): 1.50, 7.92%) to a post-vaccination median prevalence of 0.74% (95% PI: 0.42, 1.29%). The results suggest that vaccination with Gudair™ is effective in reducing shedding but as the response to vaccination is variable between flocks, use of vaccination for longer than 5 years is advisable for the majority of infected flocks.

Session 28**Theatre 1****The broken food chain information: cross border issues of risk-based meat inspection in the pig sector in Germany and the Netherlands**

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European food safety legislation allows for a new type of meat inspection in swine. This 'risk-based meat inspection without incision' or 'supply chain meat inspection' (SCMI) uses food chain information to derive a veterinary prognosis on the pigs' health prior to delivery to the slaughterhouse and allows for visual inspection of pig carcasses. Slaughter companies who want to implement SCMI must develop their risk-based system and have it approved by the competent authority. In the Dutch-German border region, slaughter companies implementing SCMI and suppliers delivering pigs in such a system have to consider the prerequisites of a number of competent authorities. In turn competent authorities have to cope with the special conditions and requirements of a cross border economic region. Within the INTERREG-IV-A project SAFEGUARD issues were addressed that arise from the conduct of SCMI in a cross border context. The main objective was to elaborate an up-to-date comparison between Germany and the Netherlands. We used an iterative approach of collecting information from project partners, external experts and scientific literature and providing feedback to the project group during a number of meetings and workshops. We discovered, among others, important differences in 'involvement of private parties', 'data exchange and communication' and 'use of epidemiological data'. We conclude that the existence of SCMI systems using different 'epidemiological data' from the holding is a barrier to inter-company acceptance of finishing pigs for slaughter. Further, current systems of data exchange fail to give a complete picture of a farm's health if farms switch deliveries between slaughterhouses. We suggest, that data exchange of food chain information and meat inspection results should be reorganized and harmonized. Further research is needed to assess economic consequences of these issues.

Traffic lights and dash boards: graphical presentation of abattoir data

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The regulatory oversight of abattoirs, boning rooms and freezers is essential to ensure safe food production. Until recently, auditors from the competent authority would pass or fail the plants based on a mixture of objective and subjective criteria. Frequently, these audit outcomes were poor predictors of food safety outcomes, for instance, microbiological contamination of product. A more modern approach has been developed by the Department of Agriculture, Fisheries and Forestry (DAFF Biosecurity, formerly AQIS). Called the Product Hygiene Index (PHI), the process results in the collection of a large data set of objective measures relating to carcass microbiology levels, pre-operation sanitation and presence of pathogens and indicator organisms on meat. First showcased at ISVEE XII in Durban, new software has now been developed which provides industry managers and regulators, a visual display which highlights aspects of the production system requiring attention through the use of coloured lights (traffic lights) and digital representation of trends and analysed data. Importantly, an individual plant's performance is compared to national averages to benchmark them against each of the approximately 20 components of the Product Hygiene Index. The Index is the major factor in determining Performance Based Auditing Frequency and provides a trigger for regulatory action against a company, where necessary. The theatre presentation will describe the components of the PHI and demonstrate the new graphical displays and outputs.

Assessment of differences in the risk to public health, animal health and animal welfare after potential modification of organ inspection at slaughter

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A public debate on the revision of meat inspection (MI) is ongoing in Europe. The question to science is whether changes to current MI practice will result in risk differences to public health (PH), animal health (AH) and also animal welfare (AW). The aim of this project was to qualitatively assess the risk to PH, AH and AW derived from potential changes to the inspection practices of green offal (GO; stomachs, intestines and mesentery). We applied the Codex Alimentarius framework to a selection of hazards: *Mycobacterium bovis* and *Mycobacterium avium* subsp. *paratuberculosis* (in bovines), toxoplasmosis (in sheep), classical swine fever, *Salmonella*, hernia and tail bites (in pigs). A risk pathway mapping the steps from lairage to chilling of the carcass was developed. For each hazard, the risk associated with three different inspection scenarios was considered: (1) traditional inspection; (2) only visual inspection; and (3) total absence of GO inspection. The capacity of each MI task to reduce the hazard in the carcass was assessed by combining three probabilities: presence of macroscopic lesions, their detection and setting corrective actions. The likelihood of a hazard being present in a carcass at chilling was used to measure the risk and compare scenarios. The risk assessment for the three scenarios showed that for the studied hazards the contribution of GO inspection was of limited value. Lesions associated with these hazards are seldom manifested in GO alone. Even if GO inspection is removed, the lesions indicative of these hazards could still be detected, with high probability, by other current MI tasks. Therefore, a modification of the GO inspection would not result in a substantial change in the risk to PH, AH and AW. However, GO inspection can still provide valuable information with regard to the prevention of AH and AW related hazards.

Estimation of surveillance system sensitivity for bovine tuberculosis in Denmark

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Denmark is officially recognised as free from bovine tuberculosis (bTB) since 1980. The Danish surveillance programme consists of *post-mortem* examinations of all slaughtered cattle and pigs (livestock) as well as tuberculin tests of exported livestock. Documentation of free status is important to ensure trade in livestock and meat. However, surveillance programmes are costly and not always that effective. The aim was to identify more cost-effective surveillance programmes for bTB. First, we evaluated the sensitivity of the current surveillance system for bTB in Denmark. Next, we simulated the effect of potential changes in the different surveillance system components on their respective sensitivities (SSCSe). The sensitivity was defined as the probability of detecting at least one infected animal with bTB at a design prevalence of 0.1%. Different scenario trees were developed to evaluate each component of the current surveillance system, namely testing imported or exported livestock, and meat inspection of livestock. The population of slaughtered livestock was divided into high-risk and low-risk groups according to the following risk factors: herd type, imports from countries not free from bTB, wildlife, animal movement rate and performance of the skin-test. The SSCSe was higher at the abattoir due to larger sample sizes for this component. However, its efficiency depends on the visual inspection sensitivity during meat inspection, which can vary greatly. Under freedom from disease status it can be assumed that import of infected cattle or pigs constitute the largest risk for re-introduction of bTB in Denmark. bTB has never been found in Danish free-ranging wildlife, making wildlife contact less important. The results of this study are relevant for the surveillance system improvement and modernisation of meat inspection currently being discussed in the EU.

Session 28**Theatre 5****A risk assessment for visual only meat inspection of both indoor and outdoor pigs within the UK**

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This project was commissioned by the UK Food Standards Agency in the context of its programme of work to modernise meat hygiene inspection. One specific example of modifying traditional inspection techniques to represent a more cost-effective approach to meat inspection is the allowance in EC Regulation 854/2004 for visual-only inspection of pigs that have been reared under controlled housing conditions since weaning. However, the definition of ‘controlled housing’ excludes outdoor pig production, hence so far UK abattoirs have yet to introduce visual-only meat inspection because of the UK having a large outdoor pig herd. We have therefore conducted a qualitative risk assessment to assess the risks to public/animal health from allowing visual-only inspection of both indoor and outdoor pigs. In order for visual-only inspection to be of higher risk to public or animal health than traditional meat inspection, the sensitivity of detection of a hazard must significantly decrease. In addition, in order for outdoor pigs to pose a greater risk than indoor pigs, the hazard must be more prevalent in the former than the latter. From a large number of hazards originally identified as worthy of investigation, only two (TB and endocarditis) were considered to be of public/animal health risk and would be less likely to be spotted through visual-only inspection. It was determined from the UK’s national meat inspection database that prevalence of TB in outdoor pigs was higher than in indoor pigs; however, endocarditis prevalence was higher in indoor pigs than outdoor pigs. Despite higher rates of TB in outdoor pigs, there was no discernable risk to public or animal health from TB-infected pigs. It was therefore concluded that visual-only inspection of both indoor and outdoor pigs in the UK posed a negligible risk to public or animal health.

Teaching statistical topics in the veterinary curriculum: what do our peers expect?

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Given the conceptual mindset of veterinary students, teaching statistical concepts to these individuals is often (seen as) a challenge. In consequence there is an ongoing debate about the best time, approach and content to teach in our statistics classes, and various faculties worldwide have established their own models. During a workshop meeting of biostatistics lecturers of the Austrian (1), German (5) and Swiss (2) veterinary schools the (additional) question was raised whether the topics that we teach in the statistics classes are of sufficient relevance to our lecturing colleagues, i.e. if our peers have certain expectations or needs what the students should know about biostatistics before entering their classes. In fall of 2011 an online survey was developed and implemented at all eight vet schools to address this issue. Over 250 lecturers (70% between 40 and 60 years of age) from the eight schools and all disciplines responded. Over 50% indicated that statistical concepts should be taught early (1st or 2nd year); for epidemiological concepts that proportion was smaller (27%). There were clear differences in perceived relevance of the 44 subtopics presented in the survey, assessed on a score from 0 (no relevance for own lecture) to 4 (very high relevance) with an overall median and mode of 1 (low relevance). Further details including possible associations with discipline of the responding colleagues and consequences on the topics we should teach in the statistics classes will be presented during the conference.

Training of veterinarians to work for government veterinary services in Europe: needs and current gaps

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A workshop was conducted to identify and discuss day-one competencies for veterinarians working for government veterinary services in Europe. The aim was to list requirements from the employer perspective and to compare the result with the current veterinary undergraduate curriculum. While veterinary education is expected to provide the basics in most of the employer-identified competencies, experience and continuing professional development or post-graduate training were seen to be essential to provide competencies at advanced level. When considering the competencies of current veterinary graduates, key gaps were identified primarily in the area of communication, but also in some technical fields such as risk analysis, impact assessment, common agricultural policy, international affairs, health economics, contingency planning and inspection/audits. While some veterinary schools are including some of these topics in their teaching, it is not currently required nor rewarded when they are audited within the European quality assurance framework governed by the European Association of Establishments in Veterinary Education. The outcomes of this workshop indicated a need to revise the current standards for veterinary undergraduate education. The introduction of electives or tracking options for students pursuing careers in veterinary services is desirable. Courses leading to post-graduate qualification and specialisation, including certificates and diplomas for veterinary officers contribute to the current training needs. Workshop participants also emphasised the importance of identifying future needs for successful management of challenges expected in the coming 10-15 years and to regularly update the undergraduate curriculum accordingly.

The global burden of congenital toxoplasmosis

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Toxoplasmosis is an important food-borne zoonosis and is a hazard to pregnant women. Primary infection during pregnancy can cause considerable harm to the developing foetus. The World Health Organization is coordinating an initiative to estimate the global burden of food-borne diseases. Toxoplasmosis is recognized as an important global food-borne pathogen. The burden of congenital toxoplasmosis (CT) is an essential part of the process of estimating the global burden of food-borne toxoplasmosis. A number of systematic reviews identified the best evidence for the incidence of CT for each country. Available data varied from country to country and hence a variety of techniques were used. These including estimates based on the numbers of actual cases where reporting systems were in place. Alternatively, the numbers of cases were estimated from cross sectional survey of new born infants who were sero-positive to toxoplasma specific IgM. Finally modeling techniques were used which utilized the incidence of specific Toxoplasma-IgM seroconversion of women during pregnancy or the increase in sero-prevalence with age. The latter technique can be used to calculate the risk of exposure during pregnancy of women of child bearing age. Whatever technique was used appropriate adjustments were made for the diagnostic accuracy of the tests used and stochastic techniques were used to model uncertainty which was dependent on the data quality. Estimates of the burden of CT in terms of Disability Adjusted Life Years (DALYs) were made based on appropriate disability weights for the syndromes associated with CT. The results suggest that globally there are approximately 193,500 infants born annually with CT. Globally the incidence is approximately 1.5 cases of CT per 1000 births resulting in a global burden of approximately 1.45 million DALYs annually

Spatial distribution of *Toxoplasma gondii* in animal populations and soil

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Toxoplasma gondii causes one of the most common zoonoses in the world. People may get infected either through meat containing tissue cysts or by oocysts after direct or indirect contact with contaminated soil. In order to estimate the relative role of each route, it is necessary to understand the distribution of oocysts in the natural environment. This aspect is poorly known due to the lack of sensitive detection methods. Here, our aim was to analyze the spatial distribution of the parasite in the populations of definitive hosts (cats), intermediate hosts (rodents) and in the soil simultaneously, using a recent sensitive method to detect *T. gondii* oocysts, based on concentration and quantitative PCR. We focused on a rural area of 1.5 km² in a French village in Ardennes. Demographic and epidemiological surveys of cats (114 captures since 2008) and rodents (357 captures since 2010) were performed. In 2011, one at random soil sampling was performed (244 soil samples) in a stratified scheme considering distance from the village center, presence of cats and soil nature. Preliminary results showed that seroprevalence was 56.4% in cats, 8% in rodents and 8% in soils. Spatial analyses allowed us to map the soil contamination and to study its relationships with soil characteristics, with the presence and infection status of intermediate and definitive hosts. Environmental contamination was both largely distributed (not restricted to the center of the village) and locally spatially clustered. The relationships with contamination of rodents and cats will be detailed. By improving our understanding of the spatial dynamics of oocysts, these results will provide elements to estimate the risk of human contamination associated with oocysts and to design preventive measures against toxoplasmosis.

An agent-based model to optimize the mitigation of a contagious animal disease

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When a contagious animal disease is introduced into a country, it is important to mitigate the spread of the disease. Often studies analyse mitigation in a setting where the optimal policy is implemented as desired by the society. However, many decisions to combat disease are taken by individual producers, without government being able to control for their decisions. It is therefore important to provide producers with private economic incentives such that they choose mitigation actions that benefit society too. The problem has spatial and time dimensions, because the optimal disease control is likely to depend on geographical proximity of disease, economic links between farms, and time elapsed after introducing the disease into a naïve population. Previous literature has not addressed time-space interaction in animal disease control, particularly when mitigation effectiveness is a function of decisions made by individual producers. This paper develops a stochastic simulation model that takes into account space and time dimensions to support policy design and resource allocation in response to a disease outbreak. The main elements of the model are: (1) a social objective function to maximise economic welfare for the society; (2) a set of policies to mitigate the disease; (3) a network of farms where the disease can spread over time; (4) a connectivity matrix defining the probability of a farm in the network to become infected at a certain time period conditional on which other farms are already infected; (5) private objective functions used to solve for how economic incentives provided to different livestock producers affect their choice of mitigation policy; and (6) a payment scheme to reward producers choosing a policy preferred by society. Simulated disease outbreak in Finland is used as a case study. The results suggest that the potential to mitigate disease spread through incentive policy depends on both the characteristics of the disease and important space-time dimensions.

An epidemiological and economic framework for evaluating the tangible and intangible impacts of emergency animal disease outbreaks

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The economics of emergency animal disease outbreak response is impacted by a range of factors, such as the likelihood of an event occurring, species affected, frequency and distribution of disease incursions, transmission cycles, host interactions and climatic anomalies. Whilst empirically focussed economic evaluation tools for analysis and evaluation of control and prevention options are in frequent use, insights can be gained from an expanded framework that incorporates value-drivers used to justify decisions. The framework is built around an extrapolated cost-benefit analysis (CBA) that incorporates tangible and intangible elements. Primary steps involve risk analysis to ascertain the magnitude, priority and impact of the potential emergency situation. The framework also allows the operator to value-add to the CBA by incorporating non-commercial intangibles (such as environment, human health and animal welfare) using a series of value multipliers. These are essentially an averaged preference for a nominated approach or intervention along a scale of potential value placements using an axiological methodology. The outcome of the framework represents a holistically adjusted parametric. Potential uses of these outcomes could include (but are not limited to): (1) development of new policy for emergency animal diseases in peace time (Preparedness phase); (2) during consultative processes where multiple perspectives and values must be identified and considered: (1) for economic (tangible and intangible) justification of adjustments to response policy during an exotic animal disease (control phase); (2) for comparing and contrasting the economic (tangible and intangible) consequences of a particular control or prevention policy. A case study using Hendra Virus will be given.

Quantitative estimation of economical losses consecutive to the 2006-2007 Bluetongue epidemics in Wallonia

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Since the summer of 2006, Central and Northern Europe faced the emergence of bluetongue (BT) in domestic ruminants and characterized by an unusual clinical picture in cattle. The disease BT spread rapidly and clinical signs of BT caused a serious concern among cattle and sheep holders, particularly because of a high incidence of reproductive disorders reported since the autumn of 2007. Consequently, BT induced major economical losses in both cattle and sheep industries. The economical consequences of BT were quantitatively estimated in Southern Belgium, on one hand, by mean of transversal epidemiological investigations submitted to ruminant holders and veterinarians and on the other hand, by identifying and interconnecting different databases compiling technical and economical information. The results of this study are representative of both bovine and ovine sectors of Wallonia. Two approaches were performed to estimate economical losses: a deterministic method (based on the mean of losses) and a probabilistic approach (taking into account the distributions of values obtained for each parameter involved in the estimation of losses). The mean technical and economical losses in Wallonia reached 32.3 million € ('mean' hypothesis based on the veterinary inquiry) and 104.8 million € ('high' hypothesis, based on investigations performed among cattle and sheep holders). Various elements compiled in the technical and economical databases validated the study. The main losses were related to reproductive disorders. Nevertheless, these losses should be re-assessed because their estimation might have been performed too early after the emergence of BT. Indeed, losses were estimated before the results of the reproduction season were known and should then be re-evaluated as they did not take into account this major post.

Impact of regulatory perturbations to disease spread through cattle movements in Great Britain

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During the past decade the British livestock industry has suffered from several major pathogen outbreaks, and a variety of regulatory and disease control measures have been applied to the movement of livestock with the express aim of mitigating the spread of infection. The Rapid Analysis and Detection of Animal-related Risks (RADAR) project, which has been collecting data on the movement of cattle since 1998, provides a relatively comprehensive record of how these policies have influenced the movement of cattle between animal holdings, markets, and slaughterhouses in Britain. Many previous studies have focused on the properties of the network that can be derived from these movements – treating farms as nodes and movements as directed (and potentially weighted) edges in the network. However, of far greater importance is how these policy changes have influenced the potential spread of infectious diseases. Here we use a stochastic fully individual-based model of cattle in Britain to assess how the epidemic potential has varied from 2000 to 2009 as the pattern of movements has changed in response to legislation and market forces. Our simulations show that the majority of policy changes lead to significant decreases in the epidemic potential (measured in multiple ways), but that this potential then increases through time as cattle farmers modify their behaviour in response. Our results suggest that the cattle industry is likely to experience boom-bust dynamics, with the actions that farmers take during epidemic-free periods to maximise their profitability likely to increase the potential for large-scale epidemics to occur.

Small-scale pig farmers' behaviour, silent release of African swine fever and consequences for persistence

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African swine fever (ASF) is present in most of Sub Saharan Africa, Sardinia, Transcaucasia and Russia. Most outbreaks affect backyard and small-scale farms (SSF), and transmission between farms involves movements of infected pigs or products. Field studies show that in case of a suspected outbreak, farmers often sell pigs with clinical signs for slaughter and pigs without signs to traders. ASF's incubation and latent periods and farmers' imperfect clinical diagnosis (sensitivity [Se] and specificity [Sp], time to detection and sale of animals [t]) facilitate the risk of selling infected pigs without detected signs to traders. This study aimed at estimating the probability that SSF release ASF infected pigs without detected signs via emergency sale and the impact of improving farmers' diagnosis. A stochastic, individual-based, discrete time, state-transition model simulating ASF spread within SSF and emergency sale was developed in R. The model was parameterised using results from field surveys in Africa and the literature. The probability of releasing infected pigs without detected signs (Pr), the proportion of the herd released and the effect of t, Se and Sp were assessed for SFF of different sizes. For SSF of 10 pigs and more, t, Se and Sp of farmers' clinical diagnosis have little effect on Pr, which remained high under all scenarios (from Pr=0.33 [n=10, t=35, Se=0.9, Sp=0.75] to Pr=0.93 [n=30, t=25, Se=0.75, Sp=0.9]). Although very small herds (n<10) constitute the majority of herds in affected regions, larger SFF (10<n<100) contributed proportionally more to ASF persistence via emergency sale. Improving farmers' diagnostic accuracy is not an effective mitigation strategy as it does not significantly reduce the release of ASF infected animals via emergency sale. Alternative control measures involving other stakeholders need to be explored, such as market-based or certification approaches.

Incentives for earlier disclosure by outbreaks of epidemics

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Early disclosure of livestock epidemics is an essential determinant for the epidemic size and its financial consequences for economies at different levels. Depending on indemnity payments and the magnitude of regulatory costs of disclosure, the farmer may have an incentive to withhold the information on possibly infected animals if the farmer expects to be worse off after disclosure. The study examines the impact of incentives on the farmers' disclosure decision, for a Dutch case in the context of Classical Swine Fever (CSF). The disclosure decision is formulated as a stochastic discrete time and discrete state finite horizon dynamic programming model, accounting for farmers perceptions of infection probabilities and a within-herd transmission. The model is run for scenarios with alternative sets of incentive parameters, represented by the proportion of public compensation for categories of animals, testing costs and quarantine costs. Per scenario, 100 replications are done. Results yield the optimal (least-cost for the farmer) strategy on disclosure timing of a CSF suspicion. In the base scenario (no compensation for dead animals; 50% compensation for diseased animals; no compensation for regulatory costs of disclosure), the optimal strategy for the farmer is to report a CSF suspicion in 3.72 weeks (after incubation period), with expected costs of €4,786. A big difference among replications shows that within-herd spread greatly affects the disclosure timing. Extra compensations for testing and quarantine costs, next to the base scenario, do not always result in notably earlier disclosure; 3.48; 3.52; 3.68 weeks in some analyzed scenarios. Penalties for dead animals is not an effective incentive policy, since the number of dead animals is rather small compared to diseased animals with specific clinical signs. Discarding compensation for (specific) clinical cases combined with compensation of regulatory costs of disclosure is the most effective policy, resulting in reporting period of 2.68 weeks.

Emergency vaccination against CSF and real animal health alternatives

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Very effective strategies exist to combat infectious diseases like Classical Swine Fever in industrial livestock areas (e.g. EU Directives). Drastic approaches, e.g. pre-emptive depletion of around detected outbreaks, however, experience doubtful publicity whenever they were applied. These concerns address the ethic perspective as well as unrelated consequences like welfare destruction of animals under movement restrictions. The issue is considered recently on the European level and we provide a model-based assessment of strategy alternatives to control CSF outbreaks. The hot-spot discussion covers different limited emergency vaccination protocols as substitute of pre-emptive destruction. We present the proposed vaccination alternatives considering vaccine concepts and pig farm types. We compare the outcome of simulations that represent the spread of the infection and the changing details of control application in a large-scale livestock area. We confirm emergency vaccination as option to substitute destruction measures in the vicinity of outbreaks. However, although emergency vaccination may be the matter of debate our simulations revealed that aspects of the control application – which do not limit the focus on the local neighbourhood of outbreaks – would help much further in providing an ethically and economically sustainable CSF management strategy. We present a comparative evaluation of ‘free-testing’ (adapted from the Belgian model) in relation to control success, control effort and accompanying losses. Finally, the improved understanding allows the manipulation of movement restrictions beyond what is currently legislated with a through breaking improvement of whole strategy outcome. We integrate the proposed activities into the socio-economically motivated debate on the practicality of alternative approaches.

Heterogeneity in animal contact networks: its measurement, modelling and consequences

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Contact networks between animals or groups of animals are typically modelled using a static structure. They are either modelled using simple summaries of the data, such as proportion of time spent in contact or numbers of animals sold or they are modelled using the details of a single observation of the network, possibly made over a period of time. Such approaches suffer because they neither consider the dynamic nature of the network, nor the randomness inherent in contacts. Furthermore they are specific to the data observed, and therefore may give erroneous inferences if used to predict future events. Although the static approach does allow comparison of networks, it only allows us to say whether the declared networks are the same or different: in the absence of an error structure, we can not quantify the statistical significance of differences relative to random variability. We have developed a stochastic framework to examine contact networks, fitting probability distributions independently to different random variables defining the network. For example, inter-contact times and contact durations between individuals within a group can each be described using gamma distributions. Fitting these distributions using two generalised linear models also allows us to incorporate covariates into the models. This approach results in a complete description of the network that can be used both to make robust predictions and to compare networks in a statistically meaningful manner. We have used this approach to demonstrate the effect of heterogeneity in contacts on the spread of disease. The model predicts that an assumption of homogeneity of contacts across all pairs of animals will lead to inaccuracies in the estimation of the basic reproductive ratio R_0 . We have also demonstrated statistically significant differences in the contact network of a group of animals before and after the introduction of an unfamiliar animal.

Multi-level survival analysis in practice

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The inclusion of random effects (frailties) in survival analysis has become a standard approach to account for hierarchical, or multi-level, data structures. It is however less common to include other components of multi-levels models, namely random regression coefficients (also called random slopes) and contextual effects. This may be due both to the computational complexity of the former and to the scarcity of datasets that support such modelling. We use a previously published analysis of data on lameness in piglets, with sows clustered in herds, to illustrate the additional insights that may be obtained from a full multi-level survival analysis based on the Cox proportional hazards model, and how such insights may substantially affect study conclusions. Our analysis includes a simulation study to compare the performance of four estimation approaches for Cox models with correlated frailties available in standard software, with ensuing recommendations for choice of analytical approach and software. As a second example we consider mortality data from a recent aquaculture field vaccine trial carried out with individually tagged fish in multiple cages each comprising multiple vaccine groups simultaneously (2). We discuss the challenges of a full multi-level survival analysis to account for cage-level variations in vaccine effects within a hierarchy with sparse replication at the upper (cage) level.

Session 32**Theatre 3****Modeling hierarchical interval censored time to intra-mammary infection data through Gibbs sampling**

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Time to infection data are commonly interval-censored in observational studies, and at the same time hierarchically organized: the event time of an udder quarter is clustered within a cow, and the cows are clustered within farms. No standard procedures exist to analyze such hierarchical interval-censored survival data. Furthermore, the low number of events (less than 5%) seems to be problematic when using the few available frequentist methods. We use Gibbs sampling based on the conditional distributions to investigate risk-factors for intramammary infections occurring at different hierarchical levels. Risk factors were considered statistically significant if the 95% Bayesian credible intervals for the hazard ratios excluded 1. The risk-factors which were significant in the uni-variable model were introduced in a forward stepwise selection procedure to produce the final model. A small simulation study was performed to validate the proposed Bayesian method. Overall, the Bayesian approach performed well with a coverage of at least 95%. Only in cases with a very low number of events the coverage decreases.

Modelling the temporal dynamics of Bovine Digital Dermatitis (BDD) using longitudinal diagnostic data and latent infection status

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Bovine digital dermatitis is a contagious epidermitis which is a leading cause of lameness in dairy cattle. Foot inspection for the typical lesions has limited diagnostic sensitivity and is prone to observer bias. Serology is a potentially more sensitive indicator of infection. Given the complex nature of BDD, we previously differentiated between a latent infection status and an observable disease status, where the latter was determined by foot inspection. We then used data from a cross-sectional study to develop a Bayesian model to estimate each individual's probability of infection, incorporating serology outcomes as well as observed lesion status and covariate data (foot hygiene score and age). We extend this work to investigate the temporal dynamics of infection. In a longitudinal study, cohorts of calves, heifers and cows (n=128) were sampled over a 22-month period during 2004-2005. At each visit, foot inspection, blood sampling and animal hygiene scoring were carried out. Serum samples were analysed by ELISA. We first modelled the latent infection status of individuals conditional on previous infection status and covariate information. We then jointly modelled the sequence of serology outcomes and lesion status conditional on this infection status and covariate information. This joint model allows the predictive probabilities of infection for each individual to be estimated at any observation time; it incorporates the fact that each individual has its own baseline serology score, and an individual-specific reaction to infection. The model outputs showed a seasonal effect on the probability of lesions for infected cows, and provided some evidence for a protective age effect, where older animals may develop resistance after repeated exposure.

Zero inflated datasets in epidemiological studies: comparing statistical test procedures: an application in tick counting in South Africa

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Data with clumping at zero frequently occur in veterinary applications. This is e.g. the case, if the occurrence of rare species is studied. Here, often a large number of locations without these species are identified, beside a small number of locations where a few counts occur. Therefore such datasets are characterized by high accumulations of zero observations in a distribution of continuous nonnegative responses. Comparing two samples with continuous nonnegative scores and substantial proportions scoring zero, presents problems in using conventional test procedures because the large number of ties leads to a distortion of the data and thus, to false test results. Even data transformations do not diminish this problem. Specific test procedures have been developed for comparing samples with data clumping at zero. In this project the power of two specialised methods was compared with three conventional statistical tests. The former includes the two-part model of Lachenbruch, 2001, and the modified Wilcoxon test introduced by Hallstrom, 2009 and the latter the application of the t-test, the Wilcoxon rank-sum test and the permutation test. Practical validation was achieved through the analysis of tick occurrence in the Eastern Cape Province in South Africa as well as performing a simulation study. For the simulations we generated 27,000 samples by producing data with zero inflation and varying the distribution parameters. It was found that the conventional t-test often presented higher power than the two-part model and the modified Wilcoxon test, especially for data with more than 60% zero observations. If the proportion of zeros counted less than 40% the modified Wilcoxon test also worked satisfactory. As a general finding the two-part model was superior to all others for data from several underlying distributions studied here.

Estimating the population impact of four pathogens on abortion rates in beef cattle using a matched case-control design

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Reproductive loss from conception to weaning in pastoral beef breeding herds in New Zealand was estimated to be 10%. This study attempted to quantify foetal loss attributable to four highly endemic pathogens, *Neospora caninum* (Nc), bovine viral diarrhoea virus (BVD), *Leptospira borgpetersenii* serovar Hardjo (Lh) and *Leptospira interrogans* serovar Pomona (Lp). In a matched case-control study, heifers/cows that aborted (cases) or calved normally (controls) were sampled from the same herd. Serum antibodies to Nc and BVD were detected by ELISA, and to Lh and Lp by the microscopic agglutination test. Multivariable, conditional logistic regression was used to generate adjusted odds ratios (aOR) for pregnancy loss at various titre cutoffs. The fraction of cases in the population (PAF) attributable to an increased titre was estimated using the proportions of exposed cases and the aOR. Between 2 and 12 aborting cows (cases) were identified and sampled in each of 45 herds. At least 1 and up to 20 controls per case were sampled in each herd. Based on 379 cases and 435 controls, significant aORs were found for Nc (aOR=3.6), Lh (aOR=1.9), Lp (aOR=11.1), and marginally significant for BVD (aOR=2.0). The PAF (95% confidence interval) for Nc was 3.0% (0.8-5.4%), for Lh was 4.9% (0.6-9.0%), for Lp was 4.2% (1.5-6.8%) and for BVD was 3.4% (0.1-6.6%). A possible bias by misclassification of a case will be discussed. If present, such a bias was regarded as being independent of the classification of exposure, thus potentially causing an underestimate of the true effect. We conclude that at least 14% abortions in the population could be prevented by controlling for Nc, BVD, Lh and Lh in beef cattle herds.

Epidemiological evaluation of air filtration in large sow herds in North America

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Air filtration systems have been demonstrated to reduce the risk of introduction of PRRSV contaminated aerosol into susceptible herds. Based on these data, several North American production companies have installed air filtration systems in boar studs or sow farms. However, a large epidemiological study evaluating the efficacy of air filtration with real farm data has not been completed. Therefore, the objective of this retrospective study was to assess the incidence of PRRSV outbreaks in filtered and non-filtered sow farms during the study period. In 2010, 20 filtered and 17 control participant sow farms from areas of high farm density were enrolled. The time line for data collections was from Oct 2004 to June 2011. Inclusion criteria were an average inventory of $\geq 2,500$ sows, use of a validated program of biosecurity, and a history of at least 3 new PRRSV introductions over the preceding 4 years. Prospective surveillance involved monthly qRT-PCR testing pools of serum from 30 piglets at weaning time (5 samples per pool). All PRRSV isolates were sequenced and represented in dendrograms (phylogenetic trees) for evaluation. For this study, an outbreak was defined as the detection of a PRRSV isolate that differed by $>2\%$ in the ORF 5 region from previous viruses of the different clusters found historically in the herd. Incidence rate for each group of farms was calculated as new outbreaks per farm-year at risk. Exhaustive analysis of the dendrograms demonstrated the seasonality of PRRSV outbreaks, although the seasonal pattern decreased noticeably during the latter periods when all filtered farms were under complete filtration. Non filtered farms (control and pre-filtered farms) had 6.4 outbreaks per 10 farm-years at risk and filtered farms, under the same conditions, 1.6 outbreaks per 10 farms-yrs at risk. During the study period, the incidence density ratio indicated that a PRRSV outbreak was 4 times higher in control farms when compared with filtered farms (95%CI: 1.6-9.6).

Impacts of intra-mammary infection misclassification in udder health research

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In most udder health research, intra-mammary infections (IMI) are diagnosed using milk bacteriological culture, a diagnostic procedure with imperfect sensitivity (Se) and specificity (Sp). More often than not, no formal attempt to quantify the magnitude of the resulting bias is made and inappropriate heuristics are instead used to perform an intuitive bias appraisal. The objective of this study was to evaluate the impacts of coagulase-negative staphylococci (CNS) IMI misclassification on measures of disease frequency and of association with exposures. A cohort of 4,000 cows from 90 herds was followed in 2007-2008. Series of quarter-milk samples were collected and analysed using bacteriological culture to identify prevalent, incident, and eliminated CNS IMI. Prevalence, and incidence and elimination rates were computed as well as measures of associations with specific exposures using traditional epidemiologic methods. The same epidemiological measurements were then computed using a Bayesian latent class model relating the observed bacteriological culture measurements to the true, but unmeasured, quarter IMI status. Prior distributions for bacteriological culture Se and Sp were used to establish this relationship. Ignoring CNS IMI misclassification resulted in a substantial and often counterintuitive bias of most measures of disease frequency. Important biases were also seen on measures of association with risk factors. In the incidence and prevalence models, traditional regression coefficients corresponded, in general, to roughly 50% of the misclassification adjusted coefficients. Most importantly, pretending that the outcome was measured perfectly would have led to gross underestimation of the 95% confidence intervals, to both type I and II errors, and would have ultimately led to different recommendations to the dairy producers. In udder health research, quantitative bias appraisal could certainly help safeguard against this bias and could improve comparability between studies.

Applying the SERVAL framework to evaluate animal health surveillance: examples using case studies of endemic and exotic diseases in ruminants and pigs

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This presentation will use a range of case studies of endemic and exotic diseases to demonstrate the use of the newly-developed SERVAL (SuRveillance EVALuation) framework. SERVAL is a generic framework for the evaluation of animal health surveillance which has been designed to assist evaluation of any animal health surveillance programme. The inclusion of socio-economic criteria ensures that economic evaluation is an integral part of this framework. Evaluation of animal health surveillance systems in Great Britain covering a variety of objectives will be demonstrated in this presentation, including: (1) surveillance to demonstrate freedom from infection (a serological survey for *Brucella melitensis* in sheep and goats); (2) surveillance for endemic disease (tuberculosis in cattle); and (3) surveillance for early detection of an exotic disease (classical swine fever in pigs). These examples will show the flexibility of the SERVAL framework, whose standardised methods allow for comparisons across surveillance systems. The SERVAL framework is freely available on the internet and we encourage you to give it a try. We would welcome feedback from those using it. This project is funded by Defra.

Why should disease surveillance protocols reflect the acute epidemic situation?

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Monitoring and surveillance systems (MOSS) often address implicitly the situation of an outbreak. Particularly, for wildlife diseases that cause severe morbidity and mortality, a more effective scheme of disease surveillance was constructed previously to adopt the changing epidemic situation within the host population (disease absence, outbreak, and expected eradication). The logic of the proposed system will be introduced. With this paper, however, we resolve three established misconceptions that lead to an apparent conflict with the situation-based concept: (1) ‘systematic hunting is more efficacious for disease surveillance in situation of disease presence’; (2) ‘active sampling could be equally well designed in space-and time than passive ones in order to catch a disease incursion’; (3) ‘the testing logic is equal for searching disease by active (e.g. hunt) vs. passive (e.g. suspicion) sampling.’ We exploit historic surveillance databases (rabies, CSF & FMD, AI) to support the argumentation by example data. The historic records were stratified for different epidemic situations in the geographic region at time of origin. The respective evidence from different cases will be presented statistically or spatio-temporally explicit. The historic data confirmed excitingly clear: (1) the performance of passive approaches in alerting disease incursion in the situation of disease absence; (2) the low performance of systematic sampling in hunted animals during disease presence; and (3) the irrelevance of sampling size specification to falsify disease presence without an epidemic. Therefore, during long-term application of surveillance, efforts can reasonably be limited to the actual needs for disease management. Particularly, we conclude that with the legal status of freedom from the considered diseases surveillance efforts should be adapted to the demonstrated needs.

Molecular prevalence of *Anaplasma marginale* (Rickettsiales: Anaplasmataceae) in cattle under smallholder production system in South Africa

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Little is known about the prevalence of anaplasmosis in cattle reared by smallholder farmers despite it being one of the leading causes of cattle mortality in the smallholder farming areas of South Africa. The current study’s objective was to determine the molecular prevalence of *Anaplasma marginale* in cattle under the smallholder production system in South Africa. Molecular prevalence of *A. marginale*, body condition score (BCS), packed cell volume (PCV) and tick infestation levels were determined in Nguni and local crossbred cattle reared by small-scale and communal producers in the Eastern Cape Province, South Africa. Of the 149 cattle sampled, 59.1% were infected with *A. marginale*, 47.7% of them being of the Nguni genotype while 52.3% were local crossbreeds. Cattle in the small-scale production system had higher ($P < 0.05$) tick infestation levels ($\chi^2 = 14.2$) and molecular prevalence of *A. marginale* ($\chi^2 = 46.8$) than those in the communal production system. The odds of infection by *A. marginale* were higher ($P < 0.05$) for cattle in the small-scale production system, young animals (below 2 years old) and cattle with a high BCS than for cattle in the communal production system, older animals and cattle with a lower BCS, respectively. It was concluded that bovine anaplasmosis had a moderate prevalence in the smallholder farming areas due to moderate tick infestation levels and force of infection with *A. marginale*. Reducing the frequency of dipping and vaccinating young cattle to establish endemic stability to *A. marginale* in the smallholder cattle herds was recommended.

Prevalence of anthelmintic resistance in cattle nematodes: a systematic review-meta-analysis approach
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A systematic review (SR) is a research synthesis method that follows a structured methodology minimizing biases and random errors. One of the goals of a meta-analysis (MA) is to summarize the results from similar studies (and addressing the same research question) with the aim to produce a more precise single estimate of an effect. The main goal of this study was to evaluate the prevalence of anthelmintic resistance (AR) in cattle nematodes. A systematic review protocol was designed a priori, validated and tested. A search algorithm was applied to four electronic databases and one level of relevance screening was conducted by two reviewers. Quality assessment and data extraction were performed in one single step. Random effect MA was performed with the anthelmintic resistance (AR) prevalence for each drug evaluated. Twenty three studies (5 cross-sectional, 9 prevalence surveys and 9 field trials) from 15 countries were included in this review. The overall percentage of farms with AR in at least one drug was 82.1% (95% CI=70.5 to 93.7), and the between study heterogeneity was high ($I^2=94.8\%$). The sub-group analysis showed the following prevalence by drug class: ivermectin 77.0%; moxidectin 74.2%; benzimidazole 44.3% and levamisole 35.0%. The main nematode genera involved in the AR were *Cooperia* (30.9%), *Ostertagia* (10.3%), *Haemonchus* (8.4%), *Trichostrongylus* (2.4%) and *Oesophagostomum* (1.4%). The results presented in this SR-MA suggested that AR in cattle nematodes is occurring where ivermectin and moxidectin seems to be the drugs with higher prevalence of AR. Additional results will be presented and discussed at the conference.

Variation factors of overall health score using Welfare Quality® assessment protocol in French dairy cattle farms

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There is a growing concern about the welfare of dairy cattle, especially regarding health which is the welfare criterion the most degraded according to recent EFSA reports. Among existing tools to assess animal welfare, the Welfare Quality® assessment protocol aims at assessing each of the 5 'freedoms' of welfare based on the calculation of 4 main principles scores (ranking from 0 to 100) including a special focus on health. If specific risk factors are well documented to reduce some specific diseases (eg mastitis, lameness), there is a lack of knowledge on how to broadly improve the overall health status and not only one health disorder. The objective of the study was to highlight the factors of variation of the overall health score obtained using the Welfare Quality® assessment protocol in a stratified random sample of 131 French dairy farms. We investigated several causal factors reflecting either: (1) the diversity of dairy systems in France: location area, milking system, type of housing in loose-housing barns, herd size, breed; or (2) putative herd risk factors: mean parity, percentage of primiparous cows, mean stage of lactation and mean milk production. Univariate analyses were performed to select potential risk factors ($P<0.2$) before ANOVA with forward selection ($P<0.05$) using the SAS® software. In the final model, factors that contributed mostly to the variability of the health score were in decreasing order: mean stage of lactation (better health score for mean stage of lactation ≤ 4.8 months vs. >6.2 months (32.9 vs. 26.5)), type of housing (better health score for deep-bedded vs. cubicles (32.1 vs. 27.2)) and milking system (better health score for milking parlor vs. automatic milking system (31.8 vs. 27.6)). This study offers a starting point to rank factors associated with poor welfare in dairy herds in order to improve the health status of dairy cows.

Pattern recognition of feeding and drinking behavior as a tool in early identification of diseased feedlot animals

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The health status of feedlot animals impacts calf welfare and the economic returns to the producer. GrowSafe (GrowSafe Systems Ltd., Airdrie, AB, Canada), a system that records feeding and drinking behavior continuously, has been shown to detect animal morbidity between 5 and 7 days earlier than visual appraisal by feedlot staff. However, it has only been validated using traditional observational methods for evaluating health status. The study objectives were (1) to validate GrowSafe® technology using laboratory parameters as additional indicators for disease status; and (2) to develop and validate an algorithm to identify sick animals in early stages of disease. A total of 746 auction-derived mixed breed calves from 2 southern Alberta commercial feedlots, equipped with the GrowSafe® system, were included in the study. Upon arrival, animals were processed according to a standardized protocol, ear tagged with a radio frequency tag for individual identification, bled and randomly assigned into 2 pens on each farm. Feeding and drinking behavior was recorded for 5 weeks. Animals identified as diseased by feedlot staff were examined and bled, and treated if necessary. Disease status was confirmed by complete blood count, total plasma protein, plasma fibrinogen, haptoglobin and serum amyloid α . A prediction model for morbidity using the laboratory parameters as additional assessments for disease status was developed and validated using a random sample of feedlot animals. Results and detailed methods will be presented. We anticipate that by creating a well-defined algorithm, diseased animals can be identified significantly earlier using behavior data compared to observational methods.

Risk factors for culling and death in New Zealand dairy cows, 2000-2011

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Significant changes have occurred in the New Zealand dairy industry over the past 10 years. There has been a steady increase in the payout price for milk and conversion of sheep and beef enterprises into dairy enterprises has been a growing trend, particularly in the South Island. The objective of this study was to identify risk factors for culling and death in New Zealand dairy cows, with an emphasis on identifying differences in the longevity of cattle born in herds located in the North and South Islands. Data were provided by the national milk recording authority, Livestock Improvement Corporation. The period of interest was from 1 July 2000 to 30 June 2011. To be eligible animals had to be born between the start and end date of the study and recorded as having been culled or died before 30 June 2011 or being still present in the herd on 30 June 2011. A total of 6,186,121 individual cow records were available for analysis. A multivariable Gompertz model with a shared herd-level frailty term was developed to quantify the effect of the following risk factors on culling and death: breed, the average number of cattle born in each herd per year (a proxy for herd size), and island in which the natal herd was located. Our results show a marked difference in the longevity of South Island cattle compared with those born in the North. The monthly hazard of culling and death for South Island cattle was 1.51 (95% CI 1.46 to 1.61) times that of North Island cattle. In this presentation possible reasons for these findings will be discussed and recommendations for further research into this area of dairy farm productivity will be provided.

Assessing the coverage and representativeness of early-warning disease surveillance in pigs in England
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Early-warning surveillance systems are used to identify changes in the health of animal populations, which may indicate new or exotic disease emergence. To optimise the probability of timely detection of such diseases, early-warning surveillance should include a sufficiently large and representative sample of a population. Methods for assessing the coverage and representativeness of early-warning surveillance systems were evaluated using the 'FarmFile' system and pigs as examples. Four English counties with diverse pig population characteristics were selected (Cumbria, Devon, East Riding of Yorkshire [ERY] and Norfolk). A survey of veterinary practices was used to supplement existing data on the number of practices treating pigs and the number of pig holdings and pigs in each county. The proportion of practices, holdings and pigs 'covered' by FarmFile in 2009 was estimated using submission data. Coverage estimates varied between counties and the coverage assessment method used. Between 5 and 17% of holdings submitted samples to FarmFile in 2009 and between 18 and 94% of holdings were registered with a veterinary practice that submitted samples. Coverage was lower in the low pig density counties (Cumbria and Devon), where holdings tended to be smaller and less likely registered with pig specialist practices than those in the high pig density counties (Norfolk and ERY). Coverage of small holdings and 'breeding only' holdings was lower than that of larger and 'growing' or 'mixed' holdings. Higher coverage of larger holdings meant that pig-level coverage was higher than holding-level coverage and varied less between counties. The assumptions made by different coverage estimation methods and the choice of the most appropriate method will be discussed.

Using network analysis to design an animal disease network surveillance: the case of developing countries

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For many developing countries confronting emerging and re-emerging infectious diseases such as Highly Pathogenic Avian Influenza H5N1 (HPAI H5N1), the disease surveillance networks and response systems are not capable to adequately deal with these new infectious agents. In these locations, surveillance of diseases in animals is not based on the local epidemiological and economic contexts; and the constraint in resources does not allow the network to play an efficient role. In Ethiopia, to understand and to improve the reporting of animal health surveillance data such as the highly pathogenic avian influenza H5N1, a network analysis was conducted to identify all stakeholders, determine their influence on the flow of surveillance information, and to describe all the alternative pathways for reporting. 41 stakeholders are involved in reporting data at the national and international levels, there are 7 key nodes with varying degrees of centrality serving as potential sources of primary health information. In recognition of several weaknesses in the formal pathway, an alternative system, consisting of a channel of information reported from the following groups: a peasant association, public health extension, woreda health office, regional health office, Ministry of Health, and federal veterinary services would likely improve good the reporting pathway of HPAI H5N1. Network analysis of animal health information pathways helps us to identify the existence of different animal health information pathways among stakeholders, and analyze the characteristics of each pathway. The analysis of the role of each node in the various pathways of the network allows us to further identify potential bottlenecks, and propose a network which fits with the social and economic context, and is appropriate for efficient health information reporting.

A national strategy for prioritisation, maintenance and development of animal health surveillance

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Investments in animal health surveillance (AHS) are under constant scrutiny, both from an economic and from a preparedness point-of-view. Reflecting this, new EU legislation is underway that may lead to demands on member states to present their long-term strategies for AHS. In Sweden, the responsibility for AHS activities involves many actors and is to a large extent based on industry-driven activities, paid for both by the state and by the stakeholders. Therefore, in defining long-term goals – and consequently identifying where resources have to be allocated – all parties need to have a joint vision of what is to be achieved. A 3-year project has now been launched to develop a national plan for surveillance of animal populations, which identifies short- and long term objectives and responsibilities with regard to AHS. Three main areas are covered: (1) surveillance prioritization, covering endemic, exotic and emerging infections including antimicrobial resistance, and covering all relevant species including wildlife; (2) maintenance and development of surveillance components, covering all types of processes that generate disease information; from clinical surveillance and meat inspection to hunter networks and analysis of unstructured data; and (3) maintenance and development of the infrastructure needed for efficient implementation of AHS, from design to analysis and communication of output. This includes development and use of risk-based methods, securing access to relevant data, development of models for evaluation of surveillance as well as tools for efficient use of information generated by AHS activities, by continuous processing, analysis and presentation of data and a strategic use of relevant communication channels. The National Surveillance Plan will guide the creation of a robust platform for the future and ensure that the national AHS is fit for purpose. This presentation will build on experiences obtained during the first year of the project.

Session 35**Theatre 4****New tools for planning surveillance to demonstrate freedom from disease: how much for how long?**

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The quality of surveillance to demonstrate freedom from disease can be measured in terms of surveillance sensitivity. Sensitivity can be accumulated over time, taking into account the risk of introduction of disease, to calculate the cumulative probability of freedom from disease. Using this approach, it is possible to achieve a high probability with surveillance that has low sensitivity, as long as the surveillance is continued over a long enough period and the risk of introduction of disease is low. This paper introduces three new tools to plan surveillance to demonstrate freedom from disease. Normally such calculations are implemented using an iterative model. These tools use simple formulae to immediately estimate results that would otherwise only be available after a series of iterations. The first tool determines the asymptotic limit of the probability of freedom that can be achieved, based on the surveillance sensitivity and that risk of introduction of disease, assuming that surveillance continues over time. The second tool determines how long it will take to achieve a specified probability of freedom. Based on the surveillance sensitivity, the starting prior probability of freedom, the risk of introduction of disease and target probability of freedom, the tool uses an approximation to the cumulative distribution to estimate the number of time periods required to meet the target. The third tool is used to modify surveillance once the target probability has been achieved. Rather than maintaining high levels of surveillance sensitivity, it may be possible to reduce the level of surveillance in order to just balance the risk of introduction of disease, thereby maintaining the required target probability of freedom at minimum cost. These tools can be easily implemented in a spreadsheet and are also available on the EpiTools web site. Together they provide surveillance planners with greater insights into surveillance requirements, allowing specific activities to be designed at minimum cost to meet defined targets.

Policy linked research in veterinary epidemiology: combining advancing surveillance with emergency outbreak control

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A consortium comprised of Scottish Universities and Research Institutes successfully tendered to establish a Scottish Centre of Excellence in Veterinary Epidemiology from 2006-2011. The remit was to develop a programme of policy linked research to help enhance veterinary surveillance and concurrently provide reactive decision support in the face of any infectious disease incursions/emergencies detected. The team focused upon Epidemiology, Population health and Infectious disease Control became known as EPIC. This paper will contrast these two roles. It will describe how such a consortium, comprised of previously competing research teams, formed into a successful coalition to progress academic research in parallel to outbreak control and emerged as a 'new' and expanded EPIC Centre of Expertise on Disease Outbreak Control 2011-2016. Examples of research output by the Research Fellows will be presented: exploring aspects of surveillance test interpretation; surveillance economics; denominator analyses; molecular epidemiology; environmental drivers for disease change and advanced methods of statistical inference in animal epidemiology. These outputs will be contrasted with that by the team in emergency response mode using the following examples: advice on Scottish surveillance focus for UK FMD outbreak (2007); advice on Scottish control response to bluetongue 8 (2008); advice on revisions to Scottish legislation on lairages (FMD, 2009) and guidance on bee foulbrood survey (2009). The author will discuss what has been learned and present on behalf of the extensive team that included staff from the Universities of Edinburgh and Glasgow, the Scottish Agricultural College, Moredun Research Institute, James Hutton Institute and Biomathematics and Statistics Scotland. This project was sponsored by Scottish Government.

Session 36**Theatre 1****Scenario-tree analysis for the evaluation of case-detection surveillance**

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One of the possible purposes of animal disease surveillance (along with early detection, demonstration of freedom from disease and measuring the level of disease) is case detection. This type of surveillance aims to identify cases in order to respond to them. In public health, breast or colon cancer screening programs provide examples. In animal health, examples include testing to identify infected herds in a tuberculosis control program, or testing of meat in abattoirs for bovine spongiform encephalopathy or trichinellosis. In all cases, the prime purpose is not to measure the incidence or prevalence of a disease known to be present, but to identify affected individuals or herds so that appropriate action may be taken. This paper illustrates how scenario-trees, originally developed for the analysis of surveillance to demonstrate freedom from disease, may be used to plan and analyse case-detection surveillance. In case-detection surveillance, the measure of quality is the detection fraction – the proportion of infected animals or herds in the population that are detected. Risk-based sampling may be used to target high risk populations, and scenario-trees provide a tool for estimating the benefit of these risk-based approaches. Case detection can be enhanced by the use of multiple, potentially overlapping, surveillance system components (such as on-farm testing and abattoir meat inspection). The analytical methodology captures the impact of overlapping systems, but parameterisation becomes difficult if more than two or three surveillance components are involved. The use of scenario-trees for the analysis of case-detection surveillance provides new quantitative tools to assist surveillance planners in optimising surveillance strategies in this under-recognised field.

Using capture-recapture approaches for assessing livestock disease surveillance at supra-individual level: methods and limitations

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Capture-recapture (CR) approaches have been extensively used for analyzing data produced by imperfect human epidemiological surveillance systems. Their objective is to assess the number of infected individuals that remain undetected. Two broad types of CR approaches have been used: multilist and unilist CR approaches. Multilist CR approach can in theory be applied in contexts where at least two distinct, imperfect and independent surveillance protocols detect infected epidemiological units in the study population. Through log-linear modeling, this approach allows estimating the number of infected units detected by none of the protocols. Unilist CR approach is based on repeated detections and tries to model the frequencies of detection in order to estimate the number of infected units with zero detection. Zero-truncated or zero-inflated count models are generally used in this approach. CR methods should be very useful for studying livestock diseases surveillance data since surveillance systems generating them are often of limited efficiency, producing a large number of undetected units. While studying livestock diseases, the relevant epidemiological unit is usually a supra-individual unit such as an infected holding or even an infected administrative area. Such point of view may require methodological adaptations of CR approaches and of their underlying assumptions. Referring to animal disease applications from the literature, we propose a critical review of the possibilities arising from the different methodologies available given the specificities of animal disease surveillance data at supra-individual level. As a conclusion, we propose some thoughts on the interest and limitations of these methods for quantitatively evaluating animal disease surveillance systems.

Impact of wild waterfowl incursions and holding characteristics: a step towards avian influenza virus risk based surveillance in Belgian

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International standards as well as EU legislation encourage countries to implement risk based surveillance programs to detect notifiable low pathogenic avian influenza (NLPAI) before it could mutate into highly PAI. The aim of this study was to evaluate the efficiency of Belgium NLPAI surveillance system based on the scenario tree methodology, using a methodological approach to estimate risk factors. Data on (1) the impact of different NLPAI strains on the spread of the virus in chickens and ducks; (2) continuous video recording of wild waterfowl incursions into experimental poultry pens; (3) biosecurity characteristics of professional poultry holdings were all investigated to determine what were the main risk factors affecting the epidemiology of AI, by the means of generalized linear mixed model (SAS 9.2). Results were used to feed the scenario tree model simulation model (ModelRisk). The sensitivity of detection at herd and risk group level was evaluated following stochastic simulation process. The optimal sample size in the different risk groups identified was then estimated, taking into account the results obtained from the simulations. Targeting surveillance in poultry holdings with outdoor access and with several species present provided higher sensitivity of detection. Temperature and feeding outdoor were significant risk factors for incursions of wild waterfowl into domestic poultry pens. The empirical approach of this study, which avoided bias due to assumptions, highlighted interesting features to consider when setting up a risk based NLPAI surveillance program in Belgium, as required by international standards and EU legislation.

A 'One Health' approach to quantitatively compare human and animal surveillance systems for avian influenza H5N1 in Cambodia

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Since 2003, nineteen human cases of highly pathogenic avian influenza (HPAI) have been reported in Cambodia, eight of them, all fatal, occurred in 2011 in people <19 years old. The source was mainly sporadic infection with direct exposition to sick poultry but this sudden increase of incidence was alarming for the national health authority of Cambodia. In order to assess the sensitivity of the national surveillance system of HPAI H5N1 in Cambodia, scenario tree modelling was used to describe and compare the components of the surveillance system in human and animal populations in order to make recommendations to enhance early detection of outbreaks. The human surveillance consists of two main components: one based on syndromic surveillance with weekly case reporting but with low capacity for laboratory confirmation and one, more research based, with a high sensitivity but low coverage. For the animal surveillance, several components were implemented but few were sustainable. The most established one is the passive surveillance based on the network of 12,000 Village Animal Health Workers. The sensitivity of this component was estimated to be 0.54 (95% CI 0.18-0.80) but with large variation between provinces. This study showed that some components in the animal surveillance system, like the market surveillance, need to be redefined in order to meet the objective of early warning and that there is a great effort needed to integrate human and animal surveillance together.

Why implementing co-ordinated systematic H5N1 post-vaccination systems is so hard and what needs to be done

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Vaccination against HPAI H5N1 has been practised in Indonesia since 2004, particularly in the commercial layer sector. Whilst this vaccination – combined with improved biosecurity – has successfully prevented massive mortalities and production loss, ongoing evolution of the virus requires the development of surveillance systems to ensure that vaccination continues to be effective. Nevertheless, to date this has been difficult to implement due to the need to co-ordinate, for a given vaccine H5N1 seed antigen, the appropriate sampling regime together with the most effective test antigen in the haemagglutination inhibition (HI) test. In addition, post-vaccination test results can be difficult to interpret without knowledge of the infection status of the sampled birds. To progress a solution to this complex problem, we have worked with a small number of commercial layer producers in West Java, which is one of the areas of Indonesia worst affected by H5N1. Initially we undertook a cross-sectional survey to better understand vaccination and biosecurity practices, and this enabled us to develop an effective strategy of sero-sampling at the point-of-lay stage of pullets where vaccination is routinely practised. This has also assisted us to define quantifiable baseline serological responses, and to define clearly questions that require parallel studies regarding vaccine responses to test antigens. As importantly, we have defined a role for a DIVA (Differentiating Infected from Vaccinated Animals) ELISA based upon the M2e antigen to detect birds actively excreting virus. These concepts are now being implemented in follow studies in West and Central Java in an intensive longitudinal study of about 40 Sector Three poultry farms.

Effect of lambing season on gastrointestinal nematodes periparturient egg rise

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The epidemiology of the periparturient egg rise (PPER) of gastrointestinal nematodes (GIN) in sheep remains unclear. Earlier studies have suggested that the PPER may be influenced by the lambing season. This longitudinal study was performed to determine the effect of lambing season on the PPER in sheep in Ontario. Six farms that practiced year-round lambing were enrolled, and each farm was sampled for three consecutive lambing seasons. For each lambing season, all farms were visited five times, following a specific schedule that was determined by the predicted date when 50% of the ewes scheduled to lamb during that season would have lambed. On the first visit for each lambing season for each farm, 20 pregnant ewes and 20 non-pregnant/early gestation ewes were randomly selected. On each visit, fecal samples were collected from each selected animal and processed individually to measure GIN fecal egg counts (FEC). The ewes were classified into different production stages based on information collected during farm visits and lambing dates. Descriptive statistics were performed, followed by the creation of a mixed linear model of the logarithmic-transformed outcome FEC. Lambing season, production stage, packed cell volume (PCV), lambing season×production stage and PCV×production stage were significant ($P \leq 0.05$) in the final model. In both winter and spring lambing seasons, the PPER peaked between early to late lactation; during the autumn season, the PPER peaked at late gestation and then decreased. Ewes with normal or high PCV values had low and constant FEC, while ewes with low PCV values had higher FEC, which increased over time. The results indicated that the PPER occurred during all three lambing seasons, though its magnitude and distribution varied with the lambing season.

Prediction of pregnancy toxæmia in Greek sheep

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The aim of this study was to develop a predictive model for sub-clinical pregnancy toxæmia in pregnant ewes. Worldwide, pregnancy toxæmia is the most common metabolic disease of pregnant sheep. This was a prospective cohort study; the study population was 113 housed and intensively fed, Chios and Chios-crossbred ewes from one commercial flock in Thessaly, Greece. The study ran from August to October 2009. The pregnant ewes were clinically examined each week from day 100 and blood sampled on four occasions, three times pre-lambing and once post-lambing. Blood samples were analysed for OCT, GDH, AST, ALP, GGT enzyme activity, BOH butyrate (BOHB), glucose and triglyceride concentrations. Other recorded variables were lambing date, ewe BCS, number of lambs born and age of ewe. For the purpose of this analysis those ewes with a BOHB blood result ≥ 1.0 mmol/l that were free of clinical signs were said to have sub-clinical pregnancy toxæmia. Three separate multivariable logistic regression models were built to model whether data collected from one sampling could predict sub-clinical pregnancy toxæmia identified at the next sampling. All models were built using a combination of forwards and backwards stepwise elimination with variables retained in the model at $P < 0.05$. Eight ewes developed clinical pregnancy toxæmia of which 4 died, 45 ewes developed sub-clinical pregnancy toxæmia and 60 were unaffected over the study period. The results from the 3 predictive models showed that for sample 1 high glucose levels and carrying three or more lambs predicted sub-clinical disease at sample 2, for sample 2 low glucose and being already sub-clinical predicted disease at sample 3 and for sample 3 being sub-clinical and having raised triglyceride levels predicted sub-clinical pregnancy toxæmia at sample 4 (post-lambing). Monitoring glucose levels in ewes with regard to stage of pregnancy and number of lambs could help identify those ewes at risk of developing pregnancy toxæmia.

Serum epidemiology of caprine leptospirosis at Veracruz, Mexico

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With the aim to determine the seroprevalence of caprine leptospirosis and associated risk factors at production units (PU) from 14 municipalities of Veracruz state of Mexico a polietapic stratified transectional study was conducted. Sample size was calculated by Win Episcopo Ver. 2.0, obtaining a serum sample fraction of six animals per PU. Females older than three months were randomly selected and all the stallions in the herd. The serological diagnosis was performed by microagglutination test (MAT) using 9 serovars of *Leptospira interrogans* and to determine risk factors, two questionnaires were applied (a single one for sampled animal and a general one for PU). Variables analyzed by Odds Ratio (OR). Overall seroprevalence from 564 sampled animals was 23.53%; however herd seroprevalence was 82.72% and for municipality 100%. The higher seroprevalence for specific serovars was 5.6% for *L. interrogans* Icterohemorrhagiae and 3.6 for *L. interrogans* Hardjo type hardjo-LT. The risk factors associated with leptospirosis were milking goats (OR=1.57; CI_{95%} 1.1-2.4), 25 to 36 months older (OR=3; CI_{95%} 1.9-4.9), cohabit with dogs (OR=4; CI_{95%} 1.5-11), presence of rodents (OR=300; CI_{95%} 135-675). Also it was observed that seropositive females have 1.5 more times for abortion. On the other hand, absence of wet areas was a protector factor (OR=0.9; CI_{95%} 0.88-0.9). In conclusion leptospirosis is a wide distribution disease at observed municipalities with several risk factors associated, representing a great public health risk

An investigation into the cause of high abortion rates of goats in the Limpopo Province, South Africa

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The study was carried out to investigate the cause of exceedingly high abortion rates and other reproductive failures of goats at Vhembe district, in the Limpopo Province, South Africa. Reproductive failures are of great economic importance to goat farmers and can result from various factors that include infectious agents, nutritional deficiencies and environmental factors. Additionally, goat abortion due to an infectious agent is a public health risk since most abortifacient agents are zoonotic. *Toxoplasma gondii*, *Chlamydophila abortus* and trace mineral deficiencies were investigated as possible etiologies in this situation. A total of 338 blood samples were collected from 22 herds and enzyme-linked immunosorbent assay (ELISA) was used to determine the seroprevalence of *T.gondii* and *C. abortus*. Copper and Zinc serum levels were analyzed using the Atomic Absorption Spectrophotometer (AAS) machine and Selenium was analyzed using the ICPMS 300Q machine. During sample collections, interviews were also conducted using a questionnaire to gather farm management information and to assess food safety and zoonoses knowledge amongst farmers. Seroprevalence of *T. gondii* in herds ranged from was 0 to 38.5% ($\mu=9.2\%$). An overall prevalence of 30.4% to *C. abortus* antibodies was recorded with a 100% seroprevalence detected in one herd. Zinc and Selenium deficiencies of up to 12.5 and 5,000 times respectively, lower than the minimum expected levels were revealed in all areas, whilst copper levels exceeded the maximum expected by up to 4.4 times. Interviews exposed a lack of awareness about *T. gondii*, *C. abortus* and other public health issues; furthermore they also highlighted the lack of supplementary feeding and basic herd health management practices amongst farmers. In this study *T. gondii*, *C. abortus* and trace mineral deficiency were indicated as significant contributors to the abortion in the study areas.

The role of vet in knowledge transfer in sheep industry in the UK: a study of farmer opinions

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A key government report in the UK on veterinary expertise in food animal production published in 2009 by the Environment, Food and Rural Affairs Committee, highlighted that there is a failure of delivery of knowledge transfer by vets in the livestock sector. According to a survey carried by independent rural consultants, around two thirds of sheep farmers only contact their vet for emergencies and only one fifth had all year round contact. To understand farmers' perception of the role of the vet in improving the health and productivity of their flocks and knowledge transfer across the sheep industry a study was conducted using a qualitative methodology. This included 6 focus groups of sheep farmers stratified by region (North, South and Central England) and within each region two age groups (<50 and ≥50). An additional focus group was conducted in South east of England. The eligibility criteria for the study were male sheep farmers with a flock size of at least 200 sheep. Thematic analysis of the focus group discussions indicated that most farmers used their vet as a fire-fighter, whilst on the farm for other reasons and for telephone advice. There was also a small group of farmers who were using their vet or other sheep consultant more proactively with regular contact. Farmers indicated that the key barriers to using vets included lack of consistent service, high turnover of younger vets, and lack of expertise in all round knowledge of the sheep enterprise and concern about independent advice. Although economics was also mentioned as a key barrier to using the vets more proactively, most farmers did not know where they made and lost money from their flock; there was a heavy reliance on the single farm payment.

Session 38**Theatre 1****Possible association between meat inspection lesions in finisher pigs and the yellow card anti-microbial scheme in Denmark**

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There is concern about the use of antimicrobials in livestock. Recently, a yellow card scheme was initiated by the Danish Veterinary and Food Administration aiming at reducing the consumption of antimicrobials in pigs. The scheme has resulted in a reduction in consumption of antimicrobials and an increased use of vaccines. We studied the potential association between lesions found at meat inspection and the change in antimicrobial consumption and vaccine use. Data originated from Vetstat. Moreover, data from meat inspection of finisher pigs from before and after introduction of the scheme were compared, including 1.7 million finisher pigs. Ten lesions of chronic and bacterial origin were selected. Logistic regression models with year and week as explanatory variables were used to identify whether the prevalence changed from 2010 to 2011. A repeated statement was used to identify animals originating from the same herd and to account for overdispersion. The decrease in antimicrobial consumption was pronounced for weaners and finisher pigs treated for gastro-intestinal or respiratory disease. For sows/piglets a decrease was found for treatment of respiratory disease. Use of vaccines increased in general. The most common lesion found was chronic pleuritis (~23%) while the other lesions occurred less-commonly (<1%). For osteomyelitis, pleuritis, chronic arthritis and condemnation, no differences were observed between the 2 years. Chronic enteritis, umbilical hernia and chronic peritonitis were statistically more frequent in 2011 compared to 2010 (P<0.01), whereas tail infection, chronic pneumonia and chronic pericarditis occurred less frequent (P<0.01). Hence, marked reduction in use of antimicrobials might have resulted in a higher prevalence of specific lesions found at meat inspection and higher vaccine coverage might have reduced the prevalence of chronic pneumonia.

A quantitative value chain analysis of the Dutch broiler sector with regard to the use of antibiotics
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In Netherlands, antibiotics are intensively used in broiler production. This extensive use of antibiotics in this sector plays a role in the development of antibiotics resistance. Because of the concerns about development of antimicrobial resistance, in 2010, the Dutch Ministry of Economic Affairs and Innovation established a target of 50% reduction of antibiotics in animal production (so also in poultry production) in 2013 related to the use of antibiotics in 2009. The objective of this study was to quantify the use of antibiotics in the Dutch broiler value chain, so that all actors of broiler industry, and simulate the economic effects of a reduction of antibiotic use in the Dutch broiler value chain. Using this information, stakeholders can better develop strategies to reduce the use of antibiotics. The total use of antibiotics in broiler value chain in 2010 was estimated to be 29,873 kg of active substance, mostly used on broiler farms and to a lesser extend on PS Breeder farm. The total revenues of antibiotics were estimated to range between 1.4 to 10.9 million euro. Using an enterprise budget model, the expected total profit of all actors in the Dutch broiler value chain was estimated to be 47.3 million euro per year. A reduction in the use of antibiotics would significantly impact the production performance of chickens and therefore would reduce the profit of all actors in value chain. In the lower performance scenario, the total profit is expected to decrease with 15.8 million euro per year. In the higher performance scenario, the total profit is expected to decrease 6.8 million euro per year.

Preliminary results on reduction of antimicrobial usage on pig farms after improvement interventions
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From January 2011 onwards data on antimicrobial usage and herd management were collected retrospectively on pig herds in Belgium aiming to promote prudent antimicrobial usage and optimize herd management. Twenty herds were analyzed on farm management (diagnostics, production parameters, biosecurity (www.biocheck.ugent.be)) and antimicrobial usage (www.abcheck.ugent.be). Six months later effect of given advise was evaluated. On these herds average total Treatment Incidence animal daily dose (TI_{ADD}) for sows was 53.0 (0.2-279.5, 42% prophylactic). For piglets 237.1 (1.6-770.9, 68% prophylactic) and for finishers 118.9 (0-648.9, 28% prophylactic). Antimicrobials used prophylactic in sucklers were macrolides (tulathromycin 13%), aminopenicillins (amoxicillin 31%) and cephalosporins (ceftiofur 56%). Main antimicrobials for weaners were amoxicillin (31%) and colistin (34%) and for finishers doxycycline (67%). Most advises were given on 'general' biosecurity and management measures. Higher awareness on prudent antimicrobial usage was advised and reduced use of critically important antimicrobials. Momentarily available data of 7 herds (more by august 2012), collected 6 months after advise, show an average increase of 4.6% in biosecurity-scores. Production parameters improved on 4 farms. One herd did not use prophylactic antimicrobials before and after the herd visits. Of the six that did use prophylactic antimicrobials four reduced their use after counseling. Average decrease in sows was 2.8 TI used daily dose (TI_{UDD}) (-44.5-64.2 TI) and for piglets 65.6 TI_{UDD} (0-275.4). In these herds no prophylactic antimicrobials were used in finishers before and after the advises. These results indicate that in herds with average to high antimicrobial usage, clear and guided interventions in improving biosecurity and management practices may lead to reduction of antimicrobial usage without loss of productivity.

Risk management and the use of antibiotics on dairy farms

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In accordance with increasing quality risk control demands from food processing industries on primary producers, there is a need for how to apply risk management and the HACCP principles on dairy farms. Especially, when in The Netherlands the government has set formal threshold levels for the use of antibiotics in cattle. Therefore, the objective of this study was to determine if there is an association between farm(ers) characteristics and risk management, and, more specifically, the use of antibiotics. This study is part of a longitudinal study in The Netherlands which assesses farmer's behavior and the effect of training in risk management, herd health and the use of antibiotics. In total 60 dairy farmers enrolled in a survey regarding farm(er's) characteristics, animal health, attitude towards the choice and use of antibiotics, and source of information for a correct treatment if needed. The major findings were that large farms (>100 head) compared to small farms (<100 head) more frequently had a herd treatment advisory plan (51.9% vs 30.3%; $P=0.08$), that were free of IBR (70.4% vs. 46.9%; $P=0.07$), less frequently bought in replacement animals (14.8% vs 51.5%; $P=0.006$) and less frequently had one person responsible for applying the treatments (32.7% vs 72.7%; $P=0.014$). Farmers, who decided to buy in replacement cattle, focused more on the withholding period when deciding which antibiotics to choose, but were more strict in having the proper diagnosis before treating animals ($P=0.01$). From these preliminary data, it can be concluded that there is a large variation between farmers regarding the attitude towards risk management and the choice of when and how to treat animals with antibiotics. In the near future, all the farmers participating in this initial survey will be involved in three different workshops regarding risk management, quality control systems and animal health, and be surveyed again to measure the effect of the training on their use of antibiotics.

Session 38**Theatre 5****Antimicrobial prescribing in UK equine veterinary practice**

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Antimicrobial use is a known driver for the emergence of resistant strains of bacteria; therefore prudent use in veterinary medicine is essential. This study aimed to characterise antimicrobial prescribing patterns in equine practice and evaluate factors associated with prescribing. Two methodologies were used. Firstly, postal questionnaires including four clinical scenarios were sent to 740 randomly selected veterinary surgeons that treat horses. Data were collected on the clinician and their practice. Secondly, indication-based use of antimicrobials was evaluated through the completion of prescription logs over a 5-day period. The antimicrobial used, dose, presenting complaint and total number of animals under consultation was documented. Multilevel, multivariable logistic regression analyses were used to ascertain factors associated with; prescribing off-licence drugs; prescribing 3rd or 4th generation cephalosporins and prescribing fluoroquinolones. Less than 1% of practices had an antimicrobial use policy. Trimethoprim-sulphonamides were most commonly prescribed in all clinical scenarios. 11% of prescriptions represented antimicrobials not licensed for use in horses in the UK. Veterinary surgeons working at referral practices were more likely to prescribe 3rd and 4th generation cephalosporins, fluoroquinolones and antimicrobials not licensed in horses. From the prescription logs antimicrobials were prescribed to 17% of the total equine patients. Of these prescriptions 23% were not licensed for horses. Fluoroquinolones and 3rd and 4th generation cephalosporins accounted for 5% and 3.4% of prescriptions respectively. Male vets and those holding postgraduate qualification were more likely to prescribe antimicrobials not licensed for use in horses. In conclusion broad-spectrum drugs were the most commonly prescribed antimicrobials and few practices had antimicrobial use policies. Use of preparations not licensed was common. Targeted guidelines are needed to ensure prudent use of antimicrobials.

Prioritizing zoonotic diseases in Canada and the US

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Zoonotic diseases account for considerable impact on veterinary public health. As resources are limited for the control and prevention of zoonotic diseases, it is necessary to prioritize diseases to direct resources into those with the greatest needs. We used conjoint analysis (CA), a well-established quantitative method, to identify the relative importance of 21 key characteristics of zoonotic diseases that can be used for their prioritization in Canada and the US. Relative importance weights from the CA were used to develop a point-scoring system to derive a recommended list of zoonoses for prioritization in Canada and the US. Six focus groups identified 21 characteristics for determining prioritization; this was used to construct the CA. Over 3,000 participants were recruited to complete the online survey (761 from the Canadian public; 778 from the US public; 707 Canadian professionals and 764 US professionals). Aggregate logit and individual-level Hierarchical Bayes models were fitted to compare the differences between the public and professional groups. The scoring derived from the CA was applied to 63 zoonotic diseases of public health importance in Canada and the US to rank diseases in order of priority. Similarities were observed between the combined public groups and combined professional groups while differences were observed between the public and professional groups. The public groups considered characteristics relating to the individual-level of disease burden such as case-fatality, human-to-human transmission and the duration of illness most important for prioritizing zoonotic diseases while the professional groups deemed characteristics relating to the societal- and population-level of disease burden such as socio-economic burden, disease trend and the efficacy of control measures to be the most important. The subsequent priority lists derived from the CA varied by groups and will help formulate a framework for the control and prevention of zoonoses in Canada and the US.

Session 39**Theatre 2****Prioritisation needs for scientific assessment of infectious diseases in animals in the European Union**

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The present regulatory framework for animal health in the European Union (EU) consists of almost 60 directives and regulations, some which were adopted over 45 years ago. Following the New Animal Health Strategy for the European Union, the Directorate-General for Health and Consumers (DG SANCO) of the European Commission will adopt a Proposal for an Animal Health Law in 2012 with the aim to develop a single, general regulatory framework for animal health. This new regulatory framework will require the prioritisation of diseases on the basis of sound and transparent criteria. In recent years, different organisations have developed and proposed disease prioritisation systems for animal and human diseases considering a range of disease outcomes. In this study, prioritisation systems now being proposed and implemented by national and international agencies were explored. An exhaustive list of animal diseases established through the OIE tool for categorisation of animal diseases was reviewed systematically to identify needs for further scientific assessment. In addition, a prioritisation exercise was conducted using a modified Delphi approach where a condensed list of diseases was scored based on the impact on animal health and welfare, public health, economy, society and environment to highlight priority diseases of animals at an EU level for which further scientific assessment is required. Identification of prioritisation needs is essential for efficient allocation of limited resources in the development of research activities, surveillance and intervention strategies.

A multidisciplinary and evidence-based methodology applied to prioritize diseases of food-producing animals and zoonoses

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This prioritization method is based on a multi-criteria decision making including multidisciplinary experts' opinion and evidence-based data. Hundred diseases were included in the process and five categories of criteria (n=57) were considered. International experts (n=40) first performed an intra-category weighting of criteria, then 6 multidisciplinary experts performed an inter-category weighting. Information corresponding to each criterion/disease was collected through an evidence-based methodology. An overall weighted score was calculated for each disease using a probabilistic approach (Monte Carlo simulation) to estimate the uncertainty and the consecutive ranking was established. A classification and regression tree analysis (CART) allowed the classification of diseases with the aim to obtain subgroups with minimal within-variance (grouping diseases with similar importance). A final ranking of diseases was presented according to their overall weighted scores and using a probabilistic approach. Few differences were observed between deterministic (mean of each weight) and probabilistic approaches (distribution function of weights) (Pearson correlation coefficient = 0.999; P<0.0001). This is probably linked to few subjective interpretation problems or to the dilution of individual discordances among the high number of experts. CART analysis allowed differentiating 4 groups of diseases in function of their relative importance. The present methodology is a generic and predictive tool applicable to different contexts. The standardization of criteria ensures the transparency and the reproducibility of the model. It could be easily applied for diseases affecting domestic or exotic pets or for enzootic conditions in order to better re-target surveillance and re-adapt prevention and control measures.

Multi-criteria decision analysis to prioritise exotic disease investigation for the Australian pig industry
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Australia's domestic pig industry is free from over thirty diseases that affect pig production worldwide. Geographic isolation, trade restrictions and biosecurity help maintain this freedom. However, recent disease incursions (such as equine influenza) and the increasing range of vector borne diseases (such as Japanese encephalitis), highlight that protection cannot be complete and that there is a need for disease preparedness. To aid preparedness, the Australian pig industry has initiated research – using the OIE risk analysis framework and disease modeling techniques – to investigate the most important disease threats to their industry. Defining the 'most important' disease threats to investigate requires prioritisation of diseases based on the aspects of impact that are most valued by the stakeholders. Prioritisation was carried out using multi-criteria decision analysis methods. Stakeholders were invited to participate in an online questionnaire and rank scenarios comprising nine criteria that affect disease impact. Probabilistic inversion of the responses was used to model stakeholder preferences, and preliminary results indicate that attack rate for pigs, and humans in the case of zoonoses, are the most important criteria. The weights of importance were aggregated with criteria measures gained from literature (and reviewed by experts) for each disease, to give an overall disease score weighted to reflect the stakeholder preferences. The highest scoring diseases were presented as the 'most important' diseases to the stakeholders to aid their decision about which diseases to study in greater detail. The methodology and results of the prioritisation are presented, and the value of the multi-criteria decision analysis method that was used in the context of this study is discussed.

Approaches to decision making with imperfect information, the case of emerging risks, knowledgeable experts and fit-for-all prioritization schemes: a review

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There appears to be growing reliance on prioritization techniques in health related fields, for example the prioritization of diseases of public and animal health relevance, often without formal understanding of methodological issues, which may lead to flawed outcomes. Techniques from risk and decision analysis, e.g. multi-attribute theory to handle multi-dimensional impacts, have been increasingly applied to deal with one-off prioritization problems, e.g. the ranking of farms for the risk of disease introduction. There is a need to extend robust methods to other situations in which evidence is scanty or questionable. This is most applicable to emerging risks such as new diseases. Expert opinion and expert groups are used in many instances for these purposes and scientific opinions abound. Here we present a review of the reasons for prioritization and use of expert opinion in different settings and for different events of interest, e.g. multiple competing threats, capability portfolios to address threat portfolios, and the organizational challenges for successful implementation. We also review prioritization methodologies and highlight common mistakes in the published literature, successful frameworks for the use of expert judgment in decision-making for low probability/high consequence events and the quantification of uncertainty by expert judgment using Cooke's classical model. Highly topical issues, e.g. prioritization of long term vs. short term benefits from competing and current interventions, are also discussed.

Unexpected delay in transmission between spatially separated hosts

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The lack of understanding of transmission between spatially separated hosts (indirect transmission) is an important knowledge gap in several disease control problems ranging from epidemics in livestock to outbreaks of hospital infections. In this study we carried out experiments on the transmission of *Campylobacter jejuni* between spatially separated broilers as a model to gain insight into the mechanisms of indirect transmission. The results showed an unexpected delay between the start of shedding by the source (i.e. inoculated animals) and the occurrence of the first transmission event. This delay was surprising because it is much longer than can be explained by a low overall transmission rate. To explore possible mechanisms that could underlie the observed pattern, we extended the standard basic Susceptible-Infectious (SI) model to include the environment as an infectivity reservoir, developing a class of mathematical models describing different scenarios of indirect transmission. Several scenarios from this general class were tested against the results of the transmission experiments. This revealed that the experimental observations can neither be explained in terms of purely airborne transmission, nor in terms of transmission via a simple, unstructured environmental reservoir. However, two more complex scenarios of indirect transmission were shown to be compatible with the observations, suggesting that transmission occurs through progressive (but slow) contamination of the environment surrounding the source.

Contribution of foot-and-mouth disease virus contaminated environment to the transmission of the disease in calves

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Foot-and-Mouth Disease (FMD) infected animals can contaminate the environment with their secretions and excretions. There is a lack of knowledge on the contribution of a FMD virus contaminated environment to the transmission of the disease. The aim of this study was to quantify direct and indirect transmission in naïve calves. Indirect transmission was studied by using pens that had previously housed infected calves and by introducing infection-free calves to these facilities. Oropharyngeal fluid swabs, urine, faeces and blood samples were collected and it was analysed whether they were positive for FMD virus. We used a modified SIR model to calculate the transmission rate parameter caused by direct contact, which is the average number of secondary infections caused by one infectious animal per day and, to calculate the transmission rate parameter caused by indirect contact, which is the average number of new infections caused by the environment contaminated by one infectious animal one or more days ago. The modified SIR model includes virus decay (estimated from laboratory experiments) and accumulation of virus in the environment (because of the presence of an infected animal the preceding day). Both direct and indirect transmission occurred. Using the estimates for the transmission parameters and the infectious periods, we calculated the reproduction ratio's R direct and indirect. Our findings show that a contaminated environment with FMD virus has an important role in FMD virus transmission, because even after removal of infected cattle, contact cattle can still become infected.

Effects of transmission of a live *Eimeria acervulina* vaccine strain on infection dynamics with a homologous wild-type strain in broilers

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Coccidiosis is one of the most costly diseases in broilers. Restrictions of anticoccidials will make alternative strategies, e.g. vaccination, essential for broiler production. Live vaccines are infrequently used in broilers, mainly due to variability in efficacy and high costs. Improved efficacy may increase its use. The transmission rate of vaccine and wild-type strains can affect efficacy of interventions. Therefore, we quantified transmission of a live *Eimeria acervulina* vaccine strain and determined degree of protection against a subsequent infection with a wild-type *E. acervulina* strain. An experiment was carried out with 4 groups of 22 SPF broilers. At 2 days of age, 11 birds of groups 2-4 were vaccinated directly by oral application of *E. acervulina* oocysts of the Paracox™ vaccine and 11 birds were placed in contact with these birds (contact-vaccinated). Birds in group 1 remained unvaccinated (controls) and were not exposed to vaccinated birds. At day 28 of age, 6 groups of 10 birds were formed, with 2 groups (duplo) for each treatment group, i.e. vaccinated, contact-vaccinated or unvaccinated control birds. Five birds of each group were orally inoculated with wild-type *E. acervulina* oocysts and five were contact-exposed. Individual droppings were collected daily from days 5-49 of age to quantify oocyst output and determine time of infection. The transmission rate of the vaccine was estimated at 1.6 day⁻¹. Although transmission of wild-type coccidia was not significantly reduced in vaccinated or contact-vaccinated groups, both groups were equally protected against high oocyst output after infection with the wild-type strain compared to unvaccinated groups. This suggest that factors influencing transmission of vaccine strains may be important targets for improvement of vaccine efficacy and warrant further research.

The influence of herd size on the spread of classical swine fever during the 1997-1998 epidemic in the Netherlands

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As livestock farms in The Netherlands are nowadays being scaled up in size for economic reasons, the question becomes important how disease introduction risks and risks of onward transmission scale with farm size (i.e. with the number of pigs on the farm). Here we use the epidemic data of the 1997-1998 epidemic of Classical Swine Fever Virus (CSF) in The Netherlands to address this question for CSF risks. This dataset is one of the most powerful ones statistically as in this epidemic a total of 428 pig farms were infected (with the majority of farm sizes ranging between 27 and 1,750 pigs). We have extended the earlier models for the transmission risk as a function of between-farm distance, by adding two size dependent factors: these factors describe the farm size dependence of, respectively, the susceptibility of an exposed farm and the infectivity of a source farm. Using the best-fitting model, we show that the size of a farm has a significant influence on both farm-level susceptibility and infectivity for CSF. Although larger farms are both more susceptible to CSF and, when infected, more infectious to other farms than smaller farms, the increase is less than linear. According to the best-fitting model, the higher the farm size, the smaller the effect on the susceptibility and infectivity of a farm of increments in farm size. We show that this implies, based on the pig farming characteristics of 1997-1998 in The Netherlands and assuming that the relative spatial distribution of farm locations does not change, a trend towards less but larger farms would produce a net decrease in between-farm transmission risks.

Whole genome sequencing and mathematical modelling of *Mycobacterium bovis* in sympatric cattle and badger populations

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Whole genome sequencing (WGS) holds great promise as a tool for studying the transmission dynamics of an observed epidemic involving a largely unsampled 'reservoir' host, as is the case for bovine tuberculosis (bTB) in British and Irish cattle and badgers. However, such data can require considerable interpretation, particularly if used to infer patterns of fine-scale transmission dynamics. Mathematical models are ideal vehicles for this interpretation, however approaches integrating models and genetic data require good datasets to validate them. Here, we analyse bTB transmission dynamics in Northern Irish cattle and badgers, where there are extensive demographic and livestock movement data, in combination with *Mycobacterium bovis* sequences from a spatially clustered group of infected cattle and badgers. Comparing WGS data to mathematical transmission models showed good correlations between the distributions of single nucleotide polymorphisms and the spatial and within-herd contact structure, but poor correspondence to the network of cattle movements linking them. Despite badgers being under-sampled, our data provided evidence for recent transmission events between the two host species, and an unprecedented resolution of the spatial correlation between these. These results provide the first direct genetic evidence of *M. bovis* persistence on farms over multiple outbreaks with a continued, ongoing interaction with *M. bovis* in badgers.

Factors influencing the immune response of vaccinated poultry in the Mekong region of Viet Nam

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A prospective cohort study was carried out to quantify the length of time taken for poultry to become H5 seronegative following a H5N1 vaccination event. Flocks from eight villages in two provinces (Can Tho and Bac Lieu) in the Mekong region of Viet Nam took part. One hundred and fifty seven poultry flocks were enrolled. Flocks were visited monthly between December 2008 and April 2010. A total of 14,878 serum samples were collected from 5,476 birds over the follow-up period and tested using the haemagglutination inhibition test. Survival analyses were carried out to determine how long it took for vaccinated birds to become H5 seronegative. Because birds were sampled at set times throughout the follow up period this was treated as an interval censored data set. Fifty percent of birds were seronegative by 59 (95% CI 54-64) days following vaccination. A parametric accelerated failure time model based on the Weibull distribution showed that the time taken to become seronegative for layer ducks and in-contact species (chicken) was increased by a factor of 3.26 (95% CI 2.59-4.10) and 1.96 (95% CI 1.55-2.48) respectively compared with broiler ducks. Compared with those vaccinated during the two low risk periods, the time taken to become seronegative for birds vaccinated during the two high risk periods was decreased by a factor of 0.72 (95% CI 0.61-0.84) and 0.75 (95% CI 0.64-0.89), respectively. Compared with birds vaccinated by staff from their own commune, the time taken to become seronegative for birds vaccinated by staff from other communes was decreased by a factor of 0.62 (95% CI 0.47-0.82). This study has identified some critical focus areas if vaccination is to continue to be used as a means for controlling HPAI H5N1 in village poultry populations in Viet Nam.

Faecal shedding probabilities in cattle with different *Salmonella dublin* antibody profiles

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Salmonella Dublin carriers contribute to the bacterial load in infected cattle herds by intermittent shedding of bacteria in faeces, and might be detected based on persistently high antibody levels in serum or milk. The objective was to estimate the probability of faecal *S. Dublin* shedding in individual cattle in risk groups (R1, R2, R3 and R4) based on repeated antibody measurements over a period of 1½ years in cattle in 14 infected Danish dairy herds. A total of 2,669 animals had paired faecal cultures and antibody measurements performed between 1 and 5 times each. R1 had persistently high antibody levels (>80 ODC%), R2 had moderately high antibody levels once or several times (50-80 ODC%), R3 had low to medium antibody levels (25-50 ODC%) and R4 had continuously low antibody levels (<25 ODC%). The overall shedding probability was 1.7%. In R1 it was 3.4%, in R2 2.7%, in R3 1.0% and in R4 0.6%. A logistic regression model taking into account clustering at herd level was used to estimate the probability of shedding at a given age for each antibody profile. The resulting probabilities of faecal shedding were up to 10 times higher in young stock than in cattle above approximately 4 years old, which had probabilities of shedding *S. Dublin* <2%. Younger cattle in the two high risk antibody profile groups (R1 and R2) had significantly higher risk of shedding *S. Dublin* than animals with R3 and R4 antibody profiles. The highest shedding probability predicted by the logistic regression model was 11%. The true probability is very likely 4-5 times higher, because the diagnostic sensitivity of faecal culture is poor. Hence, carrier detection by repeated antibody testing could be relevant, at least in young stock and 1st parity cows, in herds attempting to control or eradicate *S. Dublin* from the cattle population, but cost-benefit analyses are necessary to determine the value of such procedures.

Age and dose dependent susceptibility to *Mycobacterium avium* subspecies *paratuberculosis* infection in dairy calves

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Johne's Disease (JD) is a chronic enteritis of ruminants, caused by *Mycobacterium avium* subsp. *paratuberculosis* (MAP). As no cure is available, prevention programs are necessary and based on age related susceptibility, but this is supported by limited data. Additionally, diagnosis of MAP infection is hampered by low sensitivity of the commonly used diagnostics. The reason for this low sensitivity is that immune responses are localized in the gut during the long incubation period (years) and therefore difficult to detect systemically. We conducted an infection experiment to prove age related susceptibility and analyse the accuracy of diagnostics. Thirty-three calves were divided in 10 experimental groups and were infected at 5 different ages (14 days, 3, 6, 9 & 12 months) and with 2 different doses of MAP. Samples were collected monthly for serum ELISA, IFN- γ ELISA and fecal culture. All calves were euthanized when 17 months old to determine the infection status using histopathology and tissue culture. Serum ELISA results were summarized as area under the curve for each calf and analysed with Kruskal-Wallis test. A dose dependent IFN- γ response can be detected 2 months post-infection in all animals, with a peak at 3 months and a slight decrease afterwards. Animals test positive in antibody ELISA as of 3 months post infection, but antibody titers are not consistently present in all animals. Compared to younger infection groups, calves infected at an older age respond with a higher antibody titer early after infection. Fecal shedding can be noticed as of 1 month post-infection in some animals and is intermittent and low during the trial. After necropsy, most animals were confirmed to be infected with MAP. Diagnostic tests seem to detect IFN- γ , antibody titers and fecal shedding earlier than previously believed. We have proof that there is no age related susceptibility, but the dose has an impact on the progression of infection.

Use of cow characteristics to explain differences in *Mycobacterium avium* subspecies *paratuberculosis* ELISA results between serum and milk samples

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The performance of antibody ELISAs for the detection of *Mycobacterium avium* subspecies *paratuberculosis* (MAP) infection is dependent on the within-herd prevalence and differs depending on the type of matrices used (blood versus milk). The objectives of this study were to evaluate a commercially available ELISA kit in low MAP prevalence herds using serum and milk samples, and to evaluate whether cow characteristics explain the difference between ELISA results. Cows on 24 Alberta dairy farms were sampled twice within a 2-year period. During each visit, fecal and blood samples were collected from all cows over 36 months of age. Milk samples were acquired through the Canadian Herd Improvement Program (Canwest DHI) that also provided the individual cow production data records. Fecal samples were processed in pools of 5 using the TREK ESP culture system with IS900 PCR as confirmation. Individual animal fecal samples corresponding to positive pools were tested to identify positive cows in the pools. Using fecal culture as the gold standard, the performance of the 2 sample types was compared by ROC-analysis. The relationship between the outcome (milk ELISA s/p ratio) and the key predictors (serum ELISA s/p ratio, cow characteristics) was examined with multilevel linear regression on the levels herd, cow and year of observation. The individual animal prevalence determined by fecal culture was 1.2%. Greater area under the ROC-curve suggested greater cut-off independent prediction of fecal culture results by the serum ELISA than by the milk ELISA (0.71 versus 0.57). The relationship between milk and serum ELISA results was modified by the milk yield and the protein content. Based on the impact of the milk characteristics, we conclude milk yield and protein content should be considered when interpreting milk ELISA results.

Size of the iceberg: proportion of *Mycobacterium avium* subsp. *paratuberculosis* infected cattle with and without specific antibodies

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Diagnosis of chronic infections such as infections with *Mycobacterium avium* subsp. *paratuberculosis* (MAP) may be hampered by low sensitivity of diagnostic tests, because the infection remains latent. However, sensitivity increases with age because few infections remain latent. The proportion of detectable infections among all infected is often referred to as 'the tip of the iceberg'. For MAP infections, infected cattle may be divided into those with cell-mediated immune reactions (CMI) during latent infection, and those with humoral immune reactions (HI) characterized by IgG₁ antibodies. The purpose of this study was to estimate the proportion of cows having HI among all cows infected with MAP by assuming an infected cow had either CMI or HI. Prior test-records from 12,174 Danish dairy cows, which were ultimately deemed to have MAP specific IgG₁ antibodies, were used to estimate age-specific sensitivities (Se). The specificity (Sp) of the test was estimated based on prior test-results among 96,138 cows, which ultimately had no MAP IgG₁ antibodies. The Sp, age-specific Se and maximum Se were used to estimate the probability of having CMI and HI at a given age supplying the proportion of infected cows with HI at a given age. The Sp was estimated to 0.985. Se ranged from 0.22 at 2 years of age to 0.58 at 3 years of age, 0.74 at 4 years of age to a maximum of 0.83 at 10 years of age. The resulting proportions of infected cows with HI were 0.24 at 2 years of age and 0.96 at 5 years of age, i.e. a significant shift in the size of the iceberg. Although the 'iceberg' concept is well-known among paratuberculosis researchers, the size of the iceberg has not previously been characterized. Results can be used for inclusion of the distribution of cows in different infection stages at different ages in mathematical modeling of infection dynamics. In practice, positive and negative predictive values can be calculated for cows at different ages and in populations with different prevalences.

Evaluation of the *Salmonella* surveillance program in Belgian pig farms

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Belgium has implemented a national surveillance and control program for *Salmonella* in pigs in 2007. Pig farms are designated as *Salmonella* high risk farms based on serological profiles and are obliged to subsequently take part in a *Salmonella* Specific Action Plan (SSAP). The SSAP was evaluated and risk factors for the persistence of *Salmonella* on the farm were investigated. The Kaplan-Meier method was used to study the period during which a farm maintains a *Salmonella* high risk status. Farms recovered more slowly from their high risk status before the SSAP was implemented compared to after the program was implemented (P<0.001). However, results showed that 29% of the farms were withdrawn from the program possibly only because of sampling error. Secondly, the influence of several risk factors (type of farm, season of entrance into the SSAP, size of farm and farm density of the municipality) on the time to withdrawal from the high risk status was evaluated using univariable methods and a Cox multiple regression model for survival data. A statistically significant association was identified between the type of farm and the time to withdrawal from the high risk status. At any point in time after the onset of the SSAP, withdrawals from the high risk status occurred at a 39% and 28% higher rate in mixed (P=0.01) and fattening farms (P=0.05) respectively compared to closed farms. The risk attributed to closed farms is related to the presence of sows in this particular type of structure, which underlines the importance of implementing control measures in this category of animals.

Position and time related *Salmonella* findings in a swine holding

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A farm with sows and fattening pigs was visited 12 times in 2 week intervals, samples were taken from animals during their lifetime, after slaughter and from the environment (the site, buildings, equipment, persons). During this visitation period, three groups of pigs could be followed completely during their fattening period, other groups were only partly overlapping with the observation period. In total, 1956 samples were taken and examined for *Salmonella*. Isolates were then serotyped acct. to the Kauffman-White scheme. Control and prevention of *Salmonella* depends on insight and understanding. It was intended to find possible transfer routes based on the given in-farm organisation within the given structures on one farm area. Results: In total, 196 out of 1956 samples were positive (10.0%), with different results depending on the sampling occasion (minimum 5.3% and maximum 21.2%). All isolates were identified as *Salmonella* Typhimurium. Within this serotype, we identified monophasic (4,12:i:- and 4,5,12:i:-) and biphasic (4,12:i:1,2 and 4,5,12:i:1,2) variants as well. The isolates could be followed and re-identified during the period of observation, in addition, the animals were moved through the stable's compartments, which could be reflected by the isolation of identical strains (serotyping). Data indicate a stabile prevalence of a special serotype (with several variants) on a site over several months. However, within such a site, the agents may change in relation to their carriers. It was concluded, that individual analysis is needed to control the transfer of *Salmonella*, which is based on the technical and organisation structures on the farm.

Correlation between antibodies in pig slaughterhouse blood and KPIs

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Prevention in pig herd health and on farm management are rarely based on monitoring slaughterhouse blood. The objective of the present study is to assess the value of serology on pathogens associated with respiratory diseases in blood taken at slaughter for pig herd health management, including reduction of antibiotic use. For this purpose 20 herds in the Southeast of Germany were selected. A priori information about pneumonia at meat inspection in 2010, which varied from 1.23% to 33.92%, was used to select the farms. Blood was collected from 15 randomly selected pigs from two deliveries (n=300) of one fattening period (February to August 2011) and submitted for ELISA-serology. Additionally, meat inspection results of the supplies and farm performance data were collected. The Spearman's correlation coefficients between rejected lungs (middle and high pneumonia) during meat inspection and percentage of positive pigs per herd for PRRSV were respectively 0.714 (P=0.000), PCV2 0.874 (P=0.000), Influenza 0.318 (P=0.127), *M. hyopneumoniae* 0.771 (P=0.000) and APP2 0.596 (P=0.006). The Spearman's correlation coefficient between sum of positive serological parameters (SSOP) and rejected lungs was 0.676, (P=0.011). All five pathogens explain 76.1% of rejected lungs (quadratic R²=0.761). Spearman's correlation coefficient was 0.920 (P=0.000). Correlation coefficient between SOPP and growth rate was -0.496 (P=0.036) and feed conversion rate 0.564 (P=0.018). There are significant correlations between SOPPs and rejected lungs, growth and feed conversion rate. The results indicate that the information gained by slaughterhouse blood can be applied to support preventive herd health management and therefore can be used as additional service for net chain coordinators. Ongoing research is presented that investigated the relation of these serological results with farm observations, with health assessment at farm and the robustness of the data.

Effect of a disinfection strategy on the MRSA prevalence in pigs

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Livestock-associated methicillin-resistant *Staphylococcus aureus* (MRSA) is abundantly present in pigs. Since sows act as MRSA reservoir for their piglets, decontamination practices of sows might reduce MRSA prevalence in sows and their offspring. In this study, a disinfection strategy was tested on 2 Belgian farrow-to-finish pig farms for 6 months. Six sow rounds were sampled, sows were divided into either a test (3 rounds) or control group (3 rounds). Per round, 20 sows and 40 of their piglets were sampled at different time points. The farrowing and the swine nursery unit for both groups was always cleaned and disinfected. The disinfection strategy of the test groups consisted of washing the sows to remove dirt before entry in the farrowing unit followed by disinfection of the skin during 6 days prior to farrowing by spraying a solution containing chlorhexidine digluconate (<1%) and isopropanol (1-5%) (off label use). The skin of sows & piglets was swabbed behind both ears, all swab specimens were further processed as was previously described. Preliminary results of the first 4 rounds, showed a decrease of 60% in sow MRSA prevalence in the test group on the 1st day of disinfection. 10 days after start of the disinfection strategy, a decrease of 69% was found, at weaning this was only 5%. The MRSA prevalence of the piglets in the test groups was 22% lower in the 1st week of life, but just before weaning this was only 7% in comparison to the control group. In conclusion, preliminary results show that the tested disinfection strategy reduces temporary the sow and piglet MRSA status based on skin samples.

Dynamics of infectious agents associated with pleuritis and pneumonia in French farrow-to-finish pig herds

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A study was carried out in 125 farrow-to-finish pig herds to assess the relationships between five pathogens involved in respiratory disorders and to relate these findings to clinical signs of respiratory diseases and lung lesions at slaughter. Clinical examination and sampling were carried out on four different batches in each herd (pigs aged 4, 10, 16 and 22 weeks). *Mycoplasma hyopneumoniae*, *Actinobacillus pleuropneumoniae*, swine influenza viruses (SIV) of European H1N1 and H1N2 lineages, porcine reproductive and respiratory syndrome virus (PRRSV) and porcine circovirus type 2 (PCV2) were detected by serological or PCR tests. Pneumonia-like gross lesions and pleuritis were scored at the slaughterhouse on a random sample of 30 pigs per herd corresponding to the batch sampled on the farm at 22 weeks of age. The results indicated that the percentage of PCR-positive pigs for PCV2 at 4, 10 and 16 weeks old was associated with the percentage of PCR-positive pigs for *M. hyopneumoniae* at these ages. On the other hand, the percentage of pigs with antibodies against PRRSV at 10, 16 and 22 weeks of age was positively correlated with the percentage of pigs seropositive for *M. hyopneumoniae* at 22 weeks, with the percentage of pigs with antibodies against SIV H1N1 and SIV H1N2 and the percentage of pigs sero-positive for *A. pleuropneumoniae* serotype 2. The findings also showed that, among the five studied pathogens, *M. hyopneumoniae*, PRRSV and SIV H1N1 were the main pathogens related to pneumonia-like gross lesions even though PCV2 might play a role. *A. pleuropneumoniae* serotype 2, in association with PRRSV, was significantly associated with extensive pleuritis. Respiratory diseases could significantly be reduced by implementing measures including appropriate management practices to control these pathogens.

A risk-factor based pig herd index to evaluate the perspectives for a regional PRRSV eradication

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Since its emergence in the 1990ies, Porcine Reproductive and Respiratory Syndrome Virus (PRRSV) has become widely distributed in Europe, leading to production losses due to reproductive disorders and respiratory symptoms in pigs. Among stakeholders of the pig production chain, a possible eradication is intensively discussed, even though perspectives for such efforts are difficult to predict. Various strategies have proven successful to achieve freedom from PRRSV in individual herds. However, the cost-effectiveness of such efforts for whole regions depends on the risk of reintroduction of the virus once it has been eradicated. In order to provide a basis for these considerations, we created a methodological approach that can support assessing the feasibility of a sustainable PRRSV eradication in defined regions. For this purpose, we chose two exemplary counties in the pig-dense Northwest of Germany (estimated inter herd prevalence 90-95%) and received anonymized data for all pig herds (n=2,416) from the veterinary administration. Datasets included exact herd sizes, animal categories, and geo-referenced data providing information on proximity to neighboring herds. Using this information, and based on knowledge from literature and expert opinion, a risk-factor based index was calculated for each herd, relating to its respective risk of endemic virus circulation in the herd and reinfection during and after virus eradication. When mapping the geographical distribution of the indexed herds, we identified regions with comparably high risk of (re)introduction and endemic circulation of the virus as well as 'lower risk' regions with better chances for sustained disease freedom post eradication. On this basis, suggestions on implementation of eradication measures could be developed, possibly get extended to other regions, and thus provide a foundation for management and policy decisions.

Individual pig care (IPC), a new management tool for improved responsible use of medicines

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The individual pig care (IPC) is a new management tool for swine farmers in Europe, based in daily keen observation of the pigs, early detection of husbandry and health problems and prompt and accurate reaction to them, based on fast data collection and processing. The objective of this study was to validate this new management tool. A multicentric trial in 10 different herds – 7 in Germany and 3 in Spain – was rolled out in the last part of 2011 to evaluate a new management protocol to early identify sickness in nursery and in grower phase pigs. The IPC method includes daily observations and reporting in a methodical manner. In total 7 nursery herds (about 3,000 animals) and 3 growing-finishing herds (5,000 animals) were monitored over a period of 6 months. Parameters evaluated included respiratory-, enteric-, lameness-, neurological and biting signs. Specific actions are linked to the severity of the observed symptoms including decisions on type and route of treatment methods. All the data are digitally collected and transferred to a protected server in 'real time'. This system allows for daily feedback and progress monitoring. The preliminary results demonstrate that this method (IPC) when compared to traditional management on the same farms allows for significant reduction in mortality in the nursery phase (observations ranged up to 40% reduction in mortality) with a decrease of amounts of antibiotics used (observations ranged up to 47%), and an increase in average daily weight gain (observations ranged up 10% in certain periods) with a body weight homogeneity improvement within pens. In conclusion, early detection of symptoms is the key point of the IPC, allowing a faster reaction on events with a better result at the end in production and health. As a result, a more prudent use of antibiotics is promoted.

Abattoir condemn data used to identify regional swine TB event

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By combining practitioner information with broader USDA FSIS abattoir condemn data, we describe an emerging regional swine TB (STB) event. In January 2010, one abattoir reported unusually high STB condemnments and informed the producers who supplied the affected pigs. *Mycobacterium avium* was isolated from tissue samples taken from the condemned carcasses. *M. avium* is ubiquitous in the environment worldwide and occasionally affects swine, but is typically not transmissible to humans. In the spring of 2010, USDA Veterinary Services independently became aware of unusual increases in STB abattoir condemnments in an area 200 miles from the abattoir affected earlier that year. STB condemn rates in both affected areas subsided to typical low seasonal levels by June 2010. Beginning January 2011, condemn rates again rose above seasonal baselines and exceeded the 2010 rates. We identified pre-outbreak condemn baselines, quantified differences in the 2010 and 2011 STB outbreaks, and determined the geographic extent of the outbreaks. For the analysis, we grouped June 2007 to May 2011 FSIS market swine condemn data by three major swine producing areas with a fourth area representing the residual of U.S. market swine abattoirs. Periods of anomalous condemn rates were identified by production area and individual abattoir. Mean weekly STB condemn rates, which ranged from 5.7 to 21.4 per 100,000 swine between 2007 and 2009 (mean=10.7, SD=3.0), exceeded typical levels beginning Jan 2010 and rose even higher beginning Jan 2011. Most of the increase is due to condemnments in one of the four production areas, where weekly STB condemnments reached 670/100,000 at the peak of the 2011 outbreak. Data for the other three areas indicate that condemnments appeared to remain at non-outbreak rates over the four-year data series. Analysis by individual facility suggests that while condemnments in one of the presumably unaffected areas seemed to coincide with typical seasonal STB rates, the pattern for one facility implies atypically high STB rates in both outbreak periods.

Economic analysis of alternate Rift Valley fever control options from a multisector perspective

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Rift Valley fever, a viral zoonosis that primarily affects people, livestock and wild animals. The two most recent epidemics in Kenya occurred in 1998 and in 2007 with severe impacts in multiple sectors. We undertook a study to provide policy evidence on cost-effectiveness and benefits associated with alternate control options from a multisectoral perspective. Also undertaken is a one health (OH) institutional analysis for improved prevention and control. A multistage methodology involved: (1) mapping of OH stakeholders and an institutional analysis; (2) simulation of different options using an individual-based epidemiological model; and (3) economic modeling to estimate costs per disability averted and benefits to the livestock and other sectors. Up to 28 different OH relevant agencies (spanning beyond the line animal and public health sectors) were mapped and involved in the institutional analysis. Socio network analysis reveals denser networks and stronger relational linkages between the public health stakeholders while the reverse is true for animal health stakeholders. Centrality statistics measures of Degree, Betweenness and Closeness identified the two health sectors, and the community as being the actors who linked clusters within the network. A non health ministry emerged as the actor demonstrating the highest closeness to all actors, making it an important coordination organ. The study concludes that the current narrow scope of OH through collaboration of animal and human health agencies leaves out critical non health actors and the community which could impact on control of zoonoses. Preliminary cost-benefit analysis of animal vaccination demonstrates fairly good returns to investment.

Developments in risk-based decision making: responding to the threat of Rift Valley Fever (RVF) and other transboundary diseases

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Following the 2006-2007 outbreak of RVF in East Africa, the International Livestock Research Institute (ILRI), UN-FAO and US-Centers for Disease Control and Prevention organized a series of meeting for decision-makers to discuss how responses to the outbreak could have been conducted in a more timely and effective manner. Participants observed that the 'all or nothing' approach used in the decision to declare the emergency and mobilize responses did not contribute to the successful mitigation of the outbreak. Stakeholders concluded that a phased approach to decision-making utilizing incremental responses to the escalating risk of an outbreak could be more effective. They built a decision framework based on a matrix of events paired with action categories. The events served as decision points, and the action categories suggested responses at each point. Initially, the framework was named a decision support tool, but the RVF Risk-Based Decision Framework (RVF-RBDF) is now recognized as a more accurate name for this innovation. The RBDF enjoyed interest and decision-makers used the framework to mobilize actions to the RVF alarm of 2008. The framework is not prescriptive and easily incorporates technical enhancements such as new generation risk maps or more efficient vaccination strategies. In 2011, representatives of the Horn of Africa and the Middle East reviewed the RVF-RBDF at a meeting held in Dubai and hosted by ILRI and the African Union Inter-African Bureau for Animal Resources. The meeting recommended that the RVF-RBDF be developed as a framework for management of RVF risk in inter-regional trade. The meeting noted that the RVF-RBDF was a new paradigm for animal health management that merited application to other health issues as well. Plans are underway to apply the framework process in the regional context of North Africa using the lessons of the 2011 RVF outbreak in Mauritania.

Session 43**Theatre 3****A bioeconomic analysis of disease transmission between wildlife and livestock populations in Limpopo Province, South Africa: conservation vs. livelihoods**

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The establishment of national parks and protected areas has noticeably conserved wildlife that could nearly be extinct and preserved biodiversity. However, for most African countries, and developing countries in general, conservation policy has been received with resentment by the local people since this policy threatened their main source of livelihoods. In addition, wildlife often escape from protected areas into adjacent areas where they interact with the livestock of livestock farmers, competing for grazing pastures with the potential for transmitting diseases such as foot-and-mouth disease (FMD). The aim of this presentation is to determine the impact of potential transmission of FMD on the livelihoods of small-scale livestock farmers through the interface with wildlife populations. The study develops a bioeconomic model which analyzes the trade-offs between keeping wildlife in the park as a conservation value and the livestock that support the livelihoods of small-scale farmers in an overall optimal way in the presence of such disease transmission. The reduction in livelihoods is addressed through the reduction in the market value of the cattle. This scheme is compared to the situation with the absence of unified resource management policy, and also when there is no disease transmission. Data from Kruger National Park and livestock farmers living in the adjacent areas will serve as a demonstration of this model. Preliminary results show that when the park agency is steering the management of resources, the net benefit, or welfare, of the small scale farmers may be reduced by about 8% with the baseline parameter values compared to the hypothetical situation of no disease transmission. This reduction is due to lower slaughter market price, and not lower cattle stock size and total harvest. Under unified strategy, the reduction in welfare is about 5%, which is also due to fall in the slaughter market price.

Social-psychological factors likely to influence movement ban compliance during an outbreak of FMD
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The severity of an outbreak of foot-and-mouth disease (FMD) can be affected by the extent of early disease spread and the effectiveness of control measures. Movement restrictions are a key component of response plans; however, modern animal production systems rely on the ability to move animals, and producers may experience social, economic, and emotional pressure to move animals during an outbreak. Two questionnaires were developed and distributed to 2,018 and 2,022 Texas cow-calf producers, respectively, in order to determine the factors which best predict producers' intentions to obey animal movement restrictions during a hypothetical outbreak of FMD. Factor analysis, followed by multivariable, ordinal logistic regression was used to predict producers' intentions. The less unpleasant, difficult, or inconvenient producers felt that keeping their cattle in place during an outbreak would be, the greater the odds that they would intend to comply with animal movement restrictions (OR 13.48 for highest category, $P < 0.05$). In addition, producers who believed that they had access to adequate feed, facilities for calves born, and were able to set up disinfection procedures, were more likely to intend to comply (OR 88.02 for the highest category, $P < 0.001$). Producers' beliefs about what other producers like themselves would do had a significant effect on their intention to comply, and the odds of intending to comply were over 6 times greater for producers who agreed that other producers would comply with the movement restrictions ($P < 0.001$). Of concern, increased perception of the risk posed by FMD (overall risk and probability) was associated with a decreased intention to obey movement restrictions (OR for highest category 0.55, $P < 0.05$).

Newcastle disease vaccination: from technology to poverty reduction

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Newcastle disease (ND) is a major constraint to village chicken production in Africa. In endemic areas up to 50-100% of the village flock is lost annually. Women poultry-keepers lose assets, income and ability to feed their families. Vaccines are highly effective, yet use in villages is low and little is known about the reasons for this. In 2003-2005 a project worked to promote the use of the I-2 ND vaccine in Chamwino District, Tanzania. This thermotolerant vaccine, developed by the University of Queensland, is affordable, effective, and easy to administer. Five years later, we investigated vaccine uptake. Villages were stratified by delivery system (project, and active, inactive, and no extension), 2 were randomly selected from each strata, and households randomly sampled. Questionnaires ($n=456$), conjoint analysis ($n=455$), participatory appraisal ($n=100$ participants) and gender-specific focus group discussion ($n=206$) were used to assess social, cultural and economic determinants of vaccination. Losses from ND were high: households kept on average 15 poultry, and had lost 20 in the last year, 15 from ND. Only 1/3 had vaccinated in the last year. Conjoint analysis found distance and price were more important vaccine attributes than effectiveness or bundled services. Wealth, gender, knowledge, and disease impacts all influenced uptake, but more important were previous experiences of vaccination and the delivery system available. With adequate systems, vaccination delivered major benefits; with poor systems vaccination was associated with increased losses. In the study area, the major driver for vaccine uptake failure is not poultry-keepers but the services available to them. Given active extension, well-trained vaccinators, and participatory service delivery, ND vaccine can bring important benefits to poultry health and livelihoods of the poor.

Understanding socio-economic determinants associated with disease spread: HPAI H5N1 in backyard poultry marketing chains, Thailand

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Controlling the Highly Pathogenic Avian Influenza (HPAI) caused by the H5N1 virus in the poultry population is essential regarding the socioeconomic importance of the sector and for public health reasons. The disease is now endemic in several countries. Surveillance and control of HPAI H5N1 in the backyard poultry sector is particularly challenging, as farmers have been pointed out for underreporting outbreaks and avoiding control measures. However, the organization of this marketing chain is not well known. A value chain analysis was used to describe the organization of the supply chains of backyard poultry in Thailand, and identify key agents who may represent disease spreading nodes in the network. A field study was carried out to investigate the chains supplying native chickens to Phitsanulok city (a large city located in the central plain of Thailand). Quantitative data were collected on 473 backyard chicken farms, and on the 5 wet markets of the city. Qualitative data were collected on 17 poultry collectors and slaughterhouses, using semi-structured interviews. Findings from this study document the importance of native chickens and identify how bird collectors may spread the disease. The study describes the strategies developed by actors faced to an epidemic, and discusses the social and economical factors that influence those strategies. Trading sick chickens was one of the strategies developed by poultry collectors in case of outbreaks. This practice favoured disease spread but allowed limiting financial losses given the severe economic constraints. Results from this study should help tailoring the surveillance, control and incentive system to the backyard poultry sector in Thailand and in countries with similar context.

Cattle producers' economic incentives for preventing bovine brucellosis under uncertainty

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Cattle in the Greater Yellowstone Ecosystem (GYE) of the United States occasionally contract bovine brucellosis from free-ranging elk and bison. Cattle producers use a variety of prevention activities to reduce their herds' brucellosis risk, such as fencing haystacks, administering adult booster vaccination, and spaying heifers. Their prevention decisions are complicated, however, by uncertainty about their herd's baseline risk, and the cost and effectiveness of prevention activities. Our study reduces uncertainty by estimating the cost of various brucellosis prevention activities for cow/calf/yearling producers in the GYE, and the minimum level of effectiveness each prevention activity must achieve to justify investment by a risk-neutral producer. These 'breakeven levels of effectiveness' are estimated for various levels of baseline risk and government policies. When economic loss to brucellosis is \$40,181 (assuming a policy of compensated depopulation), a producer whose herd faces a 1% probability of contracting brucellosis can justify investing in few prevention activities. Only when economic loss rises to \$134,818 (under a policy of uncompensated quarantine) can a risk-neutral producer whose herd faces a 1% baseline risk justify activities such as adult booster vaccination. As baseline risk increases to 5%, spaying heifers needs to reduce a herd's baseline risk by only 52% to justify implementation, assuming the herd faces a policy of uncompensated quarantine. Producers can use breakeven levels of effectiveness to narrow down the list of brucellosis prevention activities worth considering, and determine which activities are most likely to generate positive expected net benefits. Policymakers and animal health experts can use our results to target their cost-share agreements more effectively. Epidemiologists can use our results to determine on which prevention activities to focus future research to generate the most useful information for stakeholders.

Latent-conditional individual-level models for infectious disease transmission

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Individual-level models, as described in Deardon *et al.*, are a class of statistical infectious disease transmission model that have previously been used to model the spatio-temporal spread of infectious diseases. These models can incorporate individual-level covariate information, such as vaccination status or geographic location, to account for population heterogeneity. However, incomplete or unreliable data is a common problem in infectious disease modelling, and models that are explicitly dependent on such information may not be robust to the inherent uncertainties. In this investigation, we assess an adaptation of a simple spatial individual-level model that incorporates a latent grouping structure based on some trait heterogeneous in the population. The resulting individual-level model is then only dependent upon a discrete latent grouping variable, rather than original unknown covariate information. Here we test the performance of this new 'latent-conditional' model using simulated data before applying it to data from the 2001 UK foot-and-mouth disease epidemic. Models are fitted within a data-augmented Bayesian framework using Markov chain Monte Carlo methods. This study demonstrates that the use of a discrete latent grouping variable is an effective alternative to utilizing covariate information, particularly when such information may be unreliable.

Investigating effects of between- and within- host variability on *Escherichia coli* O157 shedding pattern and transmission

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Cattle are the reservoir for the human pathogen *Escherichia coli* O157. Supershedders have been loosely defined as cattle that shed high concentrations of *E. coli* O157 ($\geq 10^3$ or $\geq 10^4$ cfu/g of feces) at a single (or multiple) cross-section in time. Interpreting cross-sectional fecal bacteria distribution is difficult due to the variability in the pathogen shedding level among animals, as well as fluctuations in the level shed by a single animal. We developed an individual-based model (IBM) that integrates individual animal data on temporal fecal shedding dynamics with pen-level *E. coli* O157 transmission to study how the temporal (and aggregation) patterns of *E. coli* O157 shedding loads and prevalence arise at the pen level. Longitudinal shedding patterns obtained from 33 orally challenged calves were integrated to an IBM that considered four epidemiological statuses for the animals: primary and secondary susceptible, and primary and secondary infectious states. We simulated two scenarios: (1) without individual variability (i.e. all animals had the same shedding pattern); and (2) with individual variability (i.e. animals had different shedding patterns). Both scenarios generated similar overall disease dynamics, time series of disease prevalence, and number of supershedders (defined as $\geq 10^4$ cfu/g of feces). The scenario without individual variation generated heterogeneous patterns of transmission. Even without between-host variability, the proportion of animals with concentration of *E. coli* O157 $> 10^4$ cfu/g in feces is similar to that observed in cross-sectional field data. These animals might be misclassified as putative supershedders based on the threshold definition. Testing efforts for finding highly infectious individuals might require longitudinal sampling.

Bovine *E. coli* O157:H7 supershedders: just a passing phase?

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Cattle are an important reservoir of *Escherichia coli* O157:H7 but exhibit transient, recurrent, fecal shedding of variable intensity. Prevalence of fecal shedding is highly variable among farms and pens within farms and even experimental challenge results in heterogeneous fecal shedding following standardized exposures. A potential result of this variability is that individuals with high fecal shedding may exert a disproportionate impact on the epidemiology of infection: a relatively small proportion of infected cattle, termed 'supershedders', are considered responsible for most fecal shedding. While previous modeling has provided support for the existence and significance of supershedding in the epidemiology of O157:H7, these studies are primarily based on cross-sectional studies that do not directly address the stability and infectiousness of high shedding within individual cattle. We utilized a unique longitudinal dataset that followed the progress of a natural infection in 200 cattle divided into 20 pens. Bacterial counts from recto-anal junction swabs and fecal pat samples were taken over 99 days. These measurements were used to parameterize discrete-time Susceptible-Infectious-Susceptible models via MCMC. This allowed us to quantify the impact of high shedding on within-pen transmission after adjusting for cattle density and test sensitivity. Four alternative definitions of supershedding were considered including a relatively stringent definition (3 consecutive +ve samples with mean cfu/g >10⁴), 'persistent shedders' (>9 positive sampling dates); 'high shedders' (mean cfu/g >10⁴); and 'bulk shedders' (sum of all cfu >10⁶). Little consistency was seen among the four definitions. Although some correlation between shedding levels and transmission was observed, the lack of concordance between model predictions and the observed data suggests that other factors such as variable susceptibility or social dynamics play an important role in the infection process.

***Salmonella* transmission in wild pigs: molecular, spatial and ecological approaches**

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We took an innovative approach to investigate wildlife infection transmission in an extensively distributed population of wild pigs (*Sus scrofa*) in northern Australia (2010-11). We combined molecular (integration of pig microsatellite data with *Salmonella* PFGE typing data), ecological and spatial methods. Several approaches were applied to the dataset to understand transmission and prevalence of infection at a very detailed scale. Firstly using presence/absence data we hypothesised plausible biological mechanisms for *Salmonella* prevalence. Separate logistic models were established for each hypothesis and information theoretic approaches used to choose the most likely model/s. This was used to infer mechanisms for *Salmonella* prevalence. Secondly *Salmonella* subtyping data was used to model pair-wise genetic relatedness of all *Salmonella* isolates against a variety of covariates with the aim to quantify levels of transmission between pigs. Thirdly, measures of diversity and similarity were used to provide an additional perspective on transmission dynamics. Preliminary findings from this study show potential to be of direct value for disease control. Results so far show prevalence of infection was associated with resource rich areas (riparian zones, water bodies and pasture) and behavioural factors. However no association between prevalence and; density, environmental contamination or individual risk factors could be found. Interim analyses of pair-wise *Salmonella* relatedness data suggest that herd membership, spatial proximity and differential sex based transmission to be strong risk factors for transmission. Final results will be presented at ISVEE.

Infections of dairy cattle with *Mycobacterium avium* subspecies paratuberculosis: bistability in an individual-based framework

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Mycobacterium avium subspecies *paratuberculosis* (MAP) is a endemic pathogen in dairy cattle herds worldwide. It is generally suggested that high-shedding adult animals (super-shedders) are predominately responsible for transmission events and that these high shedding adults are the main reason for endemic MAP stability in herds. However, this assumption has been challenged recently, with research demonstrating shedding among calves and experimental calf-to-calf transmission. Using ordinary differential equation (ODE) based mathematical models, we showed the a combination of early age-at-infection and a high dose-at-infection increased the probability of sustained early shedding. We then showed that this early shedding would allow MAP transmission cycles to be sustained even in the absence of high shedding adult animals, as it creates a backward bifurcation with two stable MAP prevalence equilibria under specific force-of-infection assumptions. We examined these bi-stable prevalence equilibria in [the effect of] an individual-based stochastic model (IBM) and ODE-based models which simulate transmission dynamics among age-cohorts of dairy cattle on US farms. The IBM incorporate fixed aging parameters and stochastic infection dynamics. These individual based models allow a more realistic distribution of exit from infectious states, whereas the ODE-based models rely on constant rates of exit. The herd-level outputs of ODE and individual based models were compared to the distribution of MAP herd prevalence within the US. A small portion of farms maintained a large proportion of shedding adults while the vast majority of farms show a low infection prevalence on the majority of farms.

Inference on the invasion and transmission of *Salmonella cerro* and *kentucky* in an adult dairy herd using approximate Bayesian computation

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Outbreaks and a high level of persistence of *Salmonella Cerro* and *Salmonella Kentucky* were recently found in an adult dairy herd under intensive sampling. To understand the invasion and transmission dynamics of *S. Cerro* and *Kentucky* in the herd, a susceptible-infectious-recovered-susceptible (SIRS) transmission model was developed. However, due to the infectious periods of *S. Cerro* and *S. Kentucky* more realistically following a gamma distribution, parameter estimation using the conventional likelihood-based inference approaches is not trivial. Therefore, we applied a likelihood-free method, Approximate Bayesian Computation, to the SIR model and estimated the key epidemiological parameters, the basic reproduction ratios, and the fecal culture test sensitivities for both strains from the longitudinal field data. The results show that, (1) the mean transmission rates for *S. Cerro* and *S. Kentucky* are 0.95 (95% credible interval (0.85, 1.11)) and 0.47 (0.42, 0.53) (animal×month)⁻¹, respectively, (2) the average infectious periods are 8.6 ((7.6, 9.7), *S. Cerro*) and 9.0 ((7.4, 10.2), *S. Kentucky*) months, (3) the basic reproduction ratios were 7.4 ((4.9, 12.0), *S. Cerro*) and 3.7 ((2.8, 4.6), *S. Kentucky*), and (4) the fecal culture test sensitivities against the SIRS model are 0.79 ((0.69, 0.94), *Cerro*) and 0.81 ((0.73, 0.95), *S. Kentucky*). This study indicates that both *Salmonella* strains are highly infectious to dairy cattle and that *S. Cerro* has higher invasion ability than *S. Kentucky*. Because of their long infectious periods and high transmission rates, both *Salmonella* strains are able to sustain high prevalence in the herd.

Mathematical modeling of lumpy skin disease virus transmission

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Lumpy skin disease (LSD) is a severe disease of cattle. It is caused by lumpy skin disease virus (LSDV), a Poxvirus from the genus Capripox. Previous experiments showed that direct transmission of the virus is inefficient. Therefore, it is believed that the virus is mainly transmitted by blood sucking flying insects. It was still not clear however what are the most important transmission routes of LSDV during naturally occurring outbreaks. We used a mathematical modeling approach in order to answer this question. Data that were collected during an outbreak that occurred in a dairy farm in Israel during 2006 were used for constructing a mathematical model of the various transmission routes of LSDV. The exact time and location of each infected cow during the outbreak was documented. Using these data along with previously published data on incubation period we simulated the probability of each infected cow to infect its herd-mates by direct contact, indirect contact or during milking procedure. The best fit transmission parameters were estimated by calculating the model maximum likelihood. Model results indicated that indirect contact was the most important transmission route and that its contribution to R0 was more than five times higher than all other transmission routes, combined. Sensitivity analysis showed that the model results were highly sensitive to the value of the indirect contact parameters but not to the other parameters. Model results were robust to various assumptions, regarding incubation period and the extent of sub-clinical infection. It is concluded that LSDV is mainly transmitted by indirect contact (which is attributed mainly to blood sucking, flying insects). These findings have important implications for the control of LSD.

Session 45**Theatre 1****Using reproductive performance data to evaluate under-reporting during an epizootic**

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Under-detection and under-reporting of cases result in an incomplete description of an epizootic. Reproductive data are routinely collected in many herds. Diseases can result in impairment of reproductive performance. The objective of this study was to evaluate whether decrease in fertility can highlight the under-reporting of cases during an epizootic. The outbreak of bluetongue virus serotype 8 (BTV-8) in France was used as a case-study. Variations in fertility were quantified for cows in reported case herds and cows in herds with uncertain infectious status (i.e. located in exposed areas and not reported as cases during the 2007 epizootic), compared to cows in herds unexposed to BTV-8 in 2007. An adjusted Cox model was used to model 90 d return to service. An estimated date of putative exposure to BTV-8 was interpolated for cows in herds with uncertain BTV-8 status, using a spatial based approach (kriging). The interpolation was based on the spatiotemporal dynamic of case herds. Variations in fertility were quantified around the observed and estimated date of exposure in case and uncertain BTV-8 status herds, respectively. Decreased fertility was evidenced for cows inseminated 6 weeks before to 10 weeks after the observed date of exposure in case herds, and 6 weeks before to 8 weeks after the estimated date of exposure in herds with uncertain BTV-8 status. Fertility was decreased by 5 and 3 percentage points, respectively. This study suggests that reproductive performance data can be used to monitor actual spread of emerging pathogens that affect reproductive performance. It provides an innovative method to account for under-reporting while evaluating the total burden of an epizootic.

A mixed method approach investigating factors influencing reporting of animal disease among smallholders in southern Bolivia

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The establishment of surveillance systems for animal diseases is particularly challenging in resource-scarce settings and smallholders are frequently not reached. Mixed methods are a relatively new methodology which collect and analyse qualitative and quantitative data; aiming to provide, in combination, a better understanding of research problems that either approach alone. An (explanatory) sequential mixed methods design was used to identify factors influencing disease reporting and investigate attitudes towards endemic and emerging animal diseases among smallholders in southern Bolivia. Quantitative data was collected by means of a questionnaire survey using a stratified random sampling. Agro-ecological regions were used as strata. The survey was carried out in 240 household. Descriptive statistics were performed and presented during communal meetings, where potential explanations of the findings were explored by means of focus groups and structured interviews. Qualitative data was managed and analysed using a framework approach, where themes were identified and data was systematically indexed and rearranged using matrixes. Result from the survey showed that in the event of incursion of an emerging disease, only 20% of smallholders in one region, and between 0 and 6% in the remaining regions, acknowledged they would notify veterinary services. Between 35 and 86% (depending on the region) were not aware of Veterinary Services visiting the community within the last year. Qualitative data revealed that the geographic location and accessibility of the community were factors which hindered diseases being reported. Absence of the official veterinary services and detachment between government programmes and smallholders' needs, were the main reasons cited for low compliance. The use of mixed methods allowed us to estimate willingness to report among smallholders and gives us insights into the possible reasons for hampering disease notification.

Host selection in vector-borne disease transmission: identifying wildlife hosts of tsetse flies

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The trypanosomes which cause human African trypanosomiasis (HAT) can be carried by both livestock and wildlife, and are vectored by tsetse flies. Control of disease is particularly challenging in wildlife protected areas where trypanosomes circulate in multiple wildlife species as the relative importance of different species as reservoirs of disease is not understood. Host choice by vectors is an important factor in a host species' reservoir potential but investigations into tsetse feeding patterns have previously been limited by the techniques available, which could often only identify hosts to the level of family (eg Bovidae). New molecular techniques now provide an opportunity to identify host species. We analysed blood meal samples from over 400 tsetse flies (*Glossina swynnertoni* and *Glossina pallidipes*) collected in six different study sites in Serengeti National Park, Tanzania and sequenced a cytochrome B fragment to identify host species. In each study site host species density was quantified by transect sampling analysed using Distance software. These data were used to calculate feeding preference indices for each wildlife species. Results suggested that tsetse feed highly selectively, with over 90% of meals identified from warthog, buffalo, elephant or giraffe, despite these species having relatively low density. The highest density species were Thomson's gazelle and impala but these species were not identified in blood meals. Quantifying feeding preferences improves our understanding of the relative roles of different wildlife species as reservoirs of trypanosomes.

Determinants of the growth rate of West Nile Virus mosquito vector (*Culex pipiens*) in north-eastern Italy

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Since 2008, West Nile virus (WNV) has expanded in several Italian regions and its yearly recurrence suggests the possibility for the virus to have become endemic in some areas. The recent expansion of WNV is likely due also to increases in the abundance and distribution of potential mosquito vectors as a consequence of environmental and demographic changes. However accurate prediction of the further expansion of vector populations and their response to control is hampered by poor understanding of the determinants of their growth rate. Here we analyzed the seasonal growth dynamics of *Culex pipiens*, the major WNV vector in Italy. Data on mosquito abundance was obtained using CDC-CO2 traps in 43 locations in Veneto region, on a bi-weekly basis from May-November 2010. Concurrent measurements of environmental variables including temperature and precipitation were recorded at nearby weather stations. A series of population growth models were fit to field data to evaluate the strength of evidence for regulation by intrinsic density-dependent and/or extrinsic environmental factors. Initial comparison of alternative models of density-dependent and independent growth revealed overwhelming support for the Gompertz-logistic model. This density-dependent model explained substantially more variation in *C. pipiens* population growth rate than any environmental factor on its own. Overall, *C. pipiens* seasonal dynamics were best described in a model that included both density-dependent regulation, and independent effects of temperature and number of rainy days during the larval development phase. This evidence of density-dependent population indicates that the per capita growth potential of *C. pipiens* populations increases as their numbers fall, potentially posing a challenge to control campaigns aiming to suppress and maintain WNV vectors at low density.

Multi-source analysis reveals latitudinal and altitudinal shifts in range of *Ixodes ricinus* at its northern distribution limit

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There is increasing evidence for a latitudinal and altitudinal shift in the distribution range of *Ixodes ricinus*. Reported incidence of tick-borne disease in humans is on the rise in many European countries and has raised political concern and attracted media attention. It is disputed which factors are responsible for these trends, though many ascribe shifts in distribution range to climate changes. Any possible climate effect would be most easily noticeable close to the tick's geographical distribution limits. In Norway – being the northern limit of this species in Europe – no documentation of changes in range has been published. The objectives of this study were to describe the distribution of *I. ricinus* in Norway and to evaluate if any range shifts have occurred relative to historical descriptions. Multiple data sources – such as tick-sighting reports from veterinarians, hunters, and the general public – and surveillance of human and animal tick-borne diseases were compared to describe the present distribution of *I. ricinus* in Norway. In order to identify the main spatial pattern of tick abundance, a principal component analysis (PCA) was used to obtain a weighted mean of four data sources. The weighted mean explained 67% of the variation of the data sources covering Norway's 430 municipalities and was used to depict the present distribution of *I. ricinus*. To evaluate if any geographical range shift has occurred in recent decades, the present distribution was compared to historical data from 1943 and 1983. Tick-borne disease and/or observations of *I. ricinus* was reported in municipalities up to an altitude of 583 metres above sea level (MASL) and is now present in coastal municipalities north to approximately 69°N.

Persistence of Rift Valley fever virus in East Africa

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Rift Valley fever virus (RVFv) is a mosquito-borne pathogen of livestock, wildlife and humans that causes severe outbreaks in intervals of several years. One of the open questions is how the virus persists between outbreaks. We developed a spatially-explicit, individual-based simulation model of the RVFv transmission dynamics to investigate this question. The model, is based on livestock and mosquito population dynamics. Spatial aspects are explicitly represented by a set of grid cells that represent mosquito breeding sites. A grid cell measures 500×500 m and the model considers a grid of 100×100 grid cells; the model thus operates on the regional scale of 2,500 km². Livestock herds move between grid cells, and provide connectivity between the cells. The model is used to explore the spatio-temporal dynamics of RVFv persistence in absence of a wildlife reservoir in an east African semi-arid context. Specifically, the model assesses the importance of local virus persistence in mosquito breeding sites relative to global virus persistence mitigated by movement of hosts. Local persistence is determined by the length of time the virus remains in a mosquito breeding site once introduced. In the model, this is a function of the number of mosquitoes that emerge infected and their lifespan. Global persistence is determined by the level of connectivity between isolated grid cells. Our work gives insights into the ecological and epidemiological conditions under which RVFv persists. The implication for disease surveillance and management are discussed.

Spatial-temporal analysis of the of the risk of Rift Valley Fever in Kenya

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Historical data on Rift Valley Fever (RVF) outbreaks in Kenya covering the period 1951-2010 were analyzed using a logistic regression model to identify factors associated with RVF occurrence. The analysis used a division as the unit of analysis. The infection status of each division was defined on a monthly time scale and used as a dependent variable. Predictors investigated include: monthly precipitation (minimum, maximum and total), normalized difference vegetation index, altitude, agro-ecological zone, presence of game, livestock and human population densities, the number of times a division has had an outbreak before and time interval in months between successive outbreaks (used as a proxy for immunity). Both univariable and multivariable analyses were conducted. The models used incorporated an autoregressive correlation matrix to account for clustering of observations in time, while spatial smoothing was done using Bayesian techniques. Functional relationships between the continuous and the outcome variables were assessed to ensure that the linearity assumption was met. Descriptive analyses indicate that a total of 91 divisions in 42 districts (of the original 69 districts in place by 1999) reported RVF outbreaks at least once over the period. The mean interval between outbreaks was determined to be about 43 months. Factors that were positively associated with RVF occurrence include increased precipitation, high outbreak interval and the number of times a division has been infected or reported an outbreak. The model will be validated and used for developing an RVF forecasting system which can then be used with the existing regional RVF prediction tools such as GLEWS to downscale RVF risk predictions to country-specific scales and subsequently link them with decision support systems. The ultimate aim is to increase the capacity of the national institutions to formulate appropriate RVF mitigation measures.

Calculation of the transmission potential of Rift Valley fever virus among livestock in the Netherlands
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Rift Valley fever virus (RVFV) is a zoonotic vector-borne infection and causes a potentially severe disease. Many mammals are susceptible to infection including important livestock species. Although currently confined to Africa and the near-East, this disease causes concern in countries in temperate climates where both hosts and vectors are present, such as the Netherlands. Currently, an assessment of the probability of an outbreak occurring in the Netherlands is missing. To evaluate the transmission potential of RVFV in the Netherlands, a mathematical model was developed and used to determine the initial and long term epidemic growth rate, which are indicators of the probability of an outbreak and of persistence. Several areas of the Netherlands have a high transmission potential and risk of persistence of the infection. Counter-intuitively, these are the sparsely populated livestock areas, due to the high vector-host ratios in these areas. *Culex pipiens* s.l. is found to be the main driver of the spread and persistence, because it is by far the most abundant mosquito. Stable flies are likely to be able to be the sole vector sustaining a local outbreak. The presence of deer can either reduce or enhance an outbreak, depending on their unknown susceptibility to RVFV. Our investigation underscores the importance to determine the vector competence for RVFV of blood feeding insects mostly associated with cattle, sheep and goat, i.e. mosquito species and the stable fly. Furthermore, it is necessary to determine the susceptibility of deer for RVFV to improve the risk assessment of nature reserves.

An outbreak of arboviral disease in Australia: are horses now at risk?

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Australia has a number of arboviruses of animal and public health importance. In 2011, there was a major epidemic of equine encephalitis associated with three Australian mosquito-borne arboviruses: Murray Valley encephalitis virus, Kunjin virus (KUNV) and Ross River Fever virus. It is thought that the epidemic was largely driven by heavy rainfall and unusual weather events that resulted in significant increases in mosquito and wild bird populations. An unusual feature of this outbreak was the paucity of human KUNV cases in areas of intense viral activity. The unprecedented number of equine encephalitis cases led to nationally-coordinated reporting and an epidemiological assessment of the situation by animal health authorities. Reports began in February 2011, peaked by March and April and significantly declined by the end of May 2011 as temperatures dropped and mosquito numbers fell. In total, there were 745 cases of encephalitis reported nationally, with a case fatality rate of 11%. The majority of cases were reported from the south east of Australia, and in particular from the states of Victoria and New South Wales. A large number of the cases were associated with infection with KUNV, and sequence analysis of KUNV isolates suggest a more virulent strain has emerged. Unlike the West Nile outbreaks in the United States in 1999, disease was not seen in wild birds over the course of the epidemic. The outbreak raises a number of important questions. Will activity of these viruses become a seasonal event or will similar 'extreme' weather events be needed for future outbreaks? What level of immunity exists in horse populations? In the future, is there a risk of disease spill-over into human or wild bird populations? These uncertainties highlight the importance of horse owners and policy makers being vigilant over coming seasons and raises the issue of using preventive vaccine for KUNV in horses. In this context, West Nile vaccines are being considered for registration in Australia.

Risk factors for foot-and-mouth disease in Tanzania, 2001-2006

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The objective of this study was to develop a model to quantify the effect of factors influencing the spatio-temporal distribution of FMD in Tanzania. Reported clinical cases of FMD for the period January 2001 to December 2006 was obtained from the Tanzanian Ministry of Livestock and Fisheries Development. Tanzania was divided into a regular grid of 20×20 km cells and the study outcome defined as the presence of at least one FMD-positive village within each cell. A mixed-effects Bayesian logistic regression model was developed to quantify the association between FMD presence and human population density as well as distance to major roads, railway lines, wildlife parks and international borders. For every year 10 km increases in the distance from a major road decreased the odds of FMD by a factor of 0.73 to 0.83. Similar associations were identified for railway lines (OR 0.92 to 0.99) and international borders (OR 0.93 to 0.99). Ten km increases in distance from a national park decreased FMD risk from 2001 to 2003 (OR 0.84 to 1.00) but increased the risk from 2004 to 2006 (OR 1.04 to 1.08). Ten thousand unit increases in human population density increased the odds of FMD in all years except 2005 (OR 1.03 to 1.14). The spatial distribution of FMD risk was variable and corresponded to endemic (2001, 2002 and 2005) and epidemic (2003, 2004 and 2006) periods. Roads were an important determinant of FMD risk in both phases. These results support the hypothesis that FMD occurrence in Tanzania is more related to animal movement and human activity via communication networks than trans-boundary movements or contact with wildlife.

FMD Asia-1 vaccine effectiveness in Turkey

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Vaccine effectiveness (VE) is the reduction in incidence in vaccinated animals compared to similarly exposed unvaccinated animals in the field [$1 - R_v/R_{nv}$, where R_v and R_{nv} are incidence in vaccinated and unvaccinated animals respectively]. It depends on various factors including vaccine quality, vaccine matching, number of doses, time since last dose, prior infection and vaccine delivery. In 2011, Foot and Mouth Disease (FMD) Asia-1 serotype was detected in Turkey for the first time in nearly ten years. Many livestock in Turkey were immunologically naïve to this serotype, lacking prior exposure or vaccination. In contrast, infection and vaccination with serotypes O and A have been widespread. In January 2012, an FMD Asia-1 outbreak was investigated in Afyon, Turkey to assess the effectiveness of a new vaccine based on the 2011 Turkish FMD Asia-1 field strain (Group I) which was used in October 2011. No animals had received more than one dose of this vaccine. The two outbreak villages consisted of many small herds of mixed dairy-beef cattle which were housed at the time of the outbreak. 229 cattle were selected by systematic sampling. Vaccination and FMD status were ascertained from the owner. FMD status was also assessed by clinical examination. In affected barns, cumulative incidence of clinical FMD amongst vaccinated cattle was 9/63=14% compared to 53/101=52% in other cattle. Unadjusted VE of the Asia-1 Group I vaccine was 73% [95% confidence interval (CI)=54%-84%], the same data as an unadjusted odds ratio (OR) gives OR: 0.15 [95%CI=0.06-0.35]. After controlling for age and sex this protective vaccine effect was OR=0.09 [95%CI=0.02-0.43]. Only 44% of examined animals were reported to have been vaccinated during the last vaccination campaign. The new vaccine appeared to be highly effective under these circumstances.

Relevance of seasonal drivers for an ongoing outbreak of foot-and-mouth disease

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Foot-and-mouth disease (FMD) is contagious between cloven-hoofed animals and had huge economic impact on livestock industries. Recent outbreaks in Mediterranean regions as well as subsequent transmission experiment indicate that FMD may spread well in wildlife populations. We investigated the impact of two seasonal mechanisms on the duration of virus circulation: half-life of infectious material in the environment and annual timing of host reproduction. Infection through contaminated environment may cause inter- and intra-species transmission of FMD. Temperature dependent decay of infectiousness of contaminated environment is well demonstrated, which induces seasonal variations in half-life. Data on reproduction ecology of wild boar and deer exhibit strict seasonality with majority of new-borns occurring in late spring or early summer. We present a new method to model transmission of the infection between species and social groups that don't share physical contact, by making excretion and intake of infectious material via the environment explicit. We parameterized an individual-based multi-species FMD model with data on disease courses, transmission, environmental infectiousness, temperature, host habitat and reproduction in the study region. The model accounts for social host behaviour and FMD epidemiology on the level of individual traits. We found seasonal decay crucial for the circulation and the distance spread of the infection, when compared to constant mean half-live. A pulsed availability of susceptible offspring could partially compensate for the detrimental effect of seasonal half-life. The affected eco-region was found ideally equipped by its particularly timed host reproduction ecology and annual temperature to maintain FMDV circulation. Nevertheless the potential to transit to an endemic situation was found very limited.

Assessment of the possible maintenance of FMDV in wildlife in Thrace

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Following the outbreaks of foot-and-mouth disease (FMD) in Bulgaria in 2011, the European Food Safety Authority was requested by the Bulgarian Food Safety Authority – Risk Assessment Centre and the European Commission to assess the role of wildlife in the Epidemiology of FMD in Thrace. There are several potential risk factors that are associated with both introduction and spread of the foot-and-mouth disease virus (FMDV) in the region. The most important of these factors are related to biosecurity, movement of animals and animal products (both domestic and wild life), animal density access by animals of food waste (in landfill sites) and the use and efficiency of vaccination programs. In addition, the interaction between these risk factors needs to be considered. This assessment focused on the potential maintenance of FMDV once it is introduced into a susceptible wild boar and deer population. The assessment was based on three aspects: (1) a systematic literature review looking at experimental studies to determine FMDV infection dynamics in deer and wild boar, as well as observational studies assessing the occurrence of FMD in wild deer and wild boar populations; (2) a dynamic, spatially explicit, individual-based eco-epidemiological model, mimicking the potential host-to-host spread of FMDV given its introduction; (3) the currently available surveillance data of wild boar and deer in Bulgaria and Turkey. Conclusions based on the systematic literature review, the output of the simulation model and the surveillance data in wildlife in Bulgaria and Turkey are presented.

Patterns and household implications of foot-and-mouth disease in rural Tanzanian communities

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Foot-and-mouth disease (FMD) is one of the world's most important livestock diseases, yet very little is known about its epidemiology and socio-economic impacts in endemic settings, where the disease affects communities heavily reliant upon livestock production. Key questions relate to the spatio-temporal distribution of FMD strains needed to inform vaccine selection, and the role of buffalo in endemic disease. Infection patterns were examined through cross-sectional studies in protected ecosystems in northern Tanzania, including questionnaires to quantify socio-economic impact. Seroprevalences and probang PCR-positivity varied among ecosystems, with high levels of exposure in livestock in pastoralist and agropastoralist communities (66.3% seropositive; 6.1% PCR positive), and lower rates in peri-urban livestock systems (33.5% seropositive; 1.4% PCR positive). Prevalence in buffaloes was high (82.0% seropositive; 35.3% PCR positive), with only a low seroprevalence detected in non-buffalo species (4.3%). Among livestock-keepers FMD was ranked amongst the most important diseases. In high prevalence areas, multiple outbreaks were reported each year in many herds, with considerable impacts on herd productivity. SAT-2 viruses isolated from livestock outbreaks across three ecosystems were closely related, suggesting that livestock contact patterns are likely to be important in understanding the source of outbreaks and spread of disease. This study supports evidence that FMD is very prevalent in rural African communities and has important consequences for rural livelihoods.

Effects of repeated cases of clinical mastitis due to different pathogens on milk yield in New York Holstein cows

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The objective of this study was to estimate, within a lactation, the effects of repeated cases of clinical mastitis (CM) due to different pathogens on milk yield in 17,265 primiparous and 27,666 multiparous lactations in 5 New York Holstein herds. Separate mixed linear models for primipara and multipara were fitted. The outcome was mean daily milk yield within a particular week of lactation. Herd was a random effect. Week within lactation was a repeated effect. In both models, fixed effects included week within lactation, calving season, retained placenta, displaced abomasum, and CM due to *Streptococcus* spp., *Staphylococcus aureus*, *Staphylococcus* spp., *Escherichia coli*, *Klebsiella* spp., and 'no important growth'. For primipara, they also included metritis and ketosis. For multipara, they also included parity and CM due to *Arcanobacterium pyogenes*. Up to 3 CM cases were modeled per lactation. A separate index for each CM type was created, denoting when milk weights were measured in relation to occurrence of that type and case number (first, second, third) of CM: free of CM; ≥ 3 weeks before first CM; 2 wk before first CM; one week before first CM; week of first CM; 2 wk after first CM; 3 wk after first CM; ...8 wk after first CM; ≥ 9 wk after first CM; and the same intervals for a second or third case. Cows with CM produced more milk before onset than did non-CM cows. Patterns of milk loss varied by pathogen and case number. In primipara, milk loss was generally greatest following a third case. *E. coli* was associated with the greatest milk loss overall; *Staphylococcus* spp. was associated with a gain. In multipara, milk loss was generally greatest following a second case. *Arcanobacterium pyogenes* was associated with the greatest milk loss overall. The study findings will help dairy farmers to better assess the impact of CM cases on milk yield.

Somatic cell count in early lactation and culling in Irish dairy heifers

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Culling is an important component of mastitis costs, and increased somatic cell count (SCC) early in the first lactation has been reported as a risk factor. The aim of this research was to assess the association between SCC of primiparous cows at 5 to 30 days in milk (SCC1), and the risk of culling cows in Irish dairy herds. A Bayesian approach was taken such that posterior predictions could be used to evaluate results on useful, intuitive scales. The dataset used for model development contained 147,458 records from 7,537 cows in 812 herds. A separate dataset was used for cross validation, which contained 144,113 records from 7,353 cows in 808 herds. Cows were censored at their last recording, if identified at a later date in other herds, or if recorded at the last test date for their herd. Otherwise, culling was assumed at the last recording for each cow. Survival time was taken as the number of days between the dates of first calving and the last recording, and was split into 50 day intervals. Data were analysed in discrete time logistic survival models that accounted for clustering of intervals within cows, and cows within herds. Model fit was assessed by comparison of posterior predictions to the observed data. The odds of culling in each interval from first calving, increased by a factor of 5%, per unit increase in log SCC1 above the mean. Despite this, when all possible variability was included in posterior predictions, risk of culling over 5 years for 1,000 simulated cows did not vary with SCC1. This suggests that in terms of culling, the impact of SCC1 in most Irish herds is of insufficient economic importance to justify investment in interventions to control mastitis pre-partum.

Is routine antibiotic treatment at dry-off necessary to maintain good udder health?

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Importance of dry cow management in maintaining good udder health has long been recognized and antibiotic dry cow therapy (DCT) is a cornerstone in most mastitis control programs. Routine antibiotic treatment of all quarters of all cows at the end of lactation (so called blanket DCT) is practiced in many countries. In recent years, however, largely due to global concerns over agricultural use of antimicrobial drugs and development of antimicrobial resistance, selective DCT has received increasing attention. The objective of our research has been to identify and develop cost-effective management practices that will promote animal health and welfare, improve milk quality and udder health, and enhance sustainability of the dairy industry. More specifically, we have evaluated the impact of milk yield level at dry-off on infection status at calving and the impact of selective treatment of cows at dry-off on milk quality and milk production of cows in Ohio dairies. Presumably uninfected, low-SCC cows were randomly assigned to receive or not to receive antibiotic treatment at dry-off. Our results suggest that in general, SCC or milk production during the following lactation did not significantly differ between the treated and untreated low SCC cows. Results, however, varied considerably between farms, indicating that some herds may benefit from blanket DCT while others can maintain good udder health with selective treatment. Additionally, our results indicate that uninfected quarters of high yielding cows at dry-off are at significantly higher odds of becoming infected during the dry period than those of lower producing cows. We conclude that good udder health can be maintained without routine treatment of healthy cows at dry-off, but advice to dairy producers should be herd-specific and that lowering milk yield prior to cessation of milking may play an important role in decreasing the risk of infections during the dry period.

Accuracy of composite somatic cell count to detect subclinical mastitis using latent class analysis

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The aims of the present research has been the evaluation of the composite somatic cell count (CSCC) validity to detect intramammary infections (IMI) considering that microbiologic culture is not a perfect test. Sensitivity (Se) and specificity (Sp) were estimated using latent class methods. One hundred seventy five Holstein cows from 2 dairies with different mastitis prevalence, was the study population. The two tests evaluated were CSCC at thresholds of 200,000 cells/ml and bacteriological culture. A quarter was considered infected when at least one major pathogen (*Staphylococcus aureus*, *Streptococcus agalactiae*, *Enterobacteria*, Environmental streptococci and *Pseudomonas* spp.) was isolated. A cow was defined as infected when at least one quarter was infected (parallel interpretation). Bayesian estimation using a Gibbs sampler in WinBUGs was utilized to estimate the parameters of both tests. The model stability was assessed using different CSCC prior distribution and the correlation of both tests was also evaluated. The estimated Se and Sp for the CSCC at cut-off 200,000 cells/ml was 0.70 (CI 95% 0.62, 0.79) and 0.67 (CI 95% 0.56, 0.78), respectively. The estimated Se and Sp for microbiologic culture was 0.83 (CI 95% 0.74, 0.9) and 0.87 (CI 95% 0.73, 0.97), respectively. To our knowledge this is the first report of CSCC Se and Sp considering microbiologic culture as non-perfect test, therefore the Se and Sp estimates would be less bias. These results will help to improve the estimation of the IMI predictive value when CSCC is being used as udder health monitoring tool.

Farmers' participation in herd health systems affects their behaviour concerning treatment of clinical mastitis

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In Denmark, it has recently become mandatory for all dairy herds with more than 100 cows to sign up for a herd health contract. Three different herd health contract systems with different characteristics regarding frequency of veterinary visits and the farmer's access to medication exist. The objective of this study was to investigate if dairy farmers have different behavioural intention to start treatment the same day as noting a mild clinical mastitis depending on their choice of herd health contract. A questionnaire survey was carried out based on the Theory of Planned Behaviour. The theory assumes that behavioural intention is correlated to the actual performance of the behaviour. Three psychological constructs determine the behavioural intention; attitude, subjective norm and perceived behavioural control. Each of these constructs is decided by a set of beliefs, which are evaluations of (1) how desirable the outcome of performing the behaviour is; (2) what others think of the behaviour; and (3) the person's power to influence his or her behaviour. A set of statements about treatment of mild clinical mastitis was identified based on interviews with 38 dairy farmers, rephrased to questions and distributed to 400 randomly sampled Danish dairy farmers with either Core or Module 1 herd health agreement and all 669 farmers with Module2 (response rate 64 and 60%). The association between intention and herd health contract were modelled using logistic analysis. We found significant differences in behavioural intention ($F=4.1$; $P=0.0435$) to perform the behaviour of interest depending on which herd health contract the farmer participated in. Attitude explained most of the variability in behavioural intention. The most important drivers were to get a quick recovery of the cow, to prevent three-teated cows and reduced milk yield.

Cost benefit analysis of the Swedish *Salmonella* control program

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Food producing animals delivered to slaughter in Sweden are virtually free from *Salmonella*. In 2011 a governmental commission suggested that an increased part of the costs of the control should be paid by the producers. Such increased costs may affect the design of the control program and therefore a preliminary cost benefit analysis was performed to evaluate the effect if the Swedish control would be relaxed so that the situation became comparable to the situation in Denmark or the Netherlands. The costs for the present control program including costs for feed control in Sweden, Denmark and the Netherlands were summarized for the countries respectively. Then the expected cost for an alternative Swedish control was calculated, i.e. the costs if a control similar to the programs in Denmark or the Netherlands was implemented in Sweden. Finally the increased costs for the Swedish program compared to the alternative programs were calculated. The benefits were the avoidance of the expected increase in the number of human *Salmonella* cases in Sweden if either of the two alternative control programs were implemented. The expected increase of reported cases was calculated in three different ways using data from three types of studies: sero-incidence studies, source attribution studies and travel data studies. The true number of cases was estimated by assessing the magnitude of the underreporting errors. Finally the economic impact of the increased number of cases, including direct costs, indirect costs and costs for life-years lost, was calculated for the different scenarios. The benefits never exceed the costs that would occur if an alternative control was implemented in Sweden. Strengths and weaknesses of the study will be discussed.

Estimating the non-monetary burden of neurocysticercosis in Mexico

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Neurocysticercosis (NCC) is a major public health problem in many developing countries where health education, sanitation and meat inspection infrastructure are insufficient. Although NCC is endemic in many areas of the world and is associated with considerable socio-economic losses, very few studies have been conducted to evaluate the burden of NCC and there are no estimates from Mexico. Disability Adjusted Life Years (DALYs) lost for clinical cases of NCC in Mexico were estimated by incorporating morbidity and mortality due to NCC-associated epilepsy, and morbidity due to NCC-associated severe chronic headaches. Latin hypercube sampling methods were employed to sample the distributions of uncertain parameters and to estimate 95% credible regions (95% CRs). In Mexico, 144,433 and 98,520 individuals were estimated to suffer from NCC-associated epilepsy and NCC-associated severe chronic headaches, respectively. A total of 25,341 (95% CR: 12,569-46,640) DALYs were estimated to be lost due to these clinical manifestations, with 0.25 (95% CR: 0.12-0.46) DALY lost per thousand person-years of which 90% was due to NCC-associated epilepsy. This is the first estimate of DALYs associated with NCC in Mexico. However, this value is likely to be underestimated since only the clinical manifestations of epilepsy and severe chronic headaches were included.

Assessing the costs versus the effectiveness of dioxin monitoring in bulk milk

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Dioxins are environmental pollutants present in the agri-food chains. The negative consequences associated with their presence in food are not only related to human health but also to the food businesses operators embedded in the food chains. Food and feed dioxin-monitoring programs aiming to detect, control and reduce the presence of dioxins in food chains have been implemented. However, to date, the costs and effectiveness of such programs have not been assessed. This study aims to quantify the costs and effectiveness of bulk milk dioxin monitoring to optimize the sampling and pooling strategies for a selected set of contamination scenarios. Two different optimization models were built using a linear programming methodology. The first model aims to minimize the monitoring costs subject to a minimum required effectiveness, while the second model aims to maximize the effectiveness of monitoring for a given monitoring budget. This study shows that a higher level of effectiveness is possible but at higher costs. Monitoring with 95% effectiveness aiming to detect a single contaminated farm with a tank milk concentration equal to the EC legal action level (i.e. 2 pg TEQ/g fat) would cost €2.6 million per month. A large reduction in monitoring costs (at the same level of effectiveness) is possible at intermediate incident sizes (i.e. 73% reduction when two farms are contaminated at 3 pg TEQ/g fat), which is close to the smallest incident aimed to be detected. Both models enable the analysis of the costs and the effectiveness of bulk milk dioxin monitoring programs, offering quantitative support to risk managers of the food industry and the food safety authority. Additionally, this study proves that the effectiveness of monitoring depends not only on the performance of the detection tests but also on the number of samples collected.

The monetary burden of cystic echinococcosis in Iran

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Cystic echinococcosis (CE) is a globally distributed parasitic infection of humans and livestock. The disease is of significant medical and economic importance in many developing countries, including Iran. However, the socioeconomic impact of the disease, in most endemic countries, is not fully understood. The purpose of the present study was to determine the monetary burden of CE in Iran. Epidemiological data, including prevalence and incidence of CE in humans and animals, were obtained from scientific literature and as well as official government reports. Economic data relating to human and animal disease, including cost of treatment, productivity losses, and livestock production losses were obtained from official national and international datasets. Monte Carlo simulation methods were used to represent uncertainty in input parameters. The overall annual cost of CE in Iran was estimated at over US\$200 million, including both direct and indirect costs. CE has a considerable economic impact on Iran, with the cost of the disease estimated to be approximately 0.03% of the country's gross domestic product. Establishment of a CE surveillance system and implementation of a control program are necessary to reduce the economic burden of CE on the country. Cost-benefit analysis of different control programs is recommended, incorporating present knowledge of the economic losses due to CE in Iran.

Value of adding nurses to veterinary teams for health communication about zoonotic bovine brucellosis

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Bovine brucellosis has been a re-emerging zoonoses amongst small-scale farmers in Zimbabwe since 2001 when Government veterinary services discontinued free vaccinations due to financial constraints. Following land invasions where uncontrolled movement of cattle led to *Brucella*-positive cattle entering naive herds, abortions were reported although the cause was unknown. This project hypothesised that increasing communities' knowledge about severity of and susceptibility to brucellosis would lead to calf vaccination and adoption of safe milk practices. Initially we formed veterinary teams who conducted health education sessions for farmer groups through a dairy cooperative network. This led to large, significant increases in awareness and improved payment for calf vaccination. However, although an increase in knowledge about the dangers of consuming raw milk was recorded, there were no corresponding behaviour changes. Only 5% of all the households sampled boiled milk before consumption with a significantly lower percentage of 'knowledgeable' farmers who consumed raw milk compared to the 'Unaware of Brucellosis' group (27% and 48% respectively). Despite the intervention, some farmers were still not making informed choices to decrease the risk of their livestock or families being exposed and infected with brucellosis. We added nurses and environmental health technicians to the education teams. This led to improved information dissemination, an increase in knowledge and boiling milk behaviour. Follow-up household interviews (n=170) recorded calf vaccination rates further increased and more free serological tests requested. The first human cases were detected in the district. More women attended the nurses' talks than previously where mostly men attended the veterinary talks. The cross-disciplinary teams were more effective in health communication and subsequent behaviour changes. This project provides evidence and recommendations for future community-directed zoonosis control when farmers are required to participate and pay for any procedures.

The impact of functional forms of the force of infection on the coexistence of two competing strains with complete cross-immunity in a population

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In the area of modeling infectious disease spread in a population, an important consideration is to select an appropriate functional form of the force of infection that is determined by transmission routes, either through close contact or through a contaminated environment. This study aimed to investigate the impacts of different functional forms of the force of infection on the coexistence of two competing strains of the same micro organism with complete cross-immunity in a population using a mathematical modeling approach. We constructed a simple compartmental model of two competing strains with complete cross-immunity and examined four types of functional forms of the force of infection including a linear form (assumed to act through close animal to animal contact), an exponential form (assumed to act through contact with a contaminated environment), and Holling's type II and III (also through a contaminated environment). The model was described by a system of nonlinear ordinary differential equations and was numerically solved for these four types of force of infection. The results demonstrate that coexistence of two competing strains with complete cross-immunity is possible for environment transmission even if their basic reproduction ratios are different and both basic reproduction ratios are greater than the threshold value of 1. It is important to note that for the conventionally used linear form of the force infection, only the strain with the larger basic reproduction ratio will eventually survive and co-existence is not an option. We explain our unusual results for coexistence of the two-strain competition model, and further discuss potential ranges of biologically relevant parameter values for two-strain coexistence in farm animal populations.

The role of the carrier class in the endemicity of foot-and-mouth disease in the Lake Chad Basin, Cameroon

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Foot-and-mouth disease (FMD) is endemic in the 650,000 cattle that populate the Lake Chad Basin, Cameroon. FMD causes debilitating symptoms including blisters on feet and mouth causing difficulty eating and lameness. These clinical signs may delay the nomadic patterns and prevent cattle from obtaining the nutrients critical to survival. Outbreaks are detrimental to herds' survival and the economics of the cattle industry in Cameroon. Little research has been done on the role of carriers on endemicity of FMD in Cameroon. This project seeks to understand this role via an SIR-type ordinary differential equations system (SEICR: susceptible, exposed, infectious, carrier, recovered) to model FMD in an endemic setting. Our field team in Cameroon gathered statistics on the number of carrier and recovered cattle. This data is used with the model to investigate associated parameters to the system, parameterize the endemic equilibria (EE), and calculate the basic reproductive number (R_0) using the second generation matrix technique. Sensitivity analysis is performed using Latin hypercube sampling to investigate R_0 and how the relative infectivity of the carriers affects R_0 , assuming EE. Results suggest the relative infectivity of the carrier class has a minimal effect on R_0 . However, the carrier class still contributes to the spread of the disease. In fact, results suggest that a carrier class with relative infectivity of only 6.55% is sufficient to drive the system to be endemic from the carriers alone. Sensitivity analysis reveals R_0 to vary widely over biologically plausible parameter ranges with a long tail to its distribution. Current work seeks to find the source of this variability. A counter-intuitive result is an inverse relationship between the size of R_0 and the relative infectivity of the carrier class. Forcing the model EE to match the observed data appears to result in a trade-off between R_0 and carrier infectivity.

Modeling of *Mycobacterium avium* subsp. *paratuberculosis* in farm bulk tank milk

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Mycobacterium avium subsp. *paratuberculosis* (MAP) in milk of bovine origin is suspected of being implicated Crohn's disease in humans. Pasteurization is considered to reduce the concentration of MAP by at least 4 to 5 \log_{10} . This study aimed at estimating the level of MAP in milk at farm level and simulating the effect of different control options at different infection prevalences. The concentration of MAP in milk was estimated using a hierarchical simulation model representing individual cows in a herd while taking both direct and indirect contamination with MAP into account. Parameters included true within-herd infection prevalences with cows in different infection stages, which were used to estimate prevalences of milk and fecal shedders, and subsequently MAP concentrations in milk and feces. Cows in different infection stages were considered with different risks of excreting MAP testing positive. Furthermore, direct MAP contamination of milk was related to infection stages while indirect contamination was associated to within-herd prevalence and distribution of infection stages. Control options implemented included discarding of milk based on diagnostic test results. Median MAP load in farm bulk tank milk at within-herd infection prevalences from 7.5 to 60% were estimated to 0.74-6.81 cfu/ml, of which the contribution of direct contamination was less than 1%. Maximum concentration at the prevalence of 60% could be 1186 cfu/ml caused by shedding of high amounts of MAP in feces from super-shedders. At the prevalence of 15%, discarding milk from test positive cows would result in discarding 11% of milk and reduce the MAP level by 80%. The model was relatively simple yet capable of capturing true infection status and associated contributions from milk and feces. Further knowledge on distribution of fecal excretion from infected cows is required because very few 'super-shedders' might play a major role. The results can be used for a formal risk assessment including effects such as pasteurization.

A Bayesian approach to study the risk variables for the interactions between domestic and wild ungulates for tuberculosis occurrence in South Central Spain

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Bovine tuberculosis (bTB) is a chronic infectious disease mainly caused by *Mycobacterium bovis*. Despite its eradication is a priority for the European authorities, bTB remains prevalent in many countries, causing significant economic losses. The identification of epidemiological factors contributing to TB transmission is crucial to more cost-effectively allocate control measures and, ultimately, achieve bTB eradication. The aim of this study was to identify the nature and extent of the association between TB distribution and a list of potential risk factors regarding cattle, wild ungulates and environmental aspects in Ciudad Real, one of the Spanish provinces with the highest TB herd prevalence. We used a Bayesian mixed effects multivariable logistic regression model to predict TB occurrence per municipality in 2007 by using predictors from the previous year and accounting for overdispersion and spatial autocorrelation. The risk factors (median OR) for TB occurrence identified in the final model were: incident cattle farms (1.83); number of years of veterinary inspection in hunting events (1.73); prevalence in wild boar (1.94); number of sampled cattle (1.85); bTB-infected cattle farms in 2006 (1.94); prevalence in red deer (1.69); beef farms (1.47); and bullfighting cattle farms (1.15). The spatial distribution of these factors together with particular Mediterranean features that favour the wildlife-livestock interface (WLI) may explain why TB is transmitted between both, contributing to the *M. bovis* persistence in this region. Sanitary actions should be allocated towards specific areas and epidemiological situations where the WLI seems to critically hamper the definitive bTB eradication success.

The spread of rabies in Ethiopian wolves: from field data to transmission parameters

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With fewer than 500 individuals remaining, the Ethiopian wolf is an endangered species threatened by regular outbreaks of rabies which have occurred in 1992-1993, 2003-2004, and 2008-2009. An important step towards effective control planning is to quantify the spread of infection. However, epidemic processes are often only partially observed, making parameter inference hard. Here we explore the use of Approximate Bayesian Computation to assess rabies transmission in Ethiopian wolves during the 2008-2009 outbreak. We developed a spatially explicit stochastic SEIR model for infection spread within a metapopulation of seven packs. Two parameters were inferred: the within (β_w) and between pack (β_b) transmission rates. The data comprised pre and post-outbreak pack compositions, and date and place of vaccination events and carcass recoveries. We used the model to simulate datasets using values for β_w and β_b sampled from prior distributions. These simulated data were reduced to summary statistics (number of carcasses per group of packs, total time of outbreak, and time between the first carcass and the first carcass in a neighbouring pack). Those parameters leading to the smallest distances between simulated and observed summary statistics were accepted, using an algorithm based on local linear regression. The basic reproduction number (R_0) was then computed. The median value of β_w was approximately eight times higher than β_b , consistent with behavioral studies. The mean R_0 was 2.6, in agreement with previous estimates for the 2003 rabies outbreak. Besides biological insights following the estimation of transmission parameters, these outputs will be used to calibrate a simulation model to assess the effectiveness of different vaccination strategies in populations of Ethiopian wolves.

Is meticillin-resistant *Staphylococcus aureus* ST398 able to spread in humans?

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The emergence of the livestock-associated clone of meticillin-resistant *Staphylococcus aureus* (MRSA) ST398 is a serious public health issue in a large number of European countries. Although MRSA ST398 has been evaluated less transmissible than hospital-acquired MRSA, its incidence in the community continues to rise despite the implementation of stringent ‘search-and-destroy’ policies. The question regarding the transmissibility of MRSA ST398 in humans therefore remains of great interest. Here, we report the results of a stochastic, discrete-time metapopulation model that explores patterns of spread and persistence of MRSA ST398 in an entirely susceptible human population subject to the effect of a single MRSA-positive commercial pig farm. Notably, we investigated the role of the probability of persistent carriage and the probability of acquiring MRSA due to contact with pigs on the transmission dynamics of MRSA ST398 in humans. Simulations showed that MRSA ST398 can spread and be maintained in the human community despite its low transmissibility, mainly because the recurrent introduction from pigs. We further showed that persistent carriage should occur in less than 10% of the time for MRSA ST398 to conserve epidemiological characteristics similar to what have been previously reported. These results indicate that implementing control policy that only targets human carriers may not be sufficient to control MRSA ST398 in the community while it remains endemic in pigs. We argued that farm-level control measures are required if an eradication programme is to be considered.

The ENHanCE project: a large scale risk assessment of the most likely human and animal pathogens to be affected by climate change

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Climate change is considered a major threat to human health and well-being, with increasing evidence of it impacting infectious diseases. But how large is this threat? Will many diseases respond to climate change or only a few? Is it possible that the most significant diseases in health or economic terms could be resilient to climate change, such that its overall influence on our health and well-being could be of relatively minor importance? Within the ENHanCE project we have developed an easily repeatable, bottom-up approach which allows the examination of many pathogens using multiple steps, enabling us to answer some of these questions. Within the project, we have built a database, the open access ENHanCED Infectious Diseases (EID2) database, with which we first identified the main pathogens of man, domestic and companion animals. Second, a proxy for the impact of each pathogen upon man was then developed to ascertain those of the greatest importance to us. Automated literature searches of pathogen names and climate driver terms were then implemented to establish scientific literature which potentially contained evidence of the climate drivers of disease. It was thereafter necessary to examine the literature, for a short list of the pathogens with the highest ‘impact’, to verify the actual evidence of the effects of climate upon each pathogen. This was undertaken, finally, using a critical review tool which grades the quality of the data based on a number of factors including: the journals in which papers were published; whether they describe field or laboratory studies, analysis of collated data or review articles; and the significance of any statistical support for climate and pathogen associations. This presentation will demonstrate our methodologies, and present the main findings of our full bottom up assessment.

Development of a real-time Bayesian model of equine influenza spread in Australia

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Australia experienced its first ever outbreak of equine influenza in 2007, affecting around 70,000 horses before eradication was achieved, 5 months later. We developed a spatial simulation model of equine influenza in Australia parameterised by Bayesian inference of data from the 2007 outbreak. Our modelling objectives were to improve understanding of the underlying disease process and the effectiveness of certain control measures, and to develop a real-time decision-support tool for future outbreaks. Local spatial spread, the movement of infected horses and intra-premises transmission were explicitly modelled. A Bayesian reversible jump Markov chain Monte Carlo algorithm was used to infer posterior distributions of key epidemiological parameters for a peri-urban and a rural cluster (n=7,670 and 1,540 horse premises, respectively). We then conducted forward simulation, a sensitivity analysis and validated against a previous simulation model of the 2007 outbreak. The simulated epidemics were highly cross-correlated both temporally and spatially with the actual epidemic (Spearman's $\rho=0.81$ and 0.88 , respectively) and with outputs of the previous model ($\rho=0.84$ and 0.92). Spread dynamics differed markedly in the two clusters, with local spread occurring over longer distances but at a lower rate in the rural cluster. The duration of infectivity was established for premises holding a range of numbers of horses and the effectiveness of vaccination was assessed. Our posterior parameter distributions will provide informative priors for future real-time modelling of equine influenza outbreaks in Australia, and our findings suggest which outbreak control procedures to prioritise. This research was funded by the RIRDC and the ABCRC.

Spatial BTV-8 transmission in NW-Europe in 2007

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We analysed the 2007 bluetongue (BTV-8) epidemic data for spatial transmission aspects and compared these with the results of the spatial analysis of the 2006 BTV-8 epidemic. We evaluated the spatiotemporal dynamics of newly reported outbreaks by means of a transmission kernel, which is the distance dependent rate of between-herd infection. This evaluation posed new technical hurdles due to the fact that the 2007 epidemic occurred in the wake of the 2006 epidemic. Especially in Belgium, many farms were already infected in 2006, leading to reduced transmission levels in 2007 due to the lower remaining number of susceptible farms. Furthermore, we found that in 2007, when the weather conditions were favourable again after the winter, the virus reappeared throughout those areas in which the infection was found in the 2006 epidemic. Estimating the size of these areas and removing them from the 2007 dataset proved essential for estimating the spatial transmission kernel for BTV-8 in 2007. The shape of this transmission kernel was similar to the shape of the transmission kernel as derived from the 2006 epidemic. This indicates that the spatial transmission is not very sensitive to climatic and biological fluctuations between years. The results also show that BTV-8 persisted easily through winter and can re-emerge in previously infected areas.

Is bovine tuberculosis transmission density or frequency dependent?

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Most mathematical models of bovine tuberculosis (bTB) spread have assumed a density-dependent contact structure. However, the biology of the disease and the observed data would suggest that a frequency-dependent contact structure is more appropriate. First, transmission of bTB requires close contact between animals. Second, the number of infected animals in observed outbreaks does not appear to increase linearly with herd size, as would be expected with density-dependent transmission. We used a stochastic compartment model for bTB spread in US cattle herds to investigate the importance of the assumption of density versus frequency dependence. The simulated data were compared to observed data from 10 fully evaluated bTB case farms in the US. The model predicts that a density-dependent contact structure would result in a wider distribution in the number of infected cows with increasing herd size, while this was not observed in the case reports. By contrast, frequency-dependent contact structures resulted in similar distribution of the predicted number of infections across herd sizes. When compared to 10 successfully controlled outbreaks in US dairy herds, the frequency-dependent contact structure predicted the observed number of infected animals significantly better. The difference between the contact structures is difficult to notice in herds of similar size, but becomes apparent as variation in herd size increases. With increasing herd sizes around the world, these results are important to note for the accuracy of bTB models. The distinction between the two models is also essential for our biological understanding of bTB transmission.

Databases in Denmark: opportunities and constraints for welfare assessments

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The Danish Food and Veterinary Administration is responsible for many databases of which several are related to animals. The objective of the present project was to establish database protocols for all databases that might include variables that could be used for animal welfare assessment in cattle and pig herds and to assess, which variables are most suitable for future use. A total of 13 databases were identified as including information of potential relevance for animal welfare. For each database, a responsible person was asked to provide a full database protocol. This included information on: purpose, data accessibility, primary data recording and exact definition of the variables. Hereafter, welfare experts were asked to classify the variables according to relevance and validity. The relevance was judged according to how close a variable could be associated with welfare and the validity was judged according to sensitivity and specificity of the recordings describing the true occurrence. Finally, a summary evaluation was performed also including the actual occurrence of the indicators in the animal population as well as previous assessments and information from literature. Six databases were identified to contain useful information. The most important variables included: animal movements, duration of life, mortality, several meat inspection data related to chronic conditions, medicine consumption and infringement of welfare regulations. However, there are several constraints on the variables which should be included when interpreting the information, in particular to aspects other than health issues. Further, it will be beneficial to add information from databases owned by private organisations and information on e.g. resource related animal welfare indicators.

Diagnosing intramammary infections

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A conjoint analysis was conducted with two groups of mastitis researchers (USA and The Netherlands) in which they were provided sets of data (profiles) including culture results (organism isolated and number of colonies) and somatic cell count (SCC) from 3 consecutive quarter milk samples. Participants were asked to estimate the probability that the quarter was infected with a specific organism at the time the middle sample was collected. For most profiles, the range of estimates was from 0% to 100%, indicating complete disagreement among the 'experts'. This led to a large study, using data from 2 sources, to determine the operating characteristics of various procedures for diagnosing intramammary infections. The 4 steps in the process were: (1) develop a consensus among mastitis experts as to a reasonable gold standard based on 3 consecutive milk samples; (2) determine the sensitivity and specificity of a range of possible diagnostic criteria based on a single sample (utilizing both culture and SCC results); (3) compare the operating characteristics of tests based on duplicate or triplicate samples to those from a single sample; and (4) evaluate the operating characteristics of composite samples (milk combined from all 4 quarters) compared to 4 quarter samples. The consensus gold standard considered a quarter positive if the same organism was cultured from 2 of 3 consecutive samples, or if an organism was isolated on a single sample with >1000 colony forming units (cfu)/ml. The specificity of all diagnostic criteria based on a single sample was high. Estimates of sensitivity varied substantially across pathogens, but were often very low, particularly if anything more stringent than the most liberal definition was used. Duplicate sampling with either parallel or series interpretation could be used to enhance the sensitivity of specificity, but not both. Triplicate sampling performed only slightly better than use of a single sample. Finally, composite samples were found to have sufficient sensitivity to be considered for use in many clinical settings.

Session 51**Theatre 3****Diagnostic herd sensitivity using environmental samples**

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Due to logistic and economic benefits, the animal industry has an increased interest in using environmental samples to classify herds free of infections. For a valid interpretation of results obtained from environmental samples, the performance of the diagnostic method using these samples must be assessed. In this abstract we present an approach to evaluate the sensitivity of environmental samples used for herd classification. This is illustrated using results from samples for isolation of methicillin resistant *Staphylococcus aureus* (MRSA) in 48 pig herds that had previously been tested positive either at farm or slaughter. Three sample matrices were collected; dust samples (5 environmental swabs), nasal swabs (10 pools with 5 animals per pool) and air samples (1 filter). Based on the assumption that MRSA occurred in all 48 herds the overall herd sensitivity was 58% for nasal swabs, 33% for dust samples and 63% for air samples. However, we assumed that the sensitivity of environmental samples varies between herds due to variation in the amount of the analyte. This assumption can be tested by analyzing the association between animal prevalence and the result obtained using environmental samples. In our example, the prevalence of infected pigs in each herd was estimated from the pooled samples of nasal swabs. Logistic regression was used to estimate the effect of animal prevalence on the probability to detect MRSA in the dust and air samples at herd level. The results show a significant increase in the probability of isolating MRSA in the environmental samples by increasing within-herd prevalence. This relationship was strongest for dust where the sensitivity increased from 25% at 1% infected pigs, to 35% at a 25% infected pigs. The air sampling was more sensitive to detect infected herds irrespectively of the within herd prevalence, and performed almost perfectly at a prevalence of 25% infected pigs (sensitivity=99%). In general, the dependence of within herd prevalence should be considered in designing surveillance programs based on environmental samples.

Risk factors associated with tuberculosis diagnostic failures in infected cattle herds

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In spite of progresses achieved in the last decades in the field of bovine tuberculosis (TB) diagnosis, false negative cattle remains as a major issue for disease eradication in chronically infected herds. Implementation of ancillary diagnostic tests to the single intradermal tuberculin (SIT) test, such as the interferon-gamma (IFN- γ) assay, has increased diagnostic sensitivity, but diagnostic failures may still persist. In the present study information from *post-mortem* analysis of culled cattle from more than one hundred TB-infected herds from all productive types (beef, dairy and bullfighting) present in Castilla y Leon (Spain) were used to detect individual risk factors associated to *M. bovis* positive culture results in animals testing negative in the SIT test (strict/standard interpretation), in the IFN- γ assay (with two thresholds) and in both tests assayed in parallel. Among the risk factors evaluated, age and productive type had a crucial impact on the reliability of the SIT test for accurate detection of infected animals regardless interpretation criteria, with older negative-animals and bullfighting cattle having a significantly higher risk of yielding a positive *M. bovis* culture result. The same risk factors were detected in the analysis of the IFN- γ data, but association was weaker and in the case of the age restricted only to the oldest animals (>8 years). These results demonstrate that in spite of the high sensitivity of the diagnostic strategy in place false-negative results may occur. Thus, in chronically infected herds special attention should be paid to results of older animals. Implementation of IFN- γ assay in bullfighting herds contributed to minimize the risk of diagnostic failures.

Risk of introducing African horse sickness into the Netherlands by equine movements

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10-4 per year. The risk is highest in July and August, while equine movements in the period October till March pose a negligible risk. High and low risk regions contribute most to the risk with 31% and 53%, respectively. Importations of donkeys and zebras constitute the highest risk of AHSV introduction from high risk regions, while international movements of competition horses constitute the highest risk of AHSV introduction from low and very low risk regions due to the high numbers involved. Preventive measures currently applied reduce the introduction risk of AHSV to the Netherlands by 46%. A prolonged and more effective quarantine period in high risk regions and more stringent import regulations for low risk regions could further reduce the risk. African horse sickness (AHS) is a vector-borne viral disease of equines that is transmitted by *Culicoides* spp. Mortality in horses can reach 95%. AHS virus (AHSV) is an orbivirus belonging to the family Reoviridae, which also comprises bluetongue virus (BTV). The emergence of BTV serotype 8 in North-western Europe in 2006 has demonstrated that also Palaearctic species of *Culicoides* can be competent vectors for these orbiviruses. This, combined with the potentially severe consequences of AHS has resulted in increased awareness of the risk of AHS to the Netherlands. Therefore, a study was performed to assess the risk of introduction of AHSV into the Netherlands by equine movements. The goal of this study was to provide more insight into (1) the regions and equine species that contribute most to this risk; (2) the seasonal variation in this risk; and (3) the effectiveness of measures to prevent introduction of AHSV. A risk model was constructed calculating the probability of successful release of AHSV in the Netherlands and the probability that local vectors will subsequently transmit the virus to local hosts. Model calculations indicated that the current risk of AHSV introduction into the Netherlands by equine movements is very low with a median value of 5.1

Surveillance for an outbreak of African horse sickness in the Netherlands

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African horse sickness (AHS) is a vector-borne disease which is transmitted by midges and is often lethal for horses. To assess the impact and size of a possible outbreak of AHS in The Netherlands, it is important to analyse the spread of the infection until the moment of detection. The moment of detection strongly depends on the various surveillance options that this infection offers. We focus on clinical surveillance as the most probable method to detect AHS, since AHS is fast spreading and has clear symptoms. We interviewed several veterinarians, about their probable response to a few described clinical scenarios, and concluded that they would mostly seek help or report as soon as the second horse in a herd or in the neighbourhood dies. This information served as a detection threshold in a stochastic model, which describes the spread of AHS in a population of horses. The model is based on the limited information known about AHS and its possible transmission behaviour in The Netherlands. In a series of simulations, we estimated the time to detection and the prevalence situation at detection. Our results show that AHS is detected between 4 and 5 weeks after introduction in the herd. For the more likely values for midge density, midge biting rate and incubation period, we expect 2 horses in the herd to be infected at the moment of infection. Sensitivity analysis shows that the time until detection is not sensitive to the uncertain parameter values, but the number of infected horses at detection can increase dramatically with increased midge density, increased midge biting rate and a shortened incubation period. These three aspects are all the result of an increase in temperature. Thus, in a warm period, a much larger proportion of the herd could be infected, making control of the epidemic substantially more difficult.

Session 52**Theatre 3****Transmission and control of African Horse Sickness in the Netherlands: a model analysis**

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African horse sickness (AHS) is an equine viral disease that is spread by *Culicoides* spp. Since the closely related disease bluetongue established itself in The Netherlands in 2006, AHS is considered a potential threat for the Dutch horse population. A vector-host model that incorporates the current knowledge of the infection biology is used to explore the effect of different parameters on whether and how the disease will spread, and to assess the effect of control measures. The time of introduction is an important determinant whether and how the disease will spread, depending on temperature and vector season. Given an introduction in the most favourable and constant circumstances, our results identify the vector-to-host ratio as the most important factor, because of its high variability over the country. Furthermore, a higher temperature accelerates the epidemic, while a higher horse density increases the extent of the epidemic. Due to the short infectious period in horses, the obvious clinical signs and the presence of non-susceptible hosts, AHS is expected to invade and spread less easily than bluetongue. Moreover, detection is presumed to be earlier, which allows control measures to be targeted towards elimination of infection sources. We argue that recommended control measures are euthanasia of infected horses with severe clinical signs and vector control in infected herds, protecting horses from midge bites in neighbouring herds, and (prioritized) vaccination of herds farther away, provided that transport regulations are strictly applied. The largest lack of knowledge is the competence and host preference of the different *Culicoides* species present in temperate regions.

Identification of suitable areas for African horse sickness virus infections in Spain

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African horse sickness (AHS) is a vector-borne infectious disease, mainly transmitted by *Culicoides* spp., that causes dramatic sanitary and economic consequences for equidae populations. The AHS virus (AHSV) is closely related to the bluetongue virus (BTV) and, as a consequence, the re-emergence and endemicity of BTV in Europe has increased concerns about the potential re-introduction and further spread of AHSV in European equidae populations. Spain is the second largest European country in terms of equidae population, with animals of high economic and genetic value. Furthermore, its geographical, environmental and entomological conditions are favourable for AHS infections, as has been proved in past epidemics with different AHSV serotypes (i.e. 1966 and 1988-1990) and caused devastating socio-economic consequences for the country. The study presented here, was aimed to identify suitable areas and time periods at high risk for AHS occurrence in Spain that may be target to allocate surveillance strategies and other risk reduction measures. Specifically we use knowledge about risk factor of disease, climatic conditions, abundance of *Culicoides* spp. and equidae density, with weighted linear combination of these factors. Validation of the model was performed using historical outbreaks in Spain. Model results revealed that South-West of Spain is the most suitable area for AHS infections, particularly during late summer months. Suitability maps and other results of this study may be useful to support risk-based surveillance and control strategies, and to develop a simulation spread models for evaluate AHS spread in Spain.

Geographic and temporal variation in risk of African Horse Sickness virus transmission in Great Britain

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The horse industry has had to address several emerging 'exotic' equine infectious diseases, whose risk had been regarded as low. An example is African horse sickness (AHS), a viral infection transmitted by *Culicoides* biting midges, previously confined to sub-Saharan or tropical regions. The risk of AHS, its dependence on key parameters (e.g. temperature, host preference of the vector), its temporal and geographic variation and the efficacy of some control measures has not been adequately assessed in the light of current knowledge. The aim of the current work is twofold: (1) to estimate the risk of an outbreak of AHS in Great Britain (GB), based on the basic reproduction number (R_0); (2) to identify practical control measures that reduce R_0 to below one (a condition for the disease to die out). The first objective requires information of the spatial distribution of horses. Such data are not available for GB, as the National Equine Database (NED) records owner, not horse locations. However, combining NED and land use data in a Bayesian statistical approach, we developed an algorithm to infer a realistic distribution for the location of horses. Then we estimated R_0 for a range of scenarios including (1) presence of non-susceptible vertebrate hosts; (2) adoption of different control measures (insect repellents, vaccination); (3) different hypotheses on the relationship between *Culicoides* abundance and host densities. We produced a realistic map of the location of horses in GB, a spatio-temporal assessment of the risk of AHS and a quantitative framework to assess the efficacy of control measures. For example, although non-susceptible hosts (e.g. cattle) may increase vector abundance, their presence could reduce feeding on horses and lower R_0 . We provide an evaluation, for different cases, of the hosts-horse ratio required to reduce R_0 below one and thus to control the disease.

Epidemiological characterization of bovine brucellosis in Maranhão state, Brazil

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A cross-sectional study was conducted to estimate the prevalence of bovine brucellosis at the herd and animal level in Maranhão state, Brazil. In each selected herd, serum samples were collected at random from cows aged 24 months or more and a questionnaire was applied to identify risk factors for infection at the herd level. In total, 749 herds and 6,779 animals were surveyed. Geographic coordinates of each herd were collected and the spatial distribution of bovine brucellosis was studied using kernel density estimation. Variables influencing the risk of brucellosis at the herd level were analyzed using logistic regression. The herd-level prevalence of brucellosis was 11% (95% CI 9 to 14%) and the individual animal-level prevalence was 2.5% (95% CI 1.7 to 3.6%). Having more than 54 cows aged ≥ 24 months, renting pasture to third parties and the presence of wetlands on the farm increased the risk of a farm being brucellosis positive. Brucellosis-positive farms were identified all over the state, particularly in the centre and on the northwestern border. Little evidence of second order effects were observed up to scales of 0 to 10 km, which means that even if brucellosis had been diagnosed in one herd location, the likelihood of cases being identified on nearby farms was not increased. Analysis of the residuals of the logistic regression model identified areas of unexplained risk in the center of the state. These results may assist the animal health authorities in setting up the most appropriate strategies to control brucellosis in Maranhão.

Dairy reactors are less likely to have bovine tuberculosis confirmed at *post mortem*

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The primary field screening test for bovine tuberculosis (bTB) in Great Britain (GB) is the single intradermal cervical comparative tuberculin (SICCT) test supplemented by the gamma-interferon (IFN- γ) blood test in specified circumstances. Confirmation of infection with *Mycobacterium bovis* in reactors to field tests requires detection of typical macroscopic lesions during *post-mortem* examination or isolation of the bacteria. SICCT performance varies with infection stage in the bovine, immunosuppressive factors, environmental mycobacteria, test conduct, etc. The aim was to compare proportions of reactor cattle with confirmed infection from different production classes. A population sample of 200 reactors to the SICTT (standard interpretation), was randomly selected from 198 farms in England and Wales. All of the reactors underwent an IFN- γ test, a detailed *post-mortem* and culture of tissue samples. Farmers ascribed production class. The proportion of reactors with detectable *post-mortem* evidence of infection varied by production class: Dairy cows 34% (28/82), Finishers 72% (21/29), Heifers 65% (13/20), Suckler Cows 62% (31/50), Yearlings and Calves 90% (17/19) $P < 0.001$. The odds for non-dairy reactors to have infection confirmed was three times higher than dairy after controlling for SICCT results, bovine age, interval between routine test, herd size and number of reactors in the herd (Odds Ratio 3.3, 95%CI 1.6-6.8, $P = 0.001$). Similar results were observed with IFN- γ test results. Dairy cattle have been reported as having a higher risk of contracting bTB than beef cattle. These data, and data from routinely collected surveillance statistics in GB, suggest that it may be worthwhile investigating whether the immune response to *M. bovis* in cattle may be modified by management or breed. Funding was provided by Defra through project SE3013.

Determining precision and accuracy of clinical illness scores compared to pulmonary consolidation scores in Holstein calves with induced *Mycoplasma bovis* pneumonia

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Bovine Respiratory Disease (BRD) is frequently diagnosed based on signs of clinical illness followed by a confirmatory test. Little is known about the performance of this method for diagnosing BRD. The objective of this study was to determine the precision and accuracy of clinical illness scores (CIS) compared to pulmonary consolidation scores in calves with induced pneumonia. One hundred seventy-eight calves were inoculated with *Mycoplasma bovis* and scheduled for euthanasia and necropsy 12-24 days after challenge. Nine veterinarian observers with varying levels of experience assigned CIS to the calves within 48 hours of necropsy. At necropsy, lungs were evaluated and the level of pulmonary consolidation was determined using a standard scoring system. The probability that an observer would score a calf sick was estimated and compared with the true status of the calf as gauged by 6 cutoff levels of pulmonary consolidation considered to represent respiratory disease. Sensitivity and specificity were then calculated for individual observers at each cutoff. Agreement among observers as a measure of precision was estimated using the kappa statistic, which was 0.16 (95% CI=0.10 to 0.24). Median (min, max) sensitivity and specificity for all observers ranged from 81.7% (55.4, 96.4%) and 94.9% (81.3, 97.3%) respectively, based on 6 levels of pulmonary consolidation considered to represent respiratory disease. Current findings under our study conditions demonstrate low inter-observer agreement among observers and that the accuracy of CIS in relation to pulmonary consolidation scores varied based on the cutoff of consolidation used to represent respiratory disease.

Herd-level prevalence and risk factors associated with herds infected with *Mycobacterium avium* subsp. *paratuberculosis*, in dairy herds of Chile

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The aims of this study were; to estimate herd-level prevalence of *M. paratuberculosis* infection from bulk tank milk (BTM) and environmental samples collected from dairy herds and to estimate associations between management practices of the farm and the status of infection. A cross-sectional study was performed on a stratified (by herd size) random sample of 150 dairy herds in the main dairy area of Chile. A real-time qPCR on BTM samples and cultura of environmental were used in parallel as diagnostic tests to determine the infection status of the herd. MAP was isolated from environmental samples using the protocol recommended by the USDA. In addition, at the day of sampling, a survey was completed on each farm, that is aimed to collect information from the farm that could be associated as herd-level risk factors for the disease, assessed through a logistic regression analysis. The overall prevalence of infected herds was 60.7% (95% CI 52.8; 68.5). The prevalence for Large herds was 85.7% (95% CI 67.4; 100.0), for medium herds 70.3% (95% CI 55.5; 85.0) and for small 53.5% (95% CI 43.7; 63.4) and the differences were statistically not significant ($P < 0.05$). The final model contents 3 variables: Young stock contact with animals older than one year by paddocks rotation (Yes vs. No) OR=2.8 (1.2;6.4); Grouping production cows by milk yield (Yes vs. No) OR=3.3 (1.1;10.8); Paddocks used for calves are only used for calves (Yes vs. No) OR=2.4 (1.1;6.1). The prevalence of infected herds is high but similar to other countries and it was identified some management practices associated with infection status of the herds – mainly related with young stock – that could be added to current recommendations, to help the control the transmission. Study funded by FONDECYT # 1101020.

Factors affecting time to introduction and duration of *Salmonella* in Danish dairy herds during a 7-year surveillance period

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The objectives were to investigate factors affecting time to introduction and duration of *Salmonella* in Danish dairy herds under surveillance between 2003 and 2009. Using bulk-tank milk antibody test results measured at 3-monthly intervals in a national surveillance programme, herds were considered at risk of becoming infected when they had been test-negative for at least four consecutive year-quarters (YQs), and at risk of recovering after they had been test-positive for at least 1 YQ. Survival analysis was performed on a dataset including 7732 dairy herds representing 157181 YQs, in which 1523 new infection events and 2167 recovery events occurred. Predictors obtained from register data were tested in two multivariable, proportional hazard models allowing for recurrence within herds. The final multivariable survival models showed that purchase from test-positive cattle herds within the previous 6 months, increasing local prevalence within a 5-km area, increasing herd size and increasing bulk-tank milk somatic cell counts were associated with increasing hazard of introduction and longer duration of infection. This emphasises the need to focus on both external and internal biosecurity measures to successfully control and prevent *Salmonella* infection. The effect of prior infection on the hazard of introduction was time-dependent with highest hazard of re-introduction up to 2 years after recovery. Danish dairy herds generally became better at controlling the infection and preventing introduction or recurrence over time, most likely due to publicly available herd classifications, overall decreasing prevalence and improved awareness of the need to maintain a high level of biosecurity.

Session 54**Theatre 1****Evaluation of capture-neuter-vaccination-release (CNVR) program to control rabies and dog population in Bhutan**

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Bhutan has a large population of free-roaming dogs which has been a concern for the general public, including tourists. Rabies is still endemic in the southern part of the country and free-roaming dogs have been indicated as the source of rabies in Bhutan. As a result, the Government of Bhutan has assigned a high priority for the control of rabies and the dog population in Bhutan. Since October 2009 the Bhutanese Department of Livestock and the Humane Society International (HSI) have worked together on a long term dog and rabies control project, centered around a capture-neuter-vaccinate-release (CNVR) program. During this CNVR programme a total of 32,276 dogs were neutered and vaccinated against rabies in Bhutan until January 2012. In the month of December 2011 and January 2012, six Districts were selected and visited to monitor the progress of the CNVR programme in Bhutan. The monitoring exercise included counting the number of neutered and entire dogs, lactating bitches and puppies seen in the streets and discussion of the findings with the relevant stakeholders. Data on the dogs (age, gender, colour, neuter status and health parameters including body condition and skin condition score) were collected to characterize the free roaming dog population in Bhutan. From this study the proportion of free-roaming dogs that are neutered and vaccinated (44-79%) was determined to highlight the impact/success of the CNVR programme in Bhutan. Assessment of these results will allow further refinement of the CNVR programme to achieve the targeted level of 80% of the total dog population.

Response to a rabies epidemic in Bali, Indonesia

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Bali was historically rabies free until 2008 when the disease was confirmed in the Bukit Peninsula. Initial attempts at containment by dog vaccination and culling were unsuccessful due to factors including lack of emergency funding and contingency plans, the large free-roaming dog population and its high turnover, limited availability of long-lasting vaccines and means to identify vaccinated animals and patchy cold chain arrangements. Over the next three years more than 130 people died of rabies, at least 130,000 dog bites required post-exposure prophylaxis and over 500 cases were confirmed by the fluorescent antibody test. Following trials in 2009 to pilot dog catching teams for conducting mass vaccinations and a switch to long-lasting vaccines; successive island-wide vaccination campaigns were completed in 2010 and 2011 respectively. More than 200,000 dogs were vaccinated in each of these campaigns and coverage estimates approached or exceeded 70% in most sub-villages in Bali. At the start of the first island-wide campaign 140 villages were infected, and during the mass vaccination, rabies spread into new areas and re-infected previously rabies-free villages. However, by the end of the second campaign only 30 villages remained infected, rates of spread had declined from ~10 new infected villages each month, down to less than 2, incidence had decreased from ~45 cases/month to ~11, attack rates had dropped from 0.027% down to 0.01% and bite injuries had declined from 6,256 to 4,197 bites/month. Mass dog vaccinations to date have significantly reduced rabies incidence and spread, however bite incidence remains high and repeat dog vaccination campaigns are necessary to eradicate rabies from Bali.

Rabies in Montenegro: transboundary disease control from a small country's perspective

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Although most of Western and Central Europe is free of rabies, sylvatic rabies is endemic in the Balkan region of southeast Europe. In Montenegro, the smallest of the Balkan countries, the red fox (*Vulpes vulpes*) accounts for 80% of all rabies. From 2007 to 2011, 173 cases of fox rabies were reported, with incidence cases declining from 2010 to 2011. No human cases have ever been reported in Montenegro. With funding provided by the European Union, oral vaccination of foxes was carried out for the first time in autumn 2011 in this country. We conducted a number of epidemiological studies to monitor the success of the oral vaccination campaign. These included (1) an assessment of the post-vaccination immunity of foxes by annual sampling of four healthy foxes per 100 km²; (2) monitoring of bait uptakes using bait-removal counts and *post-mortem* testing of foxes for occurrence of bait-incorporated biomarkers; and the (3) estimation of fox population density using indirect transect counts and direct night counts. Preliminary data analysis indicated that the bait disappearance rate was 81% after 7 days with most baits being consumed by foxes. However, dogs seem to play a bigger role as bait competitor compared to western and central European countries; their possible role as rabies reservoir needs to be further monitored. Antibody responses after vaccinations will be summarised over time as well as the change in fox population density. Based on these results we will discuss the role of regional coordination of rabies control and information sharing, but also highlight ecological difficulties and challenges in controlling this transboundary disease in a small country with limited resources.

Clinical incidence and people's awareness of rabies in North West Ethiopia

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A survey was conducted to determine the incidence of rabies in humans and domestic animals, and to assess the people's awareness about the disease in north Gondar zone, North West Ethiopia. The incidence of rabies in humans and domestic animals was followed for one year from April 2009 to March 2010 based on clinical manifestation of the disease. A questionnaire was also administered to 120 residents and 5 traditional healers to assess the knowledge and practices associated with the disease in the study area. Annual rabies incidence of 23.33/million in humans, 4,128/million in dogs, 198.86/ million in cattle, 676.79/million in equines, and 144.49/million in goats was recorded. Dogs were found to be the major reservoir of the disease. Almost all community members were familiar with the disease. But serious misconception and lack of awareness about the disease's causes and means of transmissions were observed. The majority (82%) of the people attend traditional healers when they feel exposed to the disease and in some cases (16%), the traditional treatment was preceded by diagnosis. It was also observed that for people who had taken the modern post exposure treatment, the mean duration of the time between time of exposure and starting of the treatment was 17 days. In conclusion the incidence of the rabies in the study area could be considered high with significant public health and economic burden. A serious lack of awareness about the disease and high reliance on traditional treatment, some aspect which is scientifically implausible, was observed.

Costs of the current rabies control strategies on Flores Island

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Rabies is a zoonotic disease and always fatal once clinical signs appear in human. The disease transmits to humans through an animal bite. Dogs are the main vector of rabies in humans on Flores island, Indonesia, resulting in about 19 deaths annually. Therefore, it is necessary to control the disease. Currently, the rabies control program at Flores island includes post exposure treatment of humans, mass vaccination and culling of dogs, and surveillance in dogs. Although the program has been in place for several years, it seems that rabies is not yet controlled. Therefore, an evaluation of the program is needed. The objective of this study is to estimate the net costs of the current control program of rabies on Flores island. A deterministic economic model has been developed to calculate the net costs of the rabies control program and of the individual components from the year 2000-2011. Data from the Health Department and Husbandry Department of East Nusa Tenggara Province were used as inputs. The result shows that the annual net costs due to vaccination, culling of dogs and surveillance (prevention) were calculated to be respectively \$US 90,420 (Rp 809.71 million), \$US 2,670 (Rp 23.9 million) and \$US 4,755 (Rp 42.6 million). The annual net costs of the post exposure treatment in humans (cure) was estimated to be \$US 172,389 (Rp 1.5 billion). Summarizing, the annual costs involved in the rabies control program add up to \$US 270,234 (Rp 2,4 billion) in total, with the post exposure treatment program being the most expensive component. The preventive measures do not seem to be effective, but the amount of money spent in prevention is lower than the amount of money spent in cure. This means that an improved control of Rabies might become cost-effective.

Bluetongue surveillance: distribution and seasonal abundance patterns of Palaearctic *Culicoides* vector species in the Netherlands

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Surveillance systems of vector-borne diseases are based on the systematic collection of relevant information, which necessarily include data on the presence, abundance, and ecology of the vector and its interactions with the environment. Palaearctic *Culicoides* midges represented a vital link in the northward advance of the bluetongue virus serotype 8 in north-western Europe. The principal ecological determinants of weekly fluctuations in *Culicoides* vector abundances during the bluetongue epidemics in The Netherlands in 2007 and 2008 were quantified within a hurdle modelling framework. The relative role of meteorological parameters showed a broadly consistent association across species, with larger catches linked to temperature related variables and lower wind speed. Moreover, both vector abundance and species diversity were found to be influenced also by edaphic factors, likely related to the species-specific breeding habitat preferences that differed markedly amongst some species. This is the first study on the *Culicoides* vector species of The Netherlands in which an attempt is made to pinpoint those factors, which at regional scale, influence midge abundance levels and geographic range. In addition to providing key inputs into risk mitigating tools for midge-borne pathogens and disease transmission models, the adoption of methods that explicitly address certain features of abundance datasets (frequent zero count observations and over-dispersion) helped enhance the robustness of the ecological analysis.

Reliability of drag sampling for tick collection on vegetation

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Drag sampling has commonly been used to collect Ixodid ticks on vegetation, since Macleod (1932), with the aim of estimating tick densities. Only recent efforts were made for the standardization of the method, and little is known about its efficiency and repeatability. In spring 2011, a study was performed on a cattle farm near Nantes (France), selected for the presence of *Ixodes ricinus* ticks, to test the reliability of drag sampling. Forty six 10 m² transects were chosen on a priori favourable biotopes: borders of pastures adjacent to a woodland, or inside the woodland. On each transect, 1 m² flannel blanket was slowly dragged (0.5 m/s) along 10 m. Ticks were then recovered and stored for later identification and counting. Dragging was immediately repeated on the same area to accumulate 20 successive samplings. For each sampling (n#1 to n#20 on a transect), the 3 stages of *Ixodes ricinus* were counted (larvae, nymphs and adults). The evolution of the countings was then analysed for each of the 46 transects. The results were the following: (1) for nymphs, the main stage of interest, the first passage corresponded to the highest counting on 70% of the transects. The exhaustion was sometimes incomplete after 20 passages (last counting ≥ 1 for 37% of the transects, mostly on high tick densities), but very few nymphs remained at the end: the cumulative counting of nymphs on 20 passages was then considered to represent the total number of nymphs actively in search of a host. The percentage of nymphs collected at the first passage varied randomly between 0% and 50%, with a mean of 26%. With a leaf litter covering the ground, the efficiency of the first passage was improved to a mean of 30%, and it fell to 20% in the absence of leaves. (2) Among the 21 transects presenting adult ticks, only one half (10 transects) revealed this stage at the first passage. (3) Among the 11 transects presenting larvae, only one half (6 transects) revealed this stage at the first passage.

Analysis of foot and mouth disease in mainland South East Asia

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Describing Foot and Mouth Disease (FMD) as endemic throughout mainland South-East Asia is significantly understating the complexity of the epidemiological picture throughout the region. The distribution of the three serotypes in the region (O, A and Asia1) is further complicated by a number of different topotypes also being present in local pools. Continuous trade in livestock allows the introduction of differing strains of FMD into naïve populations on a regular basis, creating explosive outbreaks. This paper evolved from a collaboration with the South-East Asia and China FMD Campaign to evaluate ten years worth of reporting of FMD outbreaks from member countries. A component of the campaign is to identify sites where it may be necessary to introduce vaccination campaigns to control outbreaks of disease. The data for this analysis included 5 237 reports submitted to the campaign from the start of 2000 until mid 2010. Although date, outbreak location (at the province and district level) and serotype plus information on the outbreak size and affected species was available, not all reports had complete information on serotype, number of animals affected or population at risk. Outbreak reports were standardised by number of villages and the number per province were compared over years to identify provinces with consistently high or low reporting numbers. Spatial and spatio-temporal cluster detection methods using R and SaTScan identified a number of significant clusters of each serotype over the ten year period. A number of different real-time detection algorithms were implemented in a web based query system. Although endemic across the region, FMD is not uniformly present. Initiatives on training and reporting are helping to improve the sensitivity of the system. Advances in decentralised testing techniques offer hope for improved verification of FMD. Improvements in molecular typing and further research in livestock movements will be vital for understanding the circulation of FMD in South East Asia.

Session 55**Theatre 4****Iranian NSP-serosurvey to estimate FMD infection level where impure FMD vaccine is used**

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More than 5000 suspected Foot and Mouth Disease (FMD) outbreaks were reported in Iran in 2010 despite mass vaccination of ruminants. The Iranian Veterinary Organisation has partnered with EUFMD/FAO in a 3 year project to strengthen FMD surveillance nationwide and to progress from Stage 1 to 3 on the FMD-PCP (Progressive Control Pathway) in its most western province, West Azerbaijan (WAZB). The objective of this study was to determine the baseline level of FMD infection in WAZB through a sero-survey combined with a questionnaire about putative risk factors for FMD infection. In a 2-stage sampling design, 30 calves (6-24 months) in each of 300 randomly-selected epidemiological units (epi-units), stratified proportionally by husbandry system were sampled. Samples were tested for FMD non-structural proteins (NSP) antibodies (Ab) (Prionics). As the FMD vaccine used in Iran is impure, NSP-Ab induction may occur by vaccination. This was accounted for by increasing the cut-off value (75% instead of 50% inhibition) and a sensitivity analysis to evaluate effects of this increased cut-off value. The data were analysed using a random-effects logistic model, accounting for clustering of animals within households and clustering of households within epi-units. Over 80% of epi-units had 5 or more calves positive for NSP-Ab, whereas clinical signs of FMD were observed in only 18% of epi-units in the previous 12 months. Thirty percent of calves too young to be vaccinated during the last campaign tested positive, compared to 42% old enough to be vaccinated at least once. Calves in dairy and beef farms were more likely to test positive compared with villages as were calves from trading owners compared with non-trading owners. The same risk factors were indicated using 50% inhibition cut-off.

Rate of introduction of a low pathogenic avian influenza virus infection in different poultry production sectors in the Netherlands

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Targeted risk-based surveillance of poultry types (PT) with different risks of introduction of low pathogenic avian influenza virus (LPAIV) infection may improve the sensitivity of a surveillance programme. Thus, the objective of this study was to quantify the rate of introduction of LPAIV infections into different PT (layer-chickens, Ducks, Turkeys, etc) in the Netherlands. Data from the Dutch LPAIV surveillance programme (2007-2010) were analysed using generalised linear mixed and spatial models. The rate and relative risk of introduction of a LPAIV infection into poultry were quantified. The rate of introduction of LPAIV onto indoor-layer farms was 3.5×10^{-4} per month. Outdoor (free range) layer, turkey, duck breeder and meat-duck farms had a 11, 8, 24 and 13 times higher rate of introduction of LPAIV than indoor layer farms, respectively. Although not significant, the rate of introduction into broiler, chicken breeder and pullet farms, appears to be lower than indoor layer farms. No significant spatial clustering was identified. Differences in rate of introduction of LPAIV can be used to (re)design a targeted risk-based surveillance programme.

Detection of high risk diseases for farmed salmonids in wild fish populations surrounding salmon farms in Southern Chile

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Infectious diseases are one of the major constraints to salmon industry, for which the role of wild fish in disease maintenance and spread is an important concern. The objective here was to assess the presence of several high-risk salmonid diseases in populations of wild fish located nearby salmon farms in southern Chile. Association between outbreaks of infectious agents in salmon farms and agents detection in wild fish was also assessed. Wild fish were sampled within 5-km radius that surrounds salmon farms in the sea of 10th and 11th regions. Tissue samples were tested for specific bacterial and viral agents by PCR assays. A logistic regression model was used to test the association between fish farm variables, including outbreaks of infectious agents, and agents detection in wild fish. Most of the collected wild fish (n=1,490) were *Eleginops maclovinus* (n=763) and *Odontheistes regia* (n=275), whereas the remaining 452 fish were of different species. *Piscirickettsia salmonis* was found in 51 (6.41%) of the samples and it was the only infectious agent detected. A significant association was found between a previous outbreak of *P. salmonis* in the fish farm and detection of the agent on wild fish (P=0.003). In two sampled locations, sample size of *E. maclovinus* was sufficient to support the hypothesis that the wild population surrounding the farm was free from other agents. Unfortunately, for the remaining locations and species sample size was not sufficient to assess this. Results here show an epidemiological association between outbreaks in farmed salmon and detection of the outbreak agents in wild life populations, where wild fish may play a role in emergence and transmission of at least certain farmed salmonid diseases in southern Chile. This information is useful for developing policies for disease control in farmed salmon in the country.

Prevalence of dwarf gourami iridovirus (DGIV) in imported and domestic ornamental fish in Australia and the risk posed to native fish

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The movement of ornamental fish through exporting and importing practices is a major factor for the transboundary spread of pathogens. Australia has one of the most stringent standards for the importation of ornamental fish which includes pre-border health certification, inspection upon arrival and a mandatory 1-3 week quarantine period in a quarantine approved premise. Despite these quarantine measures, in 2003 an exotic viral pathogen known as dwarf gourami iridovirus (DGIV) was the causative agent of a mass mortality event in farmed Murray cod (*Maccullochella peelii peelii*), an iconic native species of high conservation value. This outbreak and the subsequent detection of DGIV in ornamental fish in Australian retail outlets showed that it is likely that DGIV is being translocated to Australia due to inadequacies in quarantine and as a result a review of quarantine policy was undertaken. Imported ornamental fish including those arriving at Australia's border and those released from quarantine and domestic farmed and wild ornamental fish were tested in a series of targeted surveys to determine the extent of DGIV in Australia. DGIV was detected in 21% (266/1,283) of imported fish tested prior to quarantine and 15% (90/598) of fish tested from wholesale and retail outlets post-quarantine. Of concern is the potential for the release of DGIV to the natural environment. Experimental trials demonstrated that in addition to Murray cod other important native fish are susceptible to DGIV. Due to the significant biosecurity risk posed to freshwater ecosystems a qualitative risk assessment to estimate the likelihood of DGIV entering the natural environment through the ornamental fish trade was conducted. The results of this study will be used to inform imminent changes in quarantine policy.

Incursions of cyprinid herpesvirus-2 in goldfish populations in Australia despite quarantine practices

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Nearly 18 million ornamental fish were imported into Australia in 2007, including approximately 3.9 million goldfish. A further 7 million goldfish were domestically produced from aquaculture to supply the pet fish industry. Despite quarantine regulations during importation, there have been several incidents in Australia where exotic pathogens have become established in farmed or free-living fish species. The exotic virus Cyprinid herpesvirus 2 (CyHV-2) was first found in Australia in 2003 from privately owned goldfish. At the time, this suggested that sub-clinically infected goldfish were passing quarantine regulations requiring health certification and three weeks of quarantine. Subsequently in 2008, an opportunistic survey of retail outlets reporting sick or moribund fish in Sydney, Australia revealed that CyHV-2 was detected in 17% (15/87) of goldfish. However, since retail outlets contain an assortment of imported and domestic goldfish sharing the same environment, the source of the virus could not be identified. Furthermore, domestic breeders have anecdotally claimed that their stock succumb to diseases when brought into contact with imported goldfish in wholesale and retail premises. A series of targeted surveys were conducted to determine whether CyHV-2 is has already established in farmed or wild ornamental fish in Australia. For this purpose, goldfish populations were tested to OIE standard to detect 2% prevalence with 95% confidence assuming a test of 100% sensitivity and specificity. CyHV-2 was detected in domestic goldfish at farms, wholesalers and retail outlets and in wild goldfish populations. The results of this study demonstrated that the virus is established in Australia and were used to inform quarantine policy to revoke the requirement for goldfish exported to Australia to be certified free of CyHV-2.

From introduction to eradication: Spring Viraemia of Carp (SVC) in the UK

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Spring viraemia of carp (SVC) is a cyprinid fish disease of international importance that can cause significant mortality. In the UK, SVC was first detected in 1977 with further cases occurring in fisheries, farms and retail establishments throughout England and Wales (few cyprinid populations exist in Scotland) over the subsequent 30 years. Following a control and eradication programme for the disease initiated in 2005, the UK was declared free in 2010. This study compiles historic records of SVC cases in England and Wales with a view to understanding its routes of introduction and spread, and assessing the effectiveness of the control and eradication programme with a view to improving contingency plans to prevent and control future disease incursions in the cyprinid fish sectors. Between 1977 and 2007 the presence of SVC was confirmed on 105 occasions, with 65 of the cases occurring in sport fisheries and the majority of the remainder occurring in the ornamental fish sector. The study found that throughout its 30 year history in the UK, though cases were widely distributed, their occurrence was sporadic and the virus did not become endemic. Unlike koi herpesvirus (KHV) which affects the same industry sectors, SVC was not able to persist under UK environmental conditions, suggesting that the majority of cases were a result of new introductions to the UK and not within country spread. The control and eradication programme adopted was highly effective and within two years of its implementation cases of SVC ceased. Given the non-persistent nature of the pathogen the most important aspect of the control programme focused on preventing re-introduction of the virus to the UK. Despite the effectiveness of these controls against SVC, this approach is likely to be less effective against more persistent pathogens such as KHV, which are likely to require more stringent measures to prevent within country spread.

Session 56**Theatre 5****Do imports of rainbow trout carcasses risk introducing viral haemorrhagic septicaemia virus into England and Wales?**

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A qualitative import risk analysis (IRA) was undertaken to assess the likelihood of introduction and establishment of Viral haemorrhagic septicaemia virus (VHSV) genotype 1a in England and Wales (E&W) via the processing of imported rainbow trout (RBT) carcasses. Four main routes by which populations of susceptible species could be exposed to VHSV (via processing waste) were considered: 1. run-off from solid waste to watercourses, 2. contamination of birds or rodents with VHSV by scavenging solid waste, 3. liquid waste discharge to mains drainage, and 4. discharge of liquid waste directly to watercourses. Data on the biophysical characteristics of the virus, the epidemiology of the disease, and fish processing in E&W were collated. Likelihoods for each step of the four pathways were estimated. Pathway 4, the discharge of liquid waste (which may be untreated) directly to a watercourse, was judged most likely to result in exposure that might result in infection (and thus establishment). Levels of virus entering the aquatic environment via pathways 1 to 3 were judged to be many times lower than pathway 4 due mainly to the treatment of solid waste and high levels of dilution. Close physical proximity of on farm processing facilities to susceptible farmed and wild populations increases the risk of VHSV exposure and establishment via all four pathways. Other routes of mechanical spread may also be important. The analysis was constrained by a lack of data on farm level and within farm prevalence of VHSV, volume of trade in RBT and processing practices. A more accurate assessment of the likelihood of exposure and establishment requires quantitative data on viral concentrations in waste and the minimum infectious dose. Nevertheless it was concluded that the threat of VHSV introduction into E&W could be reduced by treatment of liquid effluent and sourcing carcasses for on-farm processing from approved VHSV free areas only.

Factors affecting cure after a collective topical treatment of digital dermatitis in dairy farms

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A controlled field trial was conducted to evaluate in dairy cattle the benefit provided by different regimens of a collective topical treatment using a solution of copper and zinc chelates to cure digital dermatitis (DD), and to investigate factors that could explain variations in the clinical cure of DD lesions. The study involved 4,677 dairy cows from 52 French dairy farms where DD was endemic. The farms were quasi-randomly allocated to 1 of 4 treatment regimens for 6 months: no collective treatment (Control), walk-through footbath during 4 consecutive milkings every 4 weeks (FB/4W) or every 2 weeks (FB/2W) and collective spraying during 2 milkings fortnightly (CS/2W). For welfare reasons, all farmers also had to treat all detected active DD lesions with individual topical spraying of oxytetracycline. DD was scored on all lactating cows during milking 7 times every 4 weeks by 14 trained investigators. During these farm visits, data related to cow characteristics and farm management also were collected. The curative effectiveness of collective treatments was assessed through a Cox survival frailty model (adjusted for farm and investigators) as the probability of cure of an active DD lesion during at least 2 consecutive visits. Monthly DD cure rates were 58%, 55%, 76% and 76% in the Control, FB/4W, FB/2W and CS/2W regimens respectively. Hazard of cure of DD was increased by 1.28 and 1.41 when respectively walk-through footbath and collective spraying were applied over 2 days every fortnight compared to the control regimen, whereas the FB/4W regimen was not efficient. Three main factors were identified as quickening DD healing: cleanliness of the feet, initial small size of the DD lesion and additional individual topical treatment. Grazing tended to speed DD healing. These results highlight the need of combining several control measures to ensure a high and fast cure of digital dermatitis on endemically affected farms.

The relationship between lying time and the prevalence of lameness in free-stall dairy barns in Alberta

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Lameness is a significant problem in the dairy industry. In addition to economic losses, it causes pain and can have long-term effects on cow welfare. Extremely long or short lying times are associated with lameness. The intent of this study was to evaluate lying behavior as a diagnostic tool to detect lameness on-farm. Materials and To measure standing and lying time, accelerometers were fitted on 40 Holstein cows from 80 free stall barns. Information on the frequency and duration of lying time was monitored over a 4-day period. To assess lameness, cows were gait scored by trained observers on the presence or absence of limping, asymmetric steps and head bob at the start of data collection. Preliminary analysis showed a within herd prevalence of 21% (3-68%) lameness. The average lying time (h/day) for lame and non-lame cows was 10.9 (5.7-18.2) and 10.1 (2.3-15.2) respectively. Eighty percent of the cows with high lying times (>14 h/day) were lame and 78% with low lying times (<8 h/day) were non-lame. Through linear regression analysis, a better insight in the relation between the lying time and lameness will be provided. Within herd differences were larger compared to between herd differences, indicating a strong farm effect. There is a large variation within and between herds in terms of lying time among non-lame and lame cows. Cows showing extended lying time, independent from the farm of origin, were more likely to be identified lame when compared to cows with low lying times. This suggests that extreme lying times could be a useful tool to detect lame cows.

Nervous necrosis virus: new tests and epidemiological investigations suggest a way forward in disease control

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Nervous necrosis virus (NNV) affects >35 species of fish worldwide and causes substantial economic losses in aquaculture of marine finfish. It has also reduced options for restocking wild fisheries due to fears the disease may spread from aquaculture. In Australia, the disease has primarily affected the production of barramundi (*Lates calcarifer*), with losses of up to 100% occurring in some hatcheries. Other species such as reef fish, striped trumpeter and Australian bass have also been affected. Previously the gel-based polymerase chain reaction (PCR) was used to detect NNV but in many cases infection was present despite negative test results and so the test did not predict the likelihood of an outbreak. A new, sensitive and validated quantitative (q) PCR test is now available for NNV. This has enabled an epidemiological study which involved intensive repeated cross sectional sampling of barramundi during the production cycle over several years, and has provided key evidence that infection was derived horizontally rather than vertically from broodstock. Current research is focussed on developing and applying serological (blood) tests to complement the qPCR method. This will provide information on whether antibody status of broodstock can be used as an indicator of infection in a fish population. This project is supported by the Australian Research Council and by the Fisheries Research and Development Corporation on behalf of the Australian government.

An approach to estimating the reliability of pooled diagnostic tests for fish diseases

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Many fish disease diagnostic tests use tissue samples pooled from several individuals. It is not, however, appropriate to assume that the operational sensitivities (Se) and specificities (Sp) of tests on pools are the same as those on individuals. This is because the number of infected individuals in a pool can affect the signal generated by a test. We propose an approach which provides information on the reliability of pooled diagnostic tests, allows comparison with individual diagnostic tests, and can lead to improved cost effective surveillance. The experimental design involves sampling individuals from two or more populations with different infection prevalences and testing the infection status of these individuals using two or more diagnostic tests. The individuals are also randomly assigned to one of several pooled groups which are subject to the same diagnostic tests. Standard Bayesian non-gold standard statistical methods are used to estimate the prevalence of infected individuals in each population. An extension of these methods can also be used to estimate the Sp of pooled tests. These estimates are used to convert the observed distribution of the number of test positive and negative pools containing a given number of test positive individuals to an estimated distribution of the number of test positive and negative pools containing a given number of infected individuals. A generalised linear model is used to estimate the association between the estimated proportion of pools testing positive (dependent variable) and the number of infected individuals in a pool (explanatory variable). This equation is used to estimate the prevalence (and confidence intervals) at which 50% of pools test positive and this statistic can be used to characterise the ability of a pooled diagnostic test to detect the presence of an infected individual. The advantages and limitations of this approach will be illustrated using data for salmonid alphavirus and infectious salmon anaemia virus collected by our laboratory over the last four years.

The use of the bibliometric H-index to quantify pathogen impact in North America

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Disease surveillance requires reliable ways to identify the most likely pathogen threats and given limited resources, policy decision makers need rational methods with which to prioritise diseases. Such prioritisation often involves the use of decision support tools to identify which diseases to target and on which areas to focus resources and funding. The work presented here investigated a novel quantitative method to measure the relative impact of diseases that could complement more conventional risk assessment. It involves the use of the Hirsch index (H-index). The H-index has often been used to quantify an individual's scientific research output by measuring the number of published papers and the number of times that the papers have been cited. Recently it has been tested as an objective measure of the impact of human pathogens. Here we use it to identify and assess the characteristics of infectious diseases that have the highest impact upon health in the North American region. A previously generated list of 6073 infectious organisms known to have pathogenic effects upon humans was used, though many have zoonotic potential. We used literature searching mechanisms in PubMed (for 1900 to 2009) to determine that around 1,800 of these pathogens have been recorded in North America (Canada, USA, Mexico, Greenland). The H-index of these pathogens was calculated using Web of Science and scores ranged from 0 to 584. For a small selection of pathogens the H-index was calculated from 1900 to 2009 in order to assess how it varies over time. The H-index of pathogens was compared to their emerging and zoonotic potential.

The use of scoping studies in agri-food public health: opportunities and challenges

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Scoping studies are a research synthesis approach that aims to rapidly identify, characterize and map the research knowledge underpinning a broad topic. They can play an important role in informing policy and decision-making due to their transparent and rapid process, as well as their ability to address complex, multidisciplinary issues. This study describes the methodological characteristics and current use of scoping studies, and the opportunities and challenges for their methodological standardization and wider use in agri-food public health. Four electronic databases and the grey literature were searched to identify scoping studies written in English, French or Spanish, published by June 2011. Abstract relevance screening and characterization of relevant studies were performed by two independent reviewers using pre-tested forms. Descriptive statistics were calculated to summarize the data. Of the 182 scoping studies included in the study, 83% were conducted in the health sector (n=151). Study implementation varied from 20 days to over a year, and 50% utilized a published methodological framework (n=91). The scope of the search strategy and the number of reviewers varied among studies. Quality assessment of included studies was infrequently a part of the methodological process (n=41). Presentation of the evidence ranged from descriptive narratives to detailed tables and graphical diagrams. Scoping studies are a useful research synthesis approach for addressing broad, policy-driven issues. It is a methodology that can enhance evidence-informed policies and practice in agri-food public health by ensuring that current evidence is effectively synthesized and translated to appropriate end-users.

A stochastic mathematical model of the transmission dynamics of porcine reproductive and respiratory syndrome virus (PRRSV) in a metapopulation

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Endemic diseases such as Porcine Reproductive and Respiratory Syndrome (PRRS) and Swine Dysentery (SD) are persistent and heavy burdens on the pig industry in Great Britain. We investigate the transmission and persistence of these diseases, with emphasis on the metapopulation (i.e. between herd) processes. Mathematical models are being developed to explore potential control and intervention strategies. A continuous time stochastic model framework to simulate the demographic processes (birth, death, movement) and transmission of disease through a metapopulation has been developed. Each farm in the metapopulation is comprised of 6 demographic groups representing the life cycles of pigs in a commercial herd. Pig movement data (RADAR) are used to characterise farm-types and their connections within the metapopulation. The networks of pig farms can be complex, and do not apparently conform to 'perceived wisdom'. One result is that the impact of specific control interventions have to be considered differently at farm and network levels, and the optimum policy is not necessarily the same for both perspectives, i.e. what minimises disease in the metapopulation does not minimise disease in the individual farms. Quantitative and qualitative results of different interventions will be presented.

Bayesian analysis of risk factors for infection with a genotype of PRRS virus in Ontario swine herds using monitoring data

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Porcine Reproductive and Respiratory Syndrome (PRRS) has a worldwide distribution. The impact of PRRS is approximately \$600 million in losses annually to the US swine industry and \$130 million in Canada. This economically important endemic disease causes reproductive failure in breeding stock and respiratory tract illness in young pigs. In Ontario RFLP 1-18-4 has been determined as one of the most common virus genotypes, and one that is associated with severe clinical presentation at the herd level. Individual-level models (ILMs) for infectious diseases, fitted in a Bayesian MCMC framework, have been used to describe both the spatial and temporal spread of diseases. They are an intuitive and flexible class of models that can take into account population heterogeneity via various individual-level covariates. The objective of this study is to identify risk factors for the spread of the genotype 1-18-4 from monitoring data in southern Ontario using ILMs. Specifically, we explore networks through which resources are obtained or delivered, as well as the ownership structure of herds, and identify factors that may be contributing to high risk of infection. A population of 316 herds which experienced their PRRS outbreaks between September 2004 and August 2007 are included in the analyses, in which 194 (61%) are sow herds. During the study period, 45 herds (27 sow herds) experienced their first outbreak due to RFLP 1-18-4. Our preliminary results show that sharing the same herd owners, gilt sources and market trucks are the important factors for disease spread. Geographical locations of herds do not seem to be crucial. Risk factors such as control strategies (including vaccine used, serum inoculation and feedback), bio-security measures related to trucking information, number of infected herds in the population, and herd types are also considered in the models used.

What happened to pandemics?

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What happened to Pandemics like BSE, Bird flue, Swine flue or SARS? They were not as bad as predicted. BSE was only bad in UK, but it was not a pandemic by definition, as it was restricted by time and space. One problem was that the pandemics were explained by paraclinicians. Paraclinicians need grants and publications, as others too. Consecutive an infectious agent has to be dangerous. For example, each virus can mutate, which is a biological axiom of evolution. Therefore, what do we need? People and stakeholder need more trust. This can be achieved by better health information. „One medicine’ has to provide the required information. Who can provide this information and explain them contextual to the public? Public health professionals are needed to fill the gap between medical specialists like paraclinicians and the public. „One health’ has to focus on health information in the future. Examples of the problems and interactions are given in the presentation as well as a solution of the problem with a special focus on the ECVPH and its important possibilities in this context.

Session 62**Theatre 1****Randomized clinical field trial of the effects of viral vaccination on the incidence of bovine respiratory disease, mortality, and growth in dairy heifer calves**

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Bovine respiratory disease (BRD) is one of the major causes of morbidity and mortality in young dairy cattle. The objective of this randomized clinical trial was to determine the effectiveness of one or two doses of a modified-live viral vaccine administered to heifer calves prior to weaning. A total of 2,874 heifer calves from 19 commercial dairy farms in Minnesota, USA and Ontario, Canada were enrolled at 1 to 7 d of age. Calves were randomly assigned to receive a commercial, intramuscular, modified-live vaccine against BVDV-1 and -2, BRSV, BHV-1, and PI-3 at 15 to 21 d of age (2 weeks), 35 to 42 d (5 weeks), both 2 and 5 weeks, or sterile saline at both times. The incidence of failure of passive transfer was 11 or 32%, using cut-points of serum total protein of 5.2 and 5.7 g/dl, respectively. Overall, 22% of calves were treated for BRD, mortality was 3.5%, and average daily gain was 0.95 kg/day. These outcomes did not differ between vaccination groups. Reasons for these findings may include interference by maternal antibodies, responsiveness of the neonatal immune system, timing of immunity relative to pathogen exposure, disease caused by pathogens other than those in the vaccine, or herd immunity. However, in this population of home-raised calves, intramuscular vaccination with a multivalent, modified-live viral vaccine at 2 or 5 weeks of age or both was not associated with a decreased risk of BRD or death, or with growth to 3 months of age. In populations with a higher incidence of failure of passive transfer or risk of BRD, calves with low levels of specific antibodies may respond differently to vaccination.

Diagnosed BVDV PI-animals in Northern-Belgium: where do they go?

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The key to Bovine Viral Diarrhoea Virus (BVDV) control in cattle is the detection and consequent removal of PI-animals. Data containing all cattle that tested BVDV antigen positive from a 2-year period from October 2009 to October 2011 in Northern-Belgium was investigated. Test-positive animals (BVDV ELISA or BVDV PCR) were considered as 'highly-likely' to be PI-animals. Laboratory data were linked to the Belgian I&R database to determine the location of the herd of detection of these animals. This was compared with the actual location and animal status of the detected PI's. This way, 'where-about's' and animal status of these detected PI – animals were constructed. Data were mapped using a GIS system to explore the spatial distribution of cattle herds with detected PI animals. A total of 2,951 animals tested BVDV antigen positive. Tested animals originated from 1,076 different herds. Based on the animal status and location, we can make the following conclusions: only 55.5% (1,411) of the presumed PI-animals were classified dead without first being moved to another herd (either through removal or natural death), 13.8% (351) animals were dead but had been moved to other herds after their detection. 470 animals (18.5%) were still alive and present at the herd of the detection and finally 198 (7.8%) cattle were present on another location or 112 (4.4%) exported. The average interval between detection and removal was 49.1 days. During the study period, we retrieved a total of 1,356 cattle herds with evidence of the (temporary) presence of PI-animals (approximately 6.3% of all active cattle herds in Northern-Belgium). Although this is a non-random study, the results clearly illustrate that measures to encourage farmers to quickly eradicate PI-animals are crucial for the progress of BVDV eradication. Stakeholders should be aware of this if a future BVDV-control program is developed for Belgium.

Investigating the source and spread of Border disease virus in cattle from a persistently infected bull

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In this paper we describe an investigation to understand the epidemiology of Border disease virus (BDV) occurring from natural infection in a bull. The virus was detected in a beef breeding bull found to be persistently infected. Reports of naturally infected cattle with BDV are uncommon in the literature. Poor reproductive performance (pregnancy rate of 23% for 57 days) occurred in dairy-heifers exposed to the bull persistently infected with BDV from a team of three sires used to mate the heifers. A high prevalence (39/40, 98%; 95% CI, 87-100%) of heifers had serological evidence of exposure to BDV. Border disease virus was not detected in the ear notches of six calves born to heifers exposed to the affected bull during the early mating period. There was no evidence of BDV circulating between cattle on the farm of origin of the affected bull. No BDV was detected in serum collected from all calves and adult animals present on the farm of origin during 2010. Border disease virus was circulating in sheep, shown by multiple ages of sheep being affected and the prevalence of exposure increasing with age of sheep. Exposure events between sheep and cattle on this property must be reasonably high as cattle and sheep share grazing during the pregnancy period. Therefore it seems that infection in cattle with BDV may be a low probability event with transmission of infection requiring other factors additional to shared grazing. Phylogenetic analysis of the isolate from the affected bull revealed that it could be allocated within the BDV species in the same cluster of the BDV 1 group as New Zealand isolates. It was concluded that cattle persistently infected with BDV can act as a source of virus for infection of other cattle. The benefit of bovine viral diarrhoea testing in cattle could be enhanced by using tests that also detect BDV.

Insights into the eradication of bovine viral diarrhoea in Switzerland: planned, foreseen and unforeseen events

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Switzerland started the eradication of bovine viral diarrhoea (BVD) in 2008. The concept for the eradication without vaccination was based on testing ear-notch samples from bovines directly for BVD virus and eliminate positives – persistently infected (PI) animals – from the population. The whole national stock was tested in 2008, and since 2009 all newborn calves are tested within the first weeks of live. Initially, it was scheduled to eliminate the virus from the livestock population within the year 2009 and to move to a less costly serological surveillance in 2011 at the latest. The situation in 2012 is that newborn calves are still tested within the first weeks of life. Observed obstacles for the planned time schedule were on the one hand reasons from the field: false negative test results, mixing of stock from different farms on alpine pasture, in few cases farmer's reluctance to take improved hygiene measures. On the other hand, the Veterinary Service's attitude towards a serological surveillance was dismissive. Thus, if a very easy, communicable and effective method is to be replaced by a more complicated one an early start of information is especial necessary to inform all stakeholders. Additionally, it seems that the initial schedule was set up in spite of a lack of information on the serological status of the cattle population with respect to age and purpose. We will present data and analyses showing (1) the course of the eradication campaign; (2) examples of the observed obstacles; and (3) how information of stakeholders and the communication within the Veterinary Service was set up. We describe the current situation concerning the possibilities for serological surveillance and the data needed to schedule the time intervals in BVD eradication programs if serological surveillance is not implemented from the beginning.

A multi-country epidemiological investigation of bovine neonatal pancytopenia (BNP)

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Since 2006, a syndrome called bovine neonatal pancytopenia (BNP) has been reported from several European countries and, more recently, from New Zealand. The incidence of BNP is low but the case fatality rate is high. A causal association with Pregsure BVD vaccination of the dam has been hypothesized and the vaccine was withdrawn from the market in August 2010. The current project funded by Pfizer Animal Health is designed to identify risk factors associated with BNP occurrence both at herd level and within affected herds at animal level. It consists of two nested study components. A case-control study was conducted to compare cattle farms that experienced BNP cases with those that did not. Amongst affected herds, a second case-control study was performed to compare characteristics of affected and unaffected calves. The study was conducted in Belgium, France, Germany and The Netherlands to maximise case recruitment and to allow an assessment of the potential impact of country-specific animal management practices. Data collection was completed in December 2011, yielding a total of 448 case and 757 control herds and, from the case herds, 538 cases and 1,511 control calves. Data have been reviewed to refine case definitions before proceeding to descriptive, univariable and multivariable analyses. Results from these analyses will be presented.

Risk factor analysis for infectious salmon anaemia virus positivity of Atlantic salmon farms in southern Chile

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Infectious salmon anaemia (ISA) is a highly contagious viral disease that affects the Atlantic salmon (*Salmo salar*), caused by the infectious salmon anaemia virus (ISAV). ISA is present in Chile since 2007 and it has affected most of growing-up areas. After three years of its entry into force, the ISA Surveillance and Control Official Program (ISA-SCOP), is currently being updated, process that considers the incorporation of risk for surveillance activities. The objective of this study was to identify risk factors for positivity to ISAV at fish farm level, in order to use this information in the reformulation of official surveillance strategies. The study design was a retrospective single cohort, where the study unit was defined as the salmon farm. Study population was formed by all salmon farms in operation between January 2008 and December 2010 in Los Lagos region. Cox proportional hazards model (CPHM) was used as the statistical method. Significant risk factors for ISAV positivity were: (1) number of stocked fish (HR=1.05); and (2) type of smolt origin facility, where lakes and mixed origin had a significantly higher risk than land-based farms (hatcheries) (HR=4,68; HR=4,38, respectively). Significant protective factors for ISAV positivity were: (1) fallow period (HR=0,96); and (2) multi-species cycle (HR=0,30). These factors might be useful for classify fish farms accordingly to the risk of being positive to ISAV. In addition, these factors are commonly set at the beginning of the production cycle, which allows a better surveillance planning. Inclusion of these factors in official surveillance planning should have positive impacts in the overall surveillance system sensitivity and in effectiveness for identification of ISAV positive sites.

Phylogeographic analyses of low virulent infectious salmon anaemia (ISA) virus (HPR0) in farmed Atlantic salmon in Norway

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Infectious salmon anaemia (ISA) is a severe disease in farmed Atlantic salmon (*Salmo salar*) that has caused epidemic outbreaks worldwide. The disease is caused by virulent Isavirus (ISAV) within the family Orthomyxoviridae. ISAV has a genome consisting of 8 segments, of which the Hemagglutinin esterase (HE) glycoprotein is encoded by segment 6 (the HE gene). A low virulent variant of ISAV (HPR0) have been reported with increasing frequencies. HPR0 ISAV is characterized by a full length of nucleotides in the highly polymorphic region (HPR) of the HE gene, and is proposed to be an ancestor of virulent ISAV. Here, we aim to study the phylogeographical distribution of HPR0 ISAV in farmed salmon in Norway, as well as phylogeographical associations between virulent ISAV and HPR0. We sampled 232 fish groups of Atlantic salmon along the coast, in total 9,474 fish, including fish groups with both juvenile, on-grown marine, and brood stock salmon. Real-time rtPCR was used for the detection of ISAV, and the Hemagglutinin esterase (HE) gene was sequenced from positive samples. We used a Mantel test to test for phylogeographical associations between pairs of HPR0 HE gene sequences. Furthermore, we used a rank test to test for associations between HE gene sequences from virulent ISAV and HPR0. The results show that HPR0 is widespread in farmed populations of Atlantic salmon in Norway, especially in seawater, but also in freshwater. We found a significant positive correlation between genetic and geographic distances between pairs of HPR0, suggesting that the population of HPR0 in Norway is genetically structured. Finally, we show that there is a spatial association between virulent ISAV and HPR0, supporting the hypothesis that ancestral HPR0 may undergo a transition to virulent ISAV.

Co-infection patterns of two high-risk diseases affecting farmed Atlantic salmon in southern Chile (2007-2009)

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Infectious salmon anemia virus (ISAV) caused a large epidemic in farmed salmon in Chile (2007-2009). ISAV epidemics may be exacerbated by sea lice (SL), which increases the susceptibility of infested fish and may be a vector for ISAV. In this study, co-infections patterns of ISAV and SL were assessed from a surveillance data collected by the fish health authority. ISAV status and SL counts were registered monthly in all Atlantic salmon farms located in the 10th region, from July 2007 through December 2009. Each farm was categorized monthly according to ISAV/SL status. A multinomial time-space scan test, using an elliptical window, was implemented to identify clusters of these categories. A multivariate regression model was then fitted to quantify the association between clustering of both diseases and farm management factors. Clusters of ISAV-SL co-infection (n=3), only ISAV (n=1), only SL (n=3), and ISAV-SL free (n=1) farms were identified. Most clusters (6/8) were associated with high burdens of SL, and the risk ratio was always high (>2.5) in those with both diseases. There were significant associations (P<0.05) between characteristic of ISAV outbreaks, spatial and on farm risk factors with clusters that showed co-infections. These results provide evidence that the interaction between ISAV-SL showed to be the most likely pattern of infection during the largest ISAV epidemic. In addition, spatial techniques were able to identify areas where better management practices were associated with better sanitary results.

Within-farm spread of infectious salmon anemia virus in Atlantic salmon farms in Chile

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Spread of infectious salmon anemia virus (ISAV) at a cage-level was quantified retrospectively from a subset of 23 Atlantic salmon farms located in southern Chile. Data collected from official surveillance activities were compiled and organized systematically to obtain detailed information about ISAV outbreaks. Descriptive statistics were calculated to quantify the magnitude of an ISAV incursion including the infected proportion, outbreak duration, and time to secondary infection. Linear and multiple failure time (MFT) regression models were used to determine factors significantly associated with cumulative incidence (R_c) and hazard rate (HR) for recurrent events, respectively. In addition, the Knox and spatial scan tests were used to assess if cage-to-cage transmission was clustered in space and time. Findings suggest that ISAV outbreaks lasted 30 weeks (wk) on average (median=26 wk, 95% CI=24-37 wk) affecting 55.8% of susceptible cages (95% CI=46.2-65.6%). Median time to secondary diagnosed cages was 23 days. Clinical ISAV outbreaks was a significant predictor for an increased R_c , whereas HR was associated with smolt quality and number of fish. Spatio-temporal analyses failed to identify clustering of cage-cases, suggesting that farm structure may impose contact rates and heterogeneities that may influence the dynamics of ISAV introduction and subsequent spread. Results presented here will help to parameterize models for ISAV transmission in Chile and other regions in which salmon are intensively farmed.

Emergence, control and eradication of infectious salmon anaemia in the Shetland Islands, Scotland
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Infectious salmon anaemia (ISA) is one of the most serious diseases affecting farmed salmon. ISA has caused catastrophic declines in production in Chile and the Faeroe Islands and has been a persistent problem in Norway and Atlantic Canada. Two outbreaks of ISA have occurred in Scotland, the first in 1998/9 became widespread before its eradication. The second in 2008/9 was confined to one area of the Shetland Islands, at least in part owing to epidemiological lessons learnt from the 1998/9 outbreak. The outbreak was confined because of (1) industry codes-of-practice for good biosecurity in peace time; (2) rapid detection; (3) movement bans on confirmation over a pre-defined area; (4) rapid depopulation of confirmed sites; and (5) systematic fallowing of the area after last fish removed. Good biosecurity includes codes of practice for disinfection of harvest vessels and processing plants and risk-assessing movement of fish between seawater sites. These practices reduced the potential for ISAV to spread undiscovered. Detection used intelligence-based inspection to target sites that had had large mortalities, and diagnostic methods that were improved in accuracy since 1998/9. An official area management system, based on tidal excursion distances pre-defined the area on which controls were rigorously imposed on confirmation of the index case, these sites in this MA (and others with risk-contacts) were placed under enhanced surveillance; five further sites were confirmed, all in the MA. On confirmation sites were depopulated within 7 weeks (mean 3.7 weeks). When all the site had been cleared, by depopulation or normal harvesting, the whole area was fallowed and placed under a special surveillance regime to confirm eradication. The management regime appears to have been effective at confining and then eradicating ISA. However, the putative ancestral avirulent HPR0 remains in the area, and so vigilance must be maintained to prevent ISA re-emerging.

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Theatre 1

Farmers do not do what they know they should do

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A new conceptual animal health economics framework is proposed. It focuses on competencies (knowledge and know-how) and capabilities (measures and actions) of farmers, and is based on a 2 step analysis of the farmer's health management practices. The first step deals with the learning of farmers, i.e. the diffusion of competencies among various stake-holders involved in animal health management, and the second one with the way competencies are mobilized by farmers to make decisions and to act (capabilities), i.e. what are the determinants of the implementation of health measures, at a given level of competencies. This study aims at validating this second step of the framework, and at showing that farmers often know what to do (they have competencies) for a health issue but only do it (implementation into capacities) when necessary or useful. National identification and milk control program databases were used to calculate herd-level production and health indicators. Dairy calf mortality and composite mean somatic cell count (CMSCC) were analyzed with a linear and a dynamic panel model, respectively. Results showed that CMSCC of one month was positively associated with CMSCC of the 2 previous months, but negatively with CMSCC of the third previous month. In other words, the increase of CMSCC was associated with a decrease 3 months later. This effect is likely to be related to both external advisers and the farmer's own behavior change. The results showed that farmers had the ability to improve udder health management, but they did it only after CMSCC had increased. Moreover, an increase of the male/female ratio was associated with a decrease into the mortality of both dairy young and older heifers (from birth to first calving) during this year. It showed that the farmers were able to improve the dairy heifer management when the heifer availability decreased. The results showed that farmers, in some conditions, know how to improve health, but implement the measures only when the situation deteriorates or when they judge it useful, and not on a continuous way.

The importance of farm-level behavioural considerations in disease surveillance modelling: influence on a Scottish BVD eradication model

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Disease surveillance modelling has historically focussed on epidemiological factors such as diagnostic test performance, disease spread and demographic variability amongst farms. It is more difficult to incorporate the effects of human behaviour, mostly due to uncertain behavioural parameter estimates. As part of the 'EPIC' project we used a novel agent-based stochastic modelling framework to assess qualitatively the sensitivity of disease surveillance to the behavioural responses of individual farms to the perceived local and national disease prevalence. Farm demography and cattle movement information was taken from Scottish census and cattle movement data, and an epidemiological model of national BVD eradication was incorporated, including disease transmission, diagnostic test characteristics, vaccination, and observed abortions. A sensitivity analysis was performed using varying estimates of behavioural parameters representing the changes in propensity to use diagnostic tests based on observed disease prevalence. Incorporating behavioural effects into the model increased the stable prevalence from approximately 1-10% at the end of the simulation, due to lower observed prevalence decreasing the probability of individuals testing for and eradicating disease. These effects also resulted in auto-correlation in the observed disease prevalence, increasing the discrepancy to the true prevalence. We conclude that behavioural responses to changes in perception of disease have a potentially strong influence on the effectiveness of surveillance and control programmes, and should receive greater attention than is currently the case. This work was funded by the Scottish Government.

Session 64**Theatre 3****What motivates farmers to treat lame sheep?**

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For the last 20 years the prevalence of lameness in sheep in the UK has been around 10%; at any one time approximately three million sheep are lame. The most common cause of lameness in sheep is footrot caused by the bacteria *Dichelobacter nodosus*. Research illustrates that lameness levels in the flock can be reduced to 1-2% if lame sheep are treated rapidly with antibiotic injection. Anecdotal evidence indicates that segregation of diseased sheep and culling repeatedly diseased sheep minimise the number of diseased sheep. Reducing lameness in the flock improves animal welfare, improves productivity and reduces the amount of time and money spent on treatment. The aim of this work was to use social science methodologies to investigate sheep farmers' decisions regarding management of lameness to identify the key barriers and motivators to reduce the prevalence of lameness. Sheep farmers and industry leaders were interviewed to explore the salient cognitions. Seventeen key players in the sheep industry provided their expert opinion. This included representatives of the levy boards, the National Sheep Association, vets and independent sheep advisers. Data were collected from eight groups of 5-12 sheep farmers. To increase diversity sheep farmers were recruited from a range of sources; two groups comprised of farmers that were engaged in health and welfare improvement schemes while others were randomly selected from the Agricultural Census database. Areas that were explored in the discussions included the disease representation, empathy, social norms, legislation and economics. The key themes arising from these data will be presented.

Factors influencing veterinarians' use of personal protective equipment

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Zoonotic disease perceptions and preventative practices undertaken by Australian veterinarians are not well researched or understood. This study aimed to determine the perceptions of zoonotic diseases among Australian veterinarians, the infection control practices they use to protect themselves from zoonotic diseases, and the drivers influencing these perceptions, attitudes and practices. A questionnaire was designed and piloted prior to its administration to veterinarians at the Australian Veterinary Association Conference in May 2011. The questionnaire comprised 21 closed, semi-closed and open questions. Data from the questionnaire were analysed using univariable and multivariable ordinal logistic regression analyses to determine significant associations between veterinarians' use of personal protective equipment (PPE) and their perceptions and practices. A total of 344 veterinarians completed the questionnaire. Vets were more likely to use PPE if they perceived that zoonosis exposure from animals and procedures was likely, believed that liability issues and risks encouraged use of PPE, and spent more hours per year in continuing vet education. In contrast, vets working in private practices, practising stringent infection control practices only when necessary, and working in remote or very remote areas were less likely to use PPE. In addition, vets working in places that encouraged use of P2/N95 respirators and restricted contact with isolation patients were more likely to use PPE. The results suggest that vets' perceptions and workplace policies and culture substantially influence vets' use of PPE.

A web-based tool to explore the economic impact of test and slaughter programs on individual smallholders

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Test and slaughter programs rely on compliance from farmers in order to be successful, and yet individual farmers may not perceive a direct benefit in testing and culling their own stock, especially when the test used is imperfect. Incentives such as compensation must therefore be adequate, but if excessive the program may be inefficient and counter-productive behaviour may even be incentivized. The costs and benefits of participating in disease control programs may be distributed over a relatively long time period, and may be of uncertain value or intangible. This is a particular problem for settings with a large proportion of smallholders, for whom culling a relatively small number of animals may have a large economic impact. A simplified generic framework was developed to identify and estimate the costs and benefits for individual smallholdings undergoing test and slaughter. A spreadsheet model was then built to estimate the net benefit to an individual farm. Based on this spreadsheet, a web-based tool was developed for stakeholders to investigate the impact of different test and slaughter programs on individual smallholders. Parameters can be altered manually to investigate the effect of uncertainty, in the price of milk for example. The tool also shows the effects of chance (stochasticity), for example the number of healthy cattle that will be culled as a result of testing a small number of cattle with an imperfect test. The brucellosis test and slaughter scheme in Egypt was used as a case study to explore the potential use of the model, showing that current compensation would be sufficient for approximately 45% of farmers to break even, but would need to be increased by a factor of approximately 26 for 90% of farmers to break even.

EpiContactTrace: an R-tool for facilitating livestock contact tracing and risk based surveillance

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In many countries, livestock movement data are collected with the major objective to enable contact tracing during disease outbreaks. Livestock movement data can also be of relevance for risk based surveillance – both during outbreak or when investigating if a disease is present in the population. However, the livestock movement databases are not always structured in such a way that relevant information for contact tracing or surveillance design is easily retrieved. Therefore, an open source tool, EpiContactTrace, was developed to facilitate prompt retrieval of this information. EpiContactTrace is written in the R-language and uses the network parameters in-degree, out-degree, ingoing contact-chain and outgoing contact-chain, which are relevant for forward and backward contact-tracing respectively. The measures can also be used for identifying herds with many contacts, which can be used in risk based disease surveillance. With the network approach, the livestock movement contact structure for the entire population is analyzed at once, in contrast to manually searching stepwise from farm to farm. Different time periods for ingoing and outgoing contacts can be of interest in the contact tracing, based on possible window of introduction, and this can be adjusted in the tool. The output from the analysis is available as a dataset, but moreover, the tool automatically generates a report on farm level. This report can be either in HTML or PDF format and is intended for the end users – either at the central veterinary authority or for the veterinarian in the field. The report both contains an overview of the situation on the farm, including a graph, as well as detailed information including dates of movements on group or individual level on all contacts. A pilot version of the tool was tested during a large FMD contingency exercise in Sweden. The intention is to make EpiContactTrace available as an R-package at the The Comprehensive R Archive Network (<http://www.cran.r-project.org/>).

The application of origin-destination matrices to the visualisation of animal movement

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Animal movements are important determinants of disease spread. Recent outbreaks of livestock diseases around the world have shown that the temporal and spatial movements of livestock species are generally poorly understood. Pictures speak a thousand words, and visualisation of these movements is important for (1) communication with non-technical, senior decision makers; and (2) to assist academics, technical policy makers and operational staff to form hypotheses, assess risk and target disease investigations. Quantitative spatial statistics have long promised, but failed to provide, a solution for communicating spatial information to non-specialists. This work uses the recently developed technique of Origin-Destination (OD) matrices applied to ten years of the British Cattle Movement Service (BCMS) UK cattle movement data to illustrate the approach. The OD technique is particularly interesting, because in addition to the information on the magnitude of movements apparent in the detail of the map, there are higher level visual effects that provide an immediate indication as to any general direction / randomness of flow (see figures 1 and 2 below). The technique is entirely scalable, constrained only by the availability of data, and could be applied to e.g. sub-national movements, or patterns of global trade between countries. The practical application is illustrated in the paper by a case-study of forward and back-tracings from the 2007 UK foot and mouth disease outbreak. The spatial images produced will be demonstrated as animations to highlight seasonal patterns and longer term changes (these will be available on a website, via a hyperlink and a quick response (QR) code). Previous attempts to visualise moments have generally been vector-based, and suffer from a high level of overlap and visual occlusion; as a result animal movement data remains poorly understood and applied by academia, industry and policy teams.

Livestock movements and contact patterns in Togo: implications for disease control

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The northern Togolese savannah is the country's main livestock-raising area. An extensive survey of brucellosis and Q fever was conducted in 2011 with the local human and animal populations using a One Health approach. Substantial livestock movements occur internally within the savannah and across borders with neighbouring countries. This flow of animals is related to trade routes as well as seasonal movements due to water and pasture shortages, known as transhumance, a common phenomenon in West Africa. Both trade and transhumance could play important roles in the spread and control of infectious diseases in the region, including zoonoses. Aims: To describe in detail, for the first time, the movement patterns of livestock within northern Togo and across national borders; to assess the roles and relative importance of livestock trade and transhumance in the spread, control, and prevention of infectious diseases; to translate these findings into practical recommendations relevant to policy at the national level, as well as regionally in West Africa. A survey with transhumant cattle herds is currently underway in northern Togo. Detailed geographical data relating to transhumance pathways and contacts between herds are being collected, parallel to a brucellosis serosurvey in transhumant herds. Additionally, interviews with livestock traders in markets are being undertaken to spatially and quantitatively capture the flow of livestock through principal trade routes. Where possible, contact networks will be constructed and modelled in relation to infectious disease spread. Recommendations for brucellosis control will be developed based on serosurvey results of transhumant versus local herds and their contact patterns.

A dynamic spatio-temporal model to investigate the effect of movements of animals on the spreading of Bluetongue BTV-8 in Belgium

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With the emergence of various infectious animal diseases, several guidelines have been developed and adopted to protect farms and curtail the spreading of diseases. In the case of Bluetongue Virus Serotype 8 (BTV-8) for instance, surveillance zones around affected farms were created in which transports of animals were restricted. This however did not prevent the further rapid spread of BTV-8 across Northern Europe, which has resulted to substantial economic losses, particularly in the sheep and cattle industry. To better understand the BTV-8 transmission process, the 2006 Bluetongue outbreak in Belgium was investigated. Using the concept of compartmental models, a spatio-temporal model was developed in which each farms were classified into either susceptible or infectious. The model then quantifies the local transmission of the disease between farms within a municipality, the short-distance transmission between farms across neighboring municipalities and the transmission as a result of the movement of animals. Different municipal-level covariates (i.e. land composition variables, temperature and precipitation) were assessed as possibly influencing each component of the transmission process. The model allows to predict the dynamic spreading of the disease for different scenarios. This is especially useful in quantifying how the farm contact network (through animal movements) affects the transmission of bluetongue.

The value of animal movement tracing: a case study simulating the spread and control of foot-and-mouth disease in California

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The purpose of this study was to estimate the benefits of an electronic animal tracing system compared with those of a paper-based system in terms of the potential spread of foot-and-mouth disease (FMD) if introduced in California. A spatial, stochastic simulation model and data for California were used to simulate FMD epidemics originating from a dairy herd as the index case (IC). Results of the simulated FMD outbreak extent and duration were examined to compare the effect of improving the current, paper-based tracing system and moving to an electronic system. According to the simulations, replacing the system with an electronic tracing system would reduce the median number of infected premises (IPs) by 8-81%, depending on size of the IC herd. The benefit varied by IP herd type, e.g. >50% for sheep farms, goat farms and calf and heifer raising operations and ≤20% for swine and beef premises. The impact of an introduction of FMD into California could be reduced substantially even without an electronic system, if paper-based tracing were more efficient; however, these benefits are far less than those that could be realized from an electronic animal identification system. Results show that substantial benefits, in terms of fewer IPs and infected animals and reduced epidemic duration, may be realized as a result of an efficient electronic animal identification system, compared with the current paper-based animal tracing system; however, until then, an improvement in the current system, especially regarding the ability to trace movements the day prior to a premises being diagnosed with FMD, will be highly beneficial.

Common themes and missed opportunities of One Health and Ecohealth case studies

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Objective: The purpose of this study was to examine One Health and Ecohealth case studies from various countries and regions in order to identify common research themes as well as themes that may be considered important but are not well researched. **Methods:** The authors relied on One Health and ecohealth case studies reported through peer reviewed publications, institutional reports, documentation available online, and personal communication. Themes were pre-identified by authors of reports or extracted from these sources. In the latter case a combination of key word identification, examination of case study objectives, and personal communication was used. More than forty case studies were examined; importance of research themes was ranked subjectively. **Results:** Transdisciplinarity, disease prevention, zoonoses, complexity, and community level responses were identified as highly important elements of all case studies. Fewer case studies addressed improved risk management, training, community participation, and preparedness. Themes least addressed included association with wildlife, involvement of the environment, barriers to adoption, and private sector involvement. **Conclusions:** It was not surprising to find zoonoses and disease prevention as common themes, and it was gratifying to see transdisciplinarity and complexity accorded attention. However, it was somewhat alarming that the role of wildlife and interaction with the environment were not commonly addressed by the case studies given the theoretical and management importance of these factors in a One Health and ecohealth approach to disease prevention and management. Case studies generally did not suggest clearly recommendations for policy formulation, suggesting a loss of opportunity to influence governance.

Role of wild animals in the eco-epidemiology of *Rickettsia slovaca*

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Tick Borne Lymphadenopathy (TIBOLA) is an emerging zoonosis in Europe, caused by *Rickettsia slovaca* transmitted by *Dermacentor marginatus*. Since transovarial transmission of *R. slovaca* occurs between adult and larval ticks, it is not clear whether wild animals solely serve as the blood source for *D. marginatus*, or may amplify and transmit the agent to susceptible ticks. *R. slovaca* was previously identified in ticks and tissues collected from wild boars in Tuscany (Italy), where human cases of TIBOLA were reported. The role of small rodents in *R.slovaca* transmission was investigated in the same area in 2009-2010. Animals were live trapped, ear biopsies and all the attached ticks were collected and identified. The tick engorgement index (TEI) was calculated. A sample of *D. marginatus* and mice ear biopsies was selected to detect SFG *Rickettsiae* by PCR. We performed 22 trapping nights. A total of 145 *Apodemus* spp. and 34 *Myodes glareolus* were trapped. The prevalence of *R. slovaca* was 38.17%(n=50, 95% CI: 10.83-24.31) in *D. marginatus* collected from mice, and 26.09%(n=6, 95% CI: 10.23-48.40) in host-seeking larval ticks collected in the same area. The TEI of infected ticks was higher than non infected ones, although the difference was not statistically significant. Two out of the 45 ear biopsies were positive. *R. raoultii*, the agent of a less severe TIBOLA disease, was also detected in two ticks from mice. The high prevalence of *R. slovaca* in host-seeking tick larvae indicates the maintenance of the pathogen by transovarial transmission in the area. However, the finding for the first time of positive mouse tissues, the high infection prevalence in attached ticks, and the tendency of the infected ones to have a higher TEI, may suggest a role of mice as maintenance or amplifier hosts for *R. slovaca*.

Eco-epidemiology of *Fascioloides magna* at the interface between cattle and elk

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Dynamics of infectious diseases in multi-host systems are influenced by processes related to the host-pathogen interactions, host ecology and environmental factors. *Fascioloides magna* is a liver fluke of elk, deer and caribou that can be transmitted to sympatric livestock. Cattle are dead-end hosts: clinical disease may occur but the infection does not become patent. We investigated the dynamics of *F. magna* at the interface between cattle and elk in the Rocky Mountain foothills in Alberta. Fresh fecal samples were collected from 640 elk from 10 herds that had exposure (n=5) or no exposure (n=5) to cattle. We analyzed the samples with Flukefinder® to recover *F. magna* eggs. Elk herd home ranges were defined by minimum convex polygons and kernel density estimation. Environmental variables (e.g. vegetation type, stream density, elevation) were averaged on these home ranges. A multilevel logistic regression was fitted with herd as a grouping variable, including the level of interaction with cattle and different environmental factors compiled in a geographic information system. The 5 elk herds exposed to cattle had lower proportions of positive (Porcupine Hills: 0%, Castle Carbondale: 0%, Livingstone: 0%, Beauvais: 1.4%, Whaleback: 0%) than the unexposed herds (Waterton: 75%, Crowsnest: 5.1%, Banff: 29%, Yaha Tinda: 27%, Jasper: 71%). Univariate analysis suggested a protective effect of cattle presence (P<0.001). This effect was still significant after adjusting for environmental variables in the multilevel logistic regression. Wildlife and livestock comingling is often perceived as a threat, however interspecies interactions may also have potential positive effects. It is essential for wildlife and livestock management to understand the underlying mechanisms. Possible explanations include snail habitat modifications by cattle or a dilution effect by incompetent hosts. To explore these hypotheses, snail surveys and serological tool development to assess cattle exposure are necessary.

Avian influenza in migrating mallard populations: dynamics of strains varying in transmissibility and infection-induced migration delays

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Wild waterfowl are the natural reservoir of Avian Influenza (AI) virus and may thus initiate or propagate an AI pandemic along their migratory routes. Currently, the highest prevalence of infection is observed in fall, but AI virus infection may result in delayed departure for migration. If more virulent strains would appear, this could alter transmissibility and migration, and consequently prevalence patterns. We explore the dynamics of AI virus in a migrating mallard (*Anas platyrhynchos*) population, aiming at understanding how infection-induced delays and altered transmissibility affects the dynamics of virus spread. We develop a host-pathogen model which combines the transmission dynamics of influenza with the migration, reproduction and mortality of the host. Our main findings are: (1) delayed migration reduces the total number of cases of infection each year; (2) when the transmission rate of a strain is high, most influenza cases are seen at the staging sites in early fall migration, and a migration delay results in even more cases early fall; (3) when the transmission rate is low, infection predominantly occurs later in the season, which is further delayed in case of a migration delay, possibly destabilizing the otherwise stable yearly cycle. As such, the rise of new AI strains in waterfowl could lead to a higher prevalence of infection later in the year, which could change the exposure risk for farmed poultry. Thus, we demonstrate that considering infection-induced delays and altered transmissibility of AI virus, is critical to understanding the dynamics of AI infection along the entire flyway.

Detection of *Mycobacterium avium* ssp. *paratuberculosis* in caribou from northern Canada and Greenland

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Mycobacterium avium ssp. *paratuberculosis* (MAP) is the causative agent of Johne's disease (JD), a common problem for livestock production worldwide. JD is characterized by chronic intestinal inflammation, diarrhea and wasting. JD has been previously documented in semi-domesticated reindeer (*Rangifer tarandus tarandus*), however there has never been a systematic survey for MAP among wild caribou (*Rangifer t. ssp.*). As part of a broad health survey of caribou, herds from across northern Canada and Greenland were tested for MAP using fecal culture (TREK ESP) and polymerase chain reaction (PCR) of the IS900 target. Fecal samples from 561 individual caribou from 16 different populations were collected by collaborators in the CircumArctic Rangifer Monitoring and Assessment Network (CARMA)*. A total of 31 fecal samples (5.5%) from eight different populations were positive by PCR, and one of these samples was also culture positive. The proportion of fecal samples that tested positive by PCR varied among herds, with the highest proportions in the Akia-Maniitsoq herd (23.4%) from Greenland, and the Rivière-aux-Feuilles (11.5%) and Rivière-George (10.0%) herds from northeastern Canada. Positive samples were detected among all age groups with 3/19 calves (15.8%), 2/23 yearlings (8.7%) and 26/511 adults (5.1%) testing positive. The finding that MAP is present in several free-ranging populations of caribou indicates that MAP is able to circulate in an environment that is free of contact with domestic livestock species. Further study into the pathogenesis of MAP in Rangifer species and potential population level impacts is warranted. *CARMA partners ranged from community members to wildlife managers, with key contributions from B. Elkin, A. Kelly, A. Veitch, R. Popko, and T. Davison of Gov NWT, M. Kienzler of Gov Yukon, S.D. Côté and J. Taillon of Université Laval, and C. Cuyler of Greenland INR.

Meta-analysis of influences on the welfare of laying hens in enriched colony housing systems

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Embedded within a network project on laying hens in German enriched colony housing systems this study was to assess influencing factors on animal welfare indicators. Data from three consecutive laying periods in five field stations was retrieved from one database – with standardised data collection and data entry procedures, plausibility checks, etc. Four indicators of animal health and welfare were chosen according to acquired information in the database as most important by the superordinate network project and investigated in further analyses. Statistical inference of the indicators was drawn considering one influencing factor each. Meta-Analyses were performed to summarize these results in order to account for an incomplete study design. The field station was included as a fixed factor in every meta-analysis. The size of littered area and group size do not seem to have a notable influence on animal welfare. The laying line and housing system seems to have a marginal influence at least. The predominant influencing factor seems to be the field station, where the study was conducted. Despite providing the best possible homogeneity between the stations by investigating field stations and not ‘real’ farms in the field, differences are obvious. Therefore, a latent heterogeneous management pattern condensed behind the variable field station can be assumed to influence the animal welfare more than one or two certain factors.

Onsation evaluation of different grains as a carrier for thermostable Newcastle disease vaccine (I2), Debreziet, Ethiopia

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In the current experimental study the suitability of different local grains as a carrier for thermostable Newcastle disease (ND) vaccine I2 for oral immunization of chickens was assessed by haemagglutination inhibition (HI) test and challenge experiment. The chicks were vaccinated with I₂ vaccine by conventional methods (drinking water), cracked maize and wheat, millet, barely and sorghum which were used in untreated, parboiled and cracked form. Following the primary and the second vaccination the result showed that only chickens vaccinated with conventional methods and vaccine coated cracked maize and parboiled barely gave GM antibody titer of $\geq \log_2^3$ but at third dose of vaccine, chicken vaccinated by conventional, cracked maize and parboiled barely were found to produce the highest GM titer of $\log_2^{7.1}$, $\log_2^{6.8}$ and $\log_2^{5.1}$ respectively but the least response ($\log_2^{1.9}$) was observed in chicken vaccinated by vaccine coated cracked sorghum. The experimental challenge showed that 80% mortality rate in the unvaccinated control group. The vaccine applied by drinking-water, cracked maize, parboiled barely was found 100% protective against the challenge. High protection capacity was also observed with I2 delivered by parboiled wheat (85%). Limited survival rate (60%) was observed in the chicken under untreated sorghum, untreated millet and cracked millet treatment group. The least survival rate with high mortality was observed in chicken treated with vaccine coated sorghum. Generally in the current experimental study cracked maize, parboiled barley, parboiled wheat, parboiled sorghum and untreated wheat in general found to be good carrier for I2 vaccine virus.

Household level risk factors for Newcastle disease seropositivity and incidence in backyard chicken flocks in Eastern Shewa zone, Ethiopia

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Cross-sectional studies were conducted to investigate potential risk factors for Newcastle disease (ND) virus seropositivity and incidence in household flocks of backyard chickens during September-October, 2009 and May 2010. Data were collected from 260 households in 52 villages in Adami Tulu JidoKombolcha and Ada'a Woredas using a structured questionnaire, along with serum samples. The seroprevalence and incidence of ND at the household level were estimated in various ways using serological results from the two surveys, combined with farmers' reports of ND. The risk factors were tested using multivariable mixed-effects logistic regression models. In the first survey, reduced frequency of cleaning of poultry waste was associated with increased odds of seropositivity (OR=4.78; 95% CI: 1.42, 16.11; P=0.01) while hatching at home was associated with lower odds of seropositivity (OR=0.3; 95% CI 0.11, 0.82; P=0.02). In the second survey, hatching at home again reduced the odds of seropositivity (OR=0.23; 95% CI 0.10; 0.52; P<0.001), as did larger flock size at the time of sampling (OR=0.28; 95% CI: 0.11, 0.67; P=0.004). However, the risk of ND incidence was shown to be higher with larger flock size at the beginning of observation period (OR=3.6; 95% CI: 1.25, 10.39; P=0.02). Using an open water source (pond/river) for poultry compared to closed sources (tap/ borehole) also increased risk (OR=3.14; 95% CI: 1.12, 8.8; P=0.03). In the fourth model lower risk of ND incidence in a household flock was associated with use of a grain supplement (OR=0.14; 95% CI: 0.03, 0.69; P=0.03) and hatching at home (OR=0.23; 95% CI: 0.10, 0.52; P=0.005).

Spatio-temporal patterns and effect of presence of infected neighboring producers for the *Campylobacter* status in Danish broiler farms

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A series of analyses were conducted in order to obtain a better understanding of the spatial and temporal distribution as well as potential neighbourhood risk factors for *Campylobacter* in Danish broiler flock population. *Campylobacter* infection status of flock was identified by PCR analysis of swab samples from cloacae of broilers. Included into the study were, in total, 10,876 broiler flocks sent by 226 producers to processing plants from 2007 to 2009. Methodology for visualization and exploration were used in spatial-analyses. A multivariable logistic regression model with autocorrelation structure was used to model effect of exposure variables on probability of being tested positive to *Campylobacter*. The spatio-temporal analyses revealed a non-random spatial and temporal occurrence of *Campylobacter* infection. Highest prevalence was observed during summer and lowest during winter. Significant spatio-temporal clusters were identified in the same areas during summer months from 2007 to 2009. Range of influence between infected broiler producers were estimated at the distances 9.6 km and 13.5 km in different years. Results from the risk factor study showed a significant protective effect with the absence of infected neighbour in short distances: absence of infected neighbours in 1 km radius and in-between 1 and 2 km. The analysis was adjusted for potential confounding factors. Seasonal cyclic patterns of *Campylobacter* infection was accounted for by using sine and cosine function. Predicted probability maps showed a heterogeneous spatial and temporal risk of *Campylobacter* infection in Danish broilers.

Multi-level analysis of *Campylobacter* flock status at post-chill and prevalence at various sampling points in the broiler production and processing continuum

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The purpose of this study was two-fold: (1) to determine the grow-out and processing plant sample(s) that best predict the likelihood of *Campylobacter* presence on broilers at post-chill; and (2) estimate the amount of variability in *Campylobacter* prevalence that is within the complex, farm, and flock levels. Sampling was conducted in two broiler companies located in the Southern United States, which encompassed 10 complexes, 32 farms, and 64 flocks. Upon the day of chick placement into the grow-out house the gastrointestinal tracts of chicks were collected from each flock. Prior to transportation to the processing plant and upon arrival at the processing plant, ceca, crop, and whole bird carcass rinses were collected. During processing, samples were collected prior to entering the immersion chill tank and again after exiting the immersion chill tank. Multi-level-mixed model logistic regression was used to assess the relationships between post-chill status and other sampling points. Markov-chain Monte Carlo was used for estimation of the final models and the Deviance Information Criterion was used for the comparison of the models. The best predictor of post chill *Campylobacter* carcass status was the exterior whole carcass sample in the grow-out environment prior to transportation. In the post-chill model, the percentage of variability in *Campylobacter* prevalence occurring at the complex, farm, and flock level were 8.6%, 72.8%, and 18.6%, respectively. The intra-class correlation for flocks within the same farm, flocks within the same complex but different farms, and farms within the same complex were 0.81, 0.09, and 0.11, respectively.

Session 68**Theatre 1****Using a biological-physical model to evaluate pathogen transmission in a changing aquaculture industry**

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Scotland is the largest salmon producer in the EU with 150,000 t output valued at over £500 million, making it Scotland's largest food export by value and provides important employment in remote island and highland communities. There are aspirations for the industry to sustainably increase by a further 50% by 2020. Recently, the number of farms has diminished; as a consequence the mean output per farm has increased. Over 80% of Scottish salmon is obtained from farms producing over 1000 t. Farm management areas (FMAs) exist where coordinated management practices occur to minimise the risk of disease agent transmission. The structure of FMAs can be similar to disease management areas (DMAs) derived for the control of the notifiable disease, infectious salmon anaemia (ISA). A DMA boundary is defined where the closest pair of farms are separated by more than twice the tidal excursion (TE) distance. The fixed TE is defined as 7.2 km for the mainland, and 3.6 km in the Shetland islands and takes no account of farm production. DMAs have proved successful in managing the prevention of ISA virus transmission between sites within the current industry structure of farming moderately sized farms located in relatively sheltered inshore waters. However, licensed biomass is restricted by environmental impact assessments, partly determined by tidal conditions. Should farms increase in size they will need to be located in areas further offshore within faster currents, which may alter disease transmission. A model incorporating hydrodynamics and pathogen biology is used to evaluate the effects of increasing farm sizes and locating farms in areas where there are increased residual current speeds. DMAs are appropriate for ISA control in the current structure, but may become less effective should farms increase in size, surrounded by faster waters. Furthermore, DMA methods may not be inapplicable for controlling more conserved pathogens and parasites.

Scenario modelling for determining probability of an outbreak of heart and skeletal muscle inflammation in salmon-farming sea-sites in Norway

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Heart and skeletal muscle inflammation (HSMI) is an infectious disease causing losses to the Norwegian salmon farming industry due to increased mortality and high morbidity in infected salmon. HSMI is believed to be a viral disease, but the exact association to the recently discovered Piscine reovirus (PRV) remains to be established. Undoubtedly, other factors interplay to determine whether PRV-infected fish develop disease or not. In this study, logistic regression was used to model the probability of an outbreak of HSMI on farm level, by including spatio-temporal risk factors. The data consisted of fish cohorts grown on geo-referenced farms from 2002-2010, and the risk factors included were: Infection pressure, max number of fish at cohort, cohort character, number of months in sea, year and a geoindex calculated as the position along a local polynomial regression line based on the longitude and latitude of each farm included in the study. The results showed that the probability of getting HSMI decreases when cohorts are mixed (fish are introduced multiple times), increase with time at sea, increasing infection pressure and increasing farm size and is mostly low for farms in south-Norway, high for farms in mid-Norway and variable for farms in northern-Norway (based on the geo-index). The final model was used to explore different scenarios with regards to the probability of getting HSMI and to calculate the probability for each cohort for getting HSMI, independent of their actual disease-status. The model showed that the probability of getting HSMI is much larger in Mid-Norway than in the rest of the country. Even though PRV seems to be widely distributed in the environment, the finding that infection pressure has a large influence on the probability of getting HSMI, suggests that it might be possible to reduce clinical outbreaks, if measures are taken to reduce infection pressure.

Session 68**Theatre 3****Pacific oyster mortality syndrome: epidemiological study to reduce economic losses**

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A viral disease new to Australia – Pacific Oyster Mortality Syndrome (POMS) – emerged in New South Wales (NSW) in 2010 and caused high mortality outbreaks. Despite some evidence suggesting that the disease may spread through boat movements and appears to be associated with increases in water temperature in summer, very little objective information is available about the factors responsible for outbreaks. An epidemiological investigation was conducted in Botany Bay (NSW) during summer 2011/2012 involving random sampling of farmed oysters of different ages in different culture systems, pathogen detection and quantification, and high frequency monitoring of environmental parameters in three different sites of Botany Bay. The aim of the study was to identify major risk factors responsible for disease emergence and spread. POMS disease started in November 2011 and continued for a short period of one month. Viral prevalence and intensity as well as oyster mortality strongly differed among sites, ages, and culture systems. The outbreak was short, sudden and highly clustered within the bay with simultaneous point sources and one of the three selected sites remaining free of any sign of disease. A closer observation of disease transmission revealed that the outbreak was also clustered within each site, showing a non-uniform transmission requiring water and potentially other particles present in seawater. Spatial differences suggested an environmental trigger for release of virus into the environment from a potential reservoir host. This project is supported by funding from Fish Research and Development Corporation on behalf of the Australian government, and also by The University of Sydney and the Sydney Metropolitan Catchment Management Authority, with the strong support of oyster growers from the Georges and the Hawkesbury Rivers, Siminis Oyster Systems, Hornsby Shire Council, and I&I NSW.

Spatial map of risk of pancreas disease-outbreaks in Norwegian salmonid farming sites

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Outbreak of pancreas disease (PD) is a major challenge to aquaculture industries due to its detrimental economic impact in several countries. The present study evaluated the effect of potential risk factors on outbreaks of PD on site level in Norwegian salmonid farming. The risk factors evaluated include: local biomass density (LBD), infection pressure, site location, time when smolts were put into sea, and density of the farming sites. The study population was Norwegian salmonid farming sites in the period January 2009 to December 2010. A Bayesian modeling approach was used for estimating site-specific probability of PD occurrence accounting for spatial congruity due to neighboring infected sites. A map covering the entire area of Norwegian marine salmonid production sites was produced using kriging to interpolate the model results. Subsequently, the final model was validated by comparing the predicted probabilities with observed data of PD outbreaks in 2011. The study results can be used for selecting areas with an acceptable probability of PD occurrence for establishing new aquaculture sites, and facilitate controlling and eradication of the disease.

A mathematical model for evaluating mitigation strategies of biofouling *Ciona intestinalis* in Prince Edward Island, Canada

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Mathematical models have been applied in various research fields and have been used to investigate disease transmission in both human and animal populations. Although, the use of these approaches has been increasing in the veterinary field, there has been limited application to aquatic animal disease. Disease transmission in aquatic environments typically differs from that seen in terrestrial animals and so existing models are often not readily adaptable. Aquatic invasive species have become a global issue over the past few decades. In Atlantic Canada, *Ciona intestinalis*, the vase tunicate causes important losses to the mussel farming industry. This species out-competes mussels in terms of fecundity and growth rates resulting in heavy biomass and mussel loss. A range of mitigation strategies, utilizing high pressure spray, have been developed to control the biomass of this fouling species on the mussel lines. Biologically, it appears that the greater the number of treatments, the less *C. intestinalis* biomass. However determining cost-benefit trade-offs using field trials is resource intensive. The development of a mathematical model allows for the comparison of different *C. intestinalis* control strategies. A differential equation model was developed in AnyLogic® to represent the four key life stages of *C. intestinalis*. Stage transition rates were calculated from number of individuals for that stage, time spent in the stage, and the daily transition probability. Parameters were extracted from the scientific literature and from field data collected in Prince Edward Island. The model also incorporated temperature and the carrying capacity of each mussel site. This research will help in understanding the population dynamic of *C. intestinalis* in PEI mussel farms and to develop more efficient treatment strategies for this invasive species.

Factors contributing to rinderpest eradication

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Rinderpest is caused by a member of the Morbillivirus sub-group of the Paramyxoviridae. The eradication of rinderpest has been a goal sought over the last centuries through national, regional and international programs. The last outbreak of rinderpest was registered in 2001, and the last use of vaccine was recorded in 2006. Substantial disease search and widespread serological surveillance throughout Asia, Africa, and Middle East has been conducted without any evidence of virus circulation. The virus is today only confined to the diagnostic and research laboratories or a few vaccine production facilities. Syndromic surveillance, maintaining preparedness and virus sequestration will be the major activities in the post eradication era. This paper reviews the contributing factors to this success: understanding the virus, its characteristics and epidemiology; use of effective quality vaccine and improvement of vaccine delivery systems, regional eradication programs, use of appropriate and standardized diagnostic and epidemiological tools accompanied by harmonized epidemiological surveillance guidelines, training efforts, establishment of epidemiology and laboratory networks, effective co-ordination and collaborations in rinderpest control in the final push of eradication.

The risk of rinderpest re-introduction in the post-eradication era

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Ten years after the last reported outbreak, the global eradication of rinderpest was declared in 2011. However, as rinderpest virus stocks still exist, there remains a risk of rinderpest re-introduction. A semi-quantitative risk assessment was conducted to assess this risk, which was defined as the probability of at least one host becoming infected and infectious outside a laboratory within a one year period. Pathways leading to rinderpest re-introduction were: deliberate or accidental use of virus in laboratories, deliberate or accidental use of vaccines, host exposure to an environmental source of virus, and use of virus for anti-animal biological warfare. The number of virus and vaccine stocks was assessed through a questionnaire survey involving national veterinary authorities and laboratory staff. The probability of pathway steps occurring was estimated through expert opinion elicitation. The risk was modelled as a multilevel binomial process. It was found that 44 laboratories, in 35 countries, currently hold live rinderpest viruses, 16 of which retain field strains. Viruses are still being used for vaccine and reagent production, and for *in vivo* and *in vitro* research. Seventeen countries hold vaccine stocks of up to 4,000,000 doses. The risk estimate ranged from negligible to high, with the median being very low. The accidental use of laboratory virus stocks was the highest risk pathway. Reducing the number of virus stocks and restricting their use, as well as upgrading the laboratories to a higher biosafety level, would effectively decrease the maximum and median risks. Likewise, ensuring that remaining vaccine stocks are not used and are instead destroyed or relocated to a limited number of regional repositories would also have a high impact on these estimates. However, these measures are unlikely to eliminate the risk of rinderpest re-introduction so maintaining response preparedness is essential.

Modeling the future rate of laboratory biosafety breakdowns involving rinderpest: uncertainty in the post-eradication era

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Now we are in the rinderpest post-eradication era, attention is being focused on the risks of re-introduction. There is little data on the rates of laboratory biosafety breakdowns and any predictions based on past events are subject to uncertainty. The aim of this study was to model the future rate of biosafety breakdowns involving rinderpest (defined as accidental or malicious exposure of a susceptible animal) according to different assumptions, taking account of uncertainty and stochasticity. Data was collected from a global online survey of laboratories, a structured search of ProMED reports and discussion with experts. A spreadsheet model was constructed and Monte Carlo simulation was used to simulate the number of biosafety breakdowns involving rinderpest that may occur over the next 10 years according to different assumptions, such as a reduction in the number of laboratories with rinderpest virus. There was a high degree of uncertainty in the number of rinderpest biosafety breakdowns that will occur, even when assumptions were made. The search identified no breakdowns during the last 10 years. The most optimistic set of assumptions – that the search was 100% sensitive and the number of laboratories working on rinderpest is decreasing as suggested by our survey – therefore resulted in a prediction of no biosafety breakdowns over the next 10 years. When the last 40 years (during which five breakdowns were reported) were considered as a basis for making future predictions, the most likely number of breakdowns was still zero however the probability of having at least one breakdown was greater than 0.4. Assuming a search sensitivity of 1% resulted in a 90% chance of 32 to 156 breakdowns occurring. Although a highly simplified model, it is hoped that this is a useful tool for discussion. Even fairly optimistic predictions suggest there is a non-negligible risk of future biosafety breakdowns involving rinderpest.

Session 69**Theatre 4****The global outbreak investigation: crisis management and good emergency management practice**

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The Crisis Management Centre – Animal Health (CMC-AH) as a key international facility assists countries dealing with animal disease emergencies. Concerned with transboundary diseases, the CMC-AH has worked with some 35 countries on more than 50 occasions since establishment in 2006. Hosted by the Food and Agriculture Organization (FAO) in Rome, the Centre works in close collaboration with the OIE and WHO, and serves its 194 member countries and organizations. The CMC-AH was originally envisaged as a key part of the global initiative against highly pathogenic avian influenza (H5N1) and has conducted 25 related missions but has since addressed an equal and wide-ranging number of threats, from foot and mouth disease to Ebola virus infection. The CMC-AH has sponsored and facilitated cross-border discussions as an adjunct to disease responses, to encourage cooperative approaches to multi-national issues. FAO promotes the adoption of Good Emergency Management Practice (GEMP) as a means of creating country and regional resilience to animal disease threats, through close attention to preparedness and contingency planning. GEMP is widely endorsed as a source of ‘best practice’ and readily available to assist in prevention and control. GEMP is a freely available package of tools that will assist those responsible for animal emergencies to ensure that they are well-prepared and able to respond effectively to outbreaks. The central pivot of GEMP is ‘The Essentials – a guide to preparing for animal health emergencies’. This simple language guide, widely endorsed by leading international health agencies, establishes world best practice. It emphasizes that preparedness depends on the ability to prevent, detect, respond and recover, and canvasses a wide range of important points in preparing for animal health-related emergencies.

Leptospirosis sero-prevalence in New Zealand livestock and associated risk factors

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Leptospirosis is an endemic bacterial disease of livestock in New Zealand and an important zoonotic disease in farmers and meat-workers. The same serovars occur in livestock and humans, indicating a human health risk from animal sources. The objective of this study was to estimate the animal and herd level sero-prevalence of *Leptospira borgpetersenii* serovar *Hardjobovis* (H) and *L. interrogans* serovar *Pomona* (P) in beef cattle, deer and sheep and evaluate the association between herd/flock prevalence and region, prevalence of other animal species present on farm, vaccination, herd size, water sources and irrigation systems. We conducted a stratified-random, cross-sectional, sero-prevalence study on 238 farms selected from 1,941 client farms of 28 veterinary practices on the North and South Islands of New Zealand. Twenty blood samples per farm and species were collected from 3,361 adult sheep, 2,308 beef cattle and 1,992 deer. Farmers were interviewed by questionnaire on clinical leptospirosis and farm management. Serum antibodies were measured against H and P using the microagglutination test (MAT) at doubling dilutions from 1/24 to 1/3072. Risk factors were analyzed by multilevel modeling. Fifty percent of sheep, 58% of beef and 34% of deer were sero-positive (H and/or P) with a MAT titre cut-off of 1/48. Ninety-seven percent of sheep flocks and beef herds and 60% deer farms had one or more sero-positive animals. Results of risk factor analysis will be presented. Due to random sampling, the results are fairly representative for the population of commercial pastoral livestock producers farming sheep, deer and/or beef cattle. Recent New Zealand studies have shown up to 31% abattoir workers were sero-positive with H or P indicating transmission from carcasses to humans. Exposure to live animals on farms may result in a similar infection risk for farmers, farm workers, livestock service personnel and veterinarians.

Mitigating the risk of human occupational leptospirosis by vaccinating pastoral farmed livestock

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Leptospirosis is a disease of mammals caused by a multitude of *Leptospira* and subtypes (serovars), most of them without cross-protective host-immunity. The incidence of notified human leptospirosis cases in New Zealand (2.5 per 100,000) is the highest among OECD countries. Serovars found in 50-60% of human cases were *Leptospira borgpetersenii* serovar *Hardjobovis* (H) or *L. interrogans* serovar *Pomona* (P). A recent stratified-random survey of pastoral livestock farms found serological evidence of H or P serovars in more than 50% of adult sheep and beef cattle and in 34% of adult deer. The survey excluded dairy cattle because about 85% dairy herds are vaccinated annually. Leptospirosis is therefore an occupational disease in humans with farmers, abattoir workers and livestock service personnel including veterinarians being at 50-200 times higher risk of infection and disease than the general population. Vaccination of livestock appears to be the major if not the only effective option for control. A series of studies conducted in past years (2003-2011) described the prevalence of infection and kidney culture positive rates in sheep carcasses at slaughter, the daily contact rate of abattoir workers with carcasses shedding H or P, the prevalence and sero-conversion rate of abattoir workers processing sheep, deer and cattle, and the association of sero-conversion with influenza-like symptoms resembling clinical leptospirosis in abattoir workers. This presentation puts these findings into an ecological perspective: it describes a generic model of infection dynamics among domestic pastoral livestock, its contribution to human exposure and infection, and the consequences of human illness. The model evaluates the level of protection achievable in humans through vaccination of livestock, as this is currently a critical question for authorities and individuals engaged in public health and occupational safety and health.

Clinical features of human salmonellosis caused by bovine-associated subtypes in New York

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Salmonella enterica is a leading cause of acute bacterial enteritis in people throughout the world. Although clinical disease is generally self-limiting, *Salmonella* can also produce invasive infections that may be fatal. The objective of this study was to identify patient symptoms and case outcomes that were more likely to occur as a result of salmonellosis caused by bovine-associated subtypes, as compared to *Salmonella* infections caused by non-bovine-associated subtypes. Data were collected in 34 counties of New York that comprise the Foodborne Diseases Active Surveillance Network (FoodNet) catchment area of the Centers for Disease Control and Prevention (CDC) Emerging Infections Program (EIP). Patients with specimen collection dates between March 1, 2008 and March 1, 2010 were included. Symptoms and disease outcomes of case-patients infected with bovine-associated *Salmonella* subtypes (isolates that matched contemporary bovine isolates from New York by serovar and pulsed-field gel electrophoresis [PFGE] pattern) were compared to those of control-patients infected with *Salmonella* isolates that were not bovine-associated. The presence of blood in the stool while ill was significantly associated with status as a case (OR=2.1, P=0.03). In addition, cases were significantly more likely to have invasive salmonellosis (OR=3.6, P=0.02), after adjusting for age group, gender, and race. These findings may have implications for patient management, as a history of consuming undercooked foods of bovine origin or having direct contact with cattle in the few days prior to illness could be useful for suggesting a more proactive diagnostic approach as well as close monitoring for the need to implement more aggressive therapy.

Epidemiology of *Taenia solium* in pigs and humans in Western Kenya

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We would like to present the results of a large cross-sectional study into the zoonotic helminth *Taenia solium* in the porcine and human hosts in the Lake Victoria Crescent region, focussing on the following aspects of this study: the prevalence and risk factors for porcine and human cysticercosis (CC) and for human taeniasis, a food chain risk assessment for the risk of human infection from pork consumed in this region and potential intervention strategies. We have carried out an extensive, community-based study into the epidemiology of this parasite and many other zoonotic and non-zoonotic diseases in Western Kenya. The research team consisted of an inter-disciplinary group of medical and veterinary professionals. Blood and stool samples were obtained from all people and livestock in 413 randomly selected homesteads as well as homestead and individual level questionnaire data. A parallel survey of slaughterhouses was carried out, with blood samples taken from pigs being slaughtered for consumption within the study area. The prevalence of *T.solium* in pork entering the food chain (57.7%, 95% C.I.52.3-63.0) is one of the highest recorded in sub-Saharan Africa and a food chain risk analysis, built utilising data from these studies, indicated an unacceptably high risk of pork consumers in this region acquiring a *T. solium* infection, and in turn becoming shedders of infective eggs. Western Kenya is a severely deprived region where pig production is becoming hugely popular and is seen as a major tool for economic development, yet the data presented here indicates the area to be hyper-endemic for *T. solium*. Control of this parasite must be addressed as a key priority for both the safe-guarding of public health and also to ensure the growth of an economically viable and safe pig production system.

The epidemiology of *Clostridium difficile* in ulcerative colitis patients

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Clostridium difficile affects both animals and humans. The changing epidemiology of *C. difficile* infection and recent outbreaks have led to increased public awareness particularly among predisposed populations, such as Ulcerative Colitis (UC) patients. The objective of this study was: (1) determine if UC patients with *C. difficile* infection 90 days prior to hospital or in hospital were more likely to have an emergent colectomy and if *C. difficile* increases the risk of postoperative complications; (2) whether the frequency of *C. difficile* testing/diagnosis has changed over time. We identified all UC patients (≥18 years) admitted to hospital due to disease flare under the Calgary Health Zone between January 1, 2000 and December 31, 2009 (n=276). Multivariate logistic regression was performed to examine the association between *C. difficile* diagnosis and: (1) emergent colectomy (n=104) versus medically responsive (n=172) patients; (2) postoperative infectious complications (n=21/104). Joint point regression analysis was used to test for temporal trends in *C. difficile* testing and positive results between 2004-2009. *C. difficile* diagnosis 90 days prior or in hospital (n=18) increased the risk for having a colectomy when compared to *C. difficile* negative patients (OR=2.88; 95% CI: 1.03-8.03). Preoperative *C. difficile* diagnosis increased the risk of postoperative infectious complications (OR=3.99; 95% CI: 1.02-15.56). Between 2004-2009, 72% of UC patients admitted to hospital were tested for *C. difficile* and the proportion of positive results remained stable. Given the importance of this bacterium among UC patients, further research needs to be performed to determine the potential sources of infection.

One Health in action: experiences from Lao PDR

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One health is a term increasingly used to describe activities designed to prevent and control diseases in humans where there is a domestic animal and/or wildlife component. It has its origins in the realisation that most new and emerging diseases of humans arise from domestic and wild animals, and the experience of H5N1 where effective control was only achieved with close co-operation of public health, veterinary and wildlife experts and agencies. Laos, like the rest of the Countries in Peninsula Indochina, has experienced intermittent outbreaks of H5N1 Highly Pathogenic Avian Influenza since 2004, with two human cases in 2007. This encouraged a co-ordinated response with establishment of the National Avian and Human Influenza Co-ordination Office (NAHICO) between the Ministries of Health and Agriculture. In 2009, this office expanded its remit to cover an additional four zoonotic diseases: rabies, anthrax, Leptospirosis and Trichinellosis and renamed as National Emerging Infectious Disease Coordination Office (NEIDCO). Building on this inter-ministerial commitment to respond to zoonotic disease, in 2011 we commenced a sero-epidemiological study to determine the burden of exposure of a range of pig-related zoonotic diseases in both populations. This was carried out in two provinces – Luang Prabang in the north and Savannakhet in the south – by teams from the Central, Provincial and District Animal and Human Health Offices. Provisional results from this survey show that the viral diseases Hepatitis E and Japanese Encephalitis are widespread in both provinces, but that the parasitic diseases cysticercosis and trichinellosis are more sporadic. Through the identification of the spatial patterning of risk factors associated with these diseases, we hope to be able to better target public health interventions and control.

Contact rates between rangeland livestock and wild ungulates

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Rangeland livestock in the western U.S. interact with abundant wild-ungulate populations (e.g. elk, deer and antelope), which may complicate control of an FMD outbreak. The frequency of livestock-wildlife interactions are poorly understood though. This study estimates inter-specific contact rates using the largest known dataset on cattle-elk-deer locations, from the Starkey Project's semi-arid rangelands and forests of northeast Oregon, USA. The Starkey Project is a 10,000-hectare fenced enclosure containing 500 cow/calf pairs, 200 elk, and 200 mule deer. Each year, roughly 41 cattle, 43 elk, and 21 deer are collared, and their locations are recorded every 30-60 minutes. Between 1993 and 2007, 849,443 spatial locations were collected for cattle; 1,427,707 for elk; and 489,118 for deer. We calculate spatial and temporal distances between all observed pairs of animal locations, as well as the proportion of pairwise observations occurring within a specified distance and time from each other. Of the 130 million pairs of animal locations separated in time by six hours or less, 2.2% of intraspecies pairs, and 0.04% of interspecies pairs involved animals located less than 100 meters apart. Specifically, 5% of cow-cow pairs were within 100 m of each other at the same point in time. Less than 0.1% of cow-elk pairs, and less than 0.05% of cow-deer pairs, were within 100 m of each other. Similarly, 4% of cow-cow pairs observed 30 minutes apart were within 100 m of each other (relevant for transmission via environmental contamination). Less than 0.02% of deer locations, and less than 0.05% of elk locations, were within 100 m of a location a cow visited 30 minutes ago. Contact rates between cattle, elk, and deer are relatively low, due perhaps to inter-specific avoidance. They do in fact occur, however, and may complicate control of an FMD outbreak.

Modelling the seasonal spread of an emerging pestivirus in a structured Pyrenean chamois population

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Recently, a Pestivirus closely related to Border Disease viruses emerged in populations of Pyrenean chamois (*Rupicapra r. pyrenaica*). The infection rapidly expanded across Pyrenees, leading in some populations to large epidemics with numerous deaths (as in Spanish populations), and in some others to the persistence of infection over several years with a declining population dynamics (as in French populations). The Pestivirus can be transmitted both horizontally through direct contacts and vertically in utero. Vertical transmission leads to abortion or to the birth of permanently infected (PI) animals with a short life expectancy. Horizontal transmission involves a complex dynamics because of seasonal variation in contacts among sexes and age classes, leading to a highly structured population, a seasonal population dynamics, and a seasonal pattern of pathogen transmission. To better understand pathogen transmission and the impact of infection on population dynamics, we developed an age-sex structured stochastic model of the spread of a Pestivirus accounting for seasonal population dynamics and contact pattern. Model outputs are the probability of extinction of the infection, the mean and variance of prevalence in infected populations over time, and losses due to abortions and disease-related deaths. A sensitivity analysis of the model highlighted the main parameters influencing these outputs. Such parameters represent potential control points of this complex biological system and require to be estimated precisely to ensure relevant model predictions. The model will be used to evaluate hunting plans allowing controlling for Pestivirus spread and its impact on chamois population dynamics.

Epidemiological methodology for fecal collections from free-ranging elk in southwestern Alberta

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In southwestern Alberta, there is considerable co-mingling between elk and cattle (cow-calf operations) on natural land for pasture, leading to possible transmission of pathogens between these hosts. Fecal sample strategies for laboratory testing, from specified individuals poses some challenges, as accurate census data are not available for wildlife species and individuals are not easily identified in a herd. For elk specifically, distribution in unstable sub-groups moving across a large territory makes sampling additionally challenging. Therefore, classical randomizing methods are not easily applied. The general fecal sampling strategy was defined as the collection of fresh samples from distinct individuals in a limited time frame to avoid repetitive sampling of individuals due to subgroup structure changes, to allow disease occurrence estimations. The sampling process can be divided in: (1) observation phase: identification of subgroup dynamics and movement patterns of elk herds; (2) opportunity identification: identification of favorable situations depending on individual herd characteristics e.g. resting areas, accessibility based on habituation to human interaction; (3) sample collection of fresh fecal samples. An intense coverage of the available trails, a methodical scanning of the area with binoculars, the use of radio-frequency equipment for the detection of collared individuals and thorough searching of the known elk distribution areas, limited the bias induced by accessibility. Empirical techniques were implemented to prevent re-sampling of the individual. Our sampling methods overcame some of the challenges associated with non-randomized sampling in challenging field conditions, providing confidence in our sample strategy for disease detection.

A risk assessment of bighorn sheep viability in the Payette National Forest

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Bighorn sheep currently occupy just 30% of their historic distribution, and populations are substantially depressed from their pre-Euroamerican levels. Present-day recovery of bighorn populations is in large part limited by periodic outbreaks of respiratory disease, which can be transmitted to bighorns via contact with domestic sheep, grazing in their vicinity. In order to assess the viability of bighorn sheep populations on the Payette National Forest (PNF) under several alternative patterns of domestic sheep grazing, we developed a series of interlinked models. Using telemetry and habitat data, we characterized herd home ranges, and foray movements of bighorn sheep outside of their home ranges. Combining our home range and foray models with known locations of domestic sheep, we estimated contact rates between the species. Finally, we used demographic and epidemiologic data to construct population and disease transmission models, which enabled us to estimate bighorn sheep viability under each alternative grazing scenario. Depending on the probability of disease transmission following interspecies contact, extirpation probabilities for the seven bighorn herds examined here ranged from 20% to 100%. Results of this work are being used by the United States Forest Service to define management strategies regarding sheep allotment allocations in the Western United States.

Risk factors and seroprevalence of *Mycoplasma synoviae* infection in broiler breeder farms in Mazandaran province, north of Iran

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Mycoplasma synoviae infection occurs worldwide in commercial poultry flocks and may result in severe economic losses. This study was aimed to determine the risk factors (age, size of flock, locale and strain) and seroprevalence of *M. synoviae* in broiler breeder farms in Mazandaran province, north of Iran. The study was conducted from May 2002 to October 2008 that was based on Rapid Serum Plate Agglutination (SPA) and enzyme linked immunosorbent assay (ELISA) tests. For statistical test SPSS (chi square test and pearson correlation) was used. The highest (41.2%) and lowest (0%) prevalence of *M. synoviae* infection was found in 2003 and 2008, respectively. Seasonal variation of prevalence with *M. synoviae* infection was observed in the present study. The prevalence was highest (39.6%) in winter and lowest (30.6%) in summer. Ross, Cobb, Arian, Hubbard and Arbor Acres strains had 40%, 44%, 32%, 27% and 45% infection, respectively. The prevalence of *M. synoviae* infection increased with age. The prevalence was recorded highest in above 60 weeks of age (43.1%), but at 10-20 weeks it was lowest (12.7%). The population of the flocks was not influenced on *M. synoviae* prevalence, no significant difference was seen in flocks up to 30,000 population (37.8%), 30,000-40,000 (46.8%) and upper 40,000 (51.3%). Farms were separated in two different zones (foothills with less humidity compared with coastal area). The prevalence of Mycoplasmosis in foothills was significantly ($P<0.05$) higher (36.9%) than coastal area (30.1%). The results showed that occurrence of *M. synoviae* have a significant relationship with the age and zone of sampling.

Seroprevalence and risk factors of *Mycoplasma gallisepticum* infection in Iranian broiler breeder farms

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This study was aimed to determine the risk factors (age, size of flock, locale, sex and strain) and seroprevalence of *Mycoplasma gallisepticum* (MG) in Iranian broiler breeder farms. In addition correlation between seroprevalence in breeder with chronic respiratory disease in their progeny was analyzed. The study was conducted from May 2002 to October 2008 that was based on rapid serum plate agglutination (SPA) and enzyme linked immunosorbent assay (ELISA) tests. To find a correlation between MG in breeders with airsacculitis in their progeny, data from broiler slaughterhouses were registered. According to the results, the highest (21.4%) and lowest (0%) prevalence of MG infection was found in 2003, 2008 respectively ($P<0.05$). The prevalence was highest (18.5%) in winter and lowest (6.8%) in summer. Ross, Cobb, Arian, Hubbard and Arbor Acres had 23.2, 8, 11.4, 14 and 6.9 respectively infection. The prevalence was recorded highest at 10-20 weeks of age (28%), but in above 60 weeks it was lowest (3.4%). MG infection was higher (56.21%) in female than in male (43.79%). The population of the flocks was not influenced on *Mycoplasma gallisepticum* prevalence, no significant difference was seen in flocks up to 30,000 population (11.7%), 30,000-40,000 (19%) and upper 40,000 (23%). The prevalence of Mycoplasmosis in foothills was relatively higher (9.4%) than coastal area (7.2%), however not significantly different. The correlation between MG in breeder and chronic respiratory disease in broiler wasn't significant (respectively $P=0.743$, $P=0.103$) according to this, vertical infection couldn't be an important cause of condemnation for broiler in slaughterhouse.

Case-control study into risk factors for visible lesions or positive laboratory tests in bovine tuberculosis reactor cattle in Northern Ireland

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To determine the risk factors that affect the presence of visible lesions or positive laboratory tests in bovine tuberculosis (bTB) reactor cattle (i.e. cattle that reacted to the single intradermal comparative (SIC) tuberculin skin test) in Northern Ireland. An observational case control study was conducted of all reactor cattle in Northern Ireland in 1998, 2002 and 2006. Data were obtained from APHIS (Animal and Public Health Information System). Step wise logistic regression modelling was used to investigate potential risk factors, hypothesised to be associated with the presence of visible lesions in bTB reactor cattle or positive laboratory tests. Out of the 29,846 reactor cattle investigated, 43.0% had visible lesions at *post-mortem* and 45.4% were confirmed as bTB positive by laboratory tests. In 97.5% of the reactors the visible lesion status and bTB status were either both negative or both positive. Significant risk factors identified through the multivariable analysis ($P < 0.05$) were age at death, breed, sex, test year, net rise in bovine skin thickness, risk status of the disclosure test, total number of reactors at the disclosure test, history of being in an area with confirmed bTB and being an inconclusive at a SIC skin test previously. These risk factors are likely related to other factors including the strength of the challenge and the susceptibility of the animal. These findings are important as the detection of visible lesions and the confirmation of bTB are integral parts of the overall bTB control programme in Northern Ireland.

High *Brachyspira* colonization rates of Belgian layer flocks and boiler hen carcasses

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Brachyspira intermedia, *B. alvinipulli* and *B. pilosicoli* have been associated with diarrhea, fecal eggshell-staining and reduced egg production in laying hens. *B. pilosicoli* has also been associated with enteric disease in humans. We screened Belgian layer flocks for the presence of *Brachyspira* spp. and studied contamination of boiler hen carcasses with these bacteria as a possible source of human infections. In 2008-2009, 5 chickens per flock from 18 Belgian layer flocks (13 production and 5 rearing flocks) with symptoms as described above, and 10 chickens per flock from 10 randomly selected layer flocks at slaughter age, were screened for the presence of *Brachyspira* sp. by culturing cecal content. In 2009-2010, carcass (n=110) rinse samples, from 11 batches of boiler hens bought in Belgian supermarkets, were investigated. Nine of the 13 production flocks were positive for *Brachyspira* sp. opposed to none of the rearing flocks. On average 66% of the birds in an infected flock were positive, with an increasing morbidity rate with increasing bird age. At slaughter age, 9/10 flocks were positive for *Brachyspira* and within flocks multiple species were identified. Five of the 10 flocks were positive for *B. intermedia*. Cultures of carcass rinse samples demonstrated the presence of *Brachyspira* spp. in all batches. *B. intermedia* (7/11 batches) and *B. pilosicoli* (1/11 batches) were present at high numbers as shown by quantitative-PCRs. Multilocus sequence typing demonstrated the presence of 13 different sequence types in *B. intermedia* on the carcasses. In conclusion, the number of *Brachyspira* positive layer flocks and the colonization rates within positive flocks increased with age. The poultry pathogenic species *B. intermedia* was commonly found with a marked genetic diversity. Contamination of boiler hen carcasses with high numbers of *Brachyspira* spp., including the zoonotic agent *B. pilosicoli*, was highly prevalent.

Study of mechanisms of resistance to fipronil in field populations of *Boophilus microplus* (Acari Ixodidae)

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Nowadays, the main obstacle to the control of the cattle tick (*Boophilus microplus*) is the resistance to acaricides. The metabolic resistance to fipronil in tick populations from Brazil and Uruguay was assessed through larval immersion test (LIT) and adult immersion test (AIT) with synergists. A susceptible (Mozo) and a resistant strain (RFSan) and another three resistant field populations (JRRS, DUR, QUE) were exposed to fipronil and enzymatic inhibitors of esterases (triphenylphosphate-TPP: 0.01%), cytochrome P450 monooxygenases (P450) (piperonyl butoxide-PBO: 0.01%) and glutathione S-transferases (GST) (diethylmaleate-DEM: 0.05%). The control group was exposed only to fipronil. In adults of the RFSan (resistance ratio – RR=3.9), the resistance to fipronil was not suppressed due the addition of DEM or PBO. Nevertheless, synergism studies with larvae of the same strain revealed the involvement of P450 and esterases, with synergism ratios (SR) of 3.3 and 2.5 for PBO and TPP, respectively. Neither the LIT, nor the AIT confirmed the metabolic detoxification mediated by GST in the RFSan strain. With the field isolates, no synergism of DEM or TPP was observed with DUR (RR=2.1) and QUE (RR=87.7). However, for JRRS (RR=3.5) synergism with TPP was observed (SR=2.9). Possibly, the increase of esterase activity can be associated to the presence of resistant individuals to pyrethroids and organophosphates. All the populations tested were resistant to both acaricides, so the increment of the enzymatic detoxification activity for some pesticide could affect the efficacy of another pesticide, characterizing cross-resistance. Although the addition of PBO has enhanced fipronil toxicity against some resistant populations, the metabolic resistance do not appears to be the major mechanism of resistance to fipronil in the cattle tick.

Factors associated with *Amblyomma variegatum* presence in farms in Nevis and determination of high risks TBT areas

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Tropical Bont Tick (TBT), *Amblyomma variegatum*, is an invasive tick species of ruminants present in 10 Caribbean islands. TBT and the associated disease dermatophilosis, have been a challenge to livestock development in Nevis, Northern West Indies, for the past 30 years. After the end of a regional eradication program, active surveillance and control was conducted by veterinary services between 2007 and 2009. However, prevalence of dermatophilosis increased with some areas more infested, highlighting the need to determine the factors associated with TBT presence on farms. A case-control study was conducted to identify (1) the risk factors associated with the occurrence of the TBT on Nevis; and (2) the areas at high risk of tick persistence. Cases were selected as farms with clinical signs consistent with dermatophilosis and confirmed to have TBT present between 2007-2009. Control farms, without evidence of TBT presence or dermatophilosis cases during same period, were selected from a regularly maintained list of all active farms on the island, and matched to the cases based on parish. A questionnaire was administered to all cases and controls, which collected information on control practices, awareness level to ticks issues, etc. Univariable and multivariable logistic regression performed to explore the relationship between measured variables and the presence of TBT. Risk factors related to TBT include farmer attitudes toward TBT control and species hold on the farms. After many years of unsuccessfully employing various strategies for the control and eradication for TBT and dermatophilosis, the Veterinary Authority in Nevis anticipate using the results of this study as the scientific foundation for a more sustainable, targeted approach to the control of this pest.

Prevalence of hepatitis E virus in French domestic pigs and preliminary risk factors

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A nation-wide study was carried out in French slaughter-aged pigs to estimate the seroprevalence and prevalence of HEV contaminated livers and to further assess on-farm characteristics associated with HEV positivity at the farm level. 6565 sera and 3715 livers were randomly sampled from 186 pig farms throughout the country. Sera samples were tested for HEV IgG antibodies and livers for molecular detection of HEV using RT-PCR. Taking the sampling design into account, the farm-level seroprevalence was 65% (95% CI 57-74) and 31% (95% CI 24-38) of the slaughter-aged pigs had antibodies against HEV. The individual prevalence of HEV RNA positive livers was 4% (95% CI 2-6) and 24% (95%CI 17-31) of the farms had at least 1 positive liver. Most isolates were of genotype 3f (76.7%) with smaller amounts of 3c (18.6%) and 3e (4.6%). From the sampled 115 farms located in western France, 91 agreed to participate to the risk factor study. Farm characteristics associated with the probability of having at least 1 HEV positive liver were linked to (1) replacement gilt introductions (more than 6 weeks in the acclimatization room, no distribution of feces during acclimatization); (2) short (<3 days) down periods in farrowing and weaning facilities; (3) large rooms with more than 20 sows/room in the farrowing sector; and (4) more than 3 shipments for the slaughterhouse for a given batch of fattening pigs. These results showed that HEV contamination of slaughter-aged pigs in farrow-to-finish farms is linked to rearing conditions of the breeding herd and to the slaughter age of fattening pigs as suggested by the association between the frequency of shipments to the slaughterhouse/batch and HEV positivity.

Prevalence and spatial distribution of bovine tuberculosis in Bahia, Brazil

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Bovine tuberculosis (BT) is an infectious disease caused by the *Mycobacterium bovis* that affects humans and several mammalian species. BT is important because it inflicts far-reaching economic losses to infected regions and because of its impact on public health. Epidemiological surveys were conducted in the State of Bahia between 2008 and 2010, with the objective of estimating the prevalence and assessing the spatial distribution of the disease. The state of Bahia was stratified into four regions, each of them representing a set of homogeneous epidemiological and demographic characteristics, referred to as production circuits. A total of 18,810 >2 years old cattle in 1,305 herds, ranging 320-370 herds per region and 20-40 cattle per herd, were randomly selected. A cervical comparative test was applied to each selected animal; reactive cattle and cattle with two consecutive inconclusive tests were considered BT-positive, whereas non-reactive cattle were considered BT-negative. Case-herds were those with at least one BT-positive result, whereas herds without BT-positive results were assumed to be control-herds. Latitude and longitude were recorded for each sampled herd using a generic Global Positioning System (GPS). The Cuzick-and-Edwards' test was used to identify whether BT was spatially clustered. Herd-level prevalence, as indicated by the proportion of case-herds, was 1.6% (range 0.3-2.9% per region). No evidence of significant (P<0.05) spatial clustering was detected by the Cuzick-Edwards' test at any of the assessed levels of neighborhood, which ranged from 1 to 10, most likely, due to the low disease prevalence. Results here suggest that BT is low prevalent in the State of Bahia and that disease prevalence is independent from spatially-structured factors.

Risk factors for seropositivity to *Mycoplasma hyopneumoniae* and severity of clinical symptoms of enzootic pneumonia in fattening pigs

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Our aim was to examine potential risk factors associated with the occurrence of enzootic pneumonia in a region of high pig density (>800 pigs per 100 ha), where majority of herds is endemically infected with *Mycoplasma hyopneumoniae*. Overall 112 herds were enrolled in this study, which included collection of epidemiological data by personal interview with farmers and investigation of the pigs' environment. Clinical examination of fattening pigs included measuring the coughing index [C-Ind] and assessing seropositivity to *M. hyopneumoniae* [SP in %], SIV and PRRSV in finishing pigs. In a multinomial regression model three different groups were defined to identify risk factors for the within-herd transmission of *M. hyopneumoniae* and the occurrence of clinical symptoms: 25 'healthy' herds (C-Ind <2.5, SP <0.5), 35 herds with high 'seropositivity' only (C-Ind <2.5, SP ≥0.5) and 40 herds with 'disease' (C-Ind ≥2.5, SP ≥0.5). An increase of the age of piglets at weaning could be identified as risk for both, 'seropositivity' and 'disease'. Any contact between fattening pigs of different age during restocking of compartments increased the risk for 'disease'. The use of living animals for the exposition to replacement gilts during the acclimatisation in the herd and an increase in the number of weaned piglets per sow per year were protective in terms of 'seropositivity' and 'disease'. In this study, focusing on risks of within-herd transmission of *M. hyopneumoniae* and on the occurrence of clinical symptoms of enzootic pneumonia in fattening pigs, new aspects, namely the duration of the suckling period and the link to high sow herd productivity, likely reflecting good hygiene and management measures, were identified.

Poster topic 01

Poster 10

Prevalence and control of Bovine Viral Diarrhea in two large industrial dairies around Tehran-Iran

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BVDV is one of the commonest infectious agents with significant economical losses in dairy cow industry all over the world. Prominent impact of the consequences has mostly been ignored in Iran; therefore, this study was conducted to clarify some important features related to the infection and as a footstone for further investigations leading to serious control measures in Iran. During the summer of 2011, 2926 and 952 (overall 3,878) blood samples from 2 large industrial dairy farms around Tehran were gathered. The samples were from over 3.5 months calves and all adults. Adopted control and eradication program was based on mass testing (census), culling PI animals from the herds, taking serious biosecurity measures. All samples according to the similarities and age were categorized into pooled samples for RT-PCR and positive ones underwent AC-ELISA, individually. 46 and 35 (overall 81) samples were positive in the first test. The second sampling on the positives was carried out 3-4 weeks later. Only 3 persistently infected (PI) were discovered from the larger farm and the smaller one had no PIs. Overall, antigenic prevalence of BVDV was about 2% (TI) and PI prevalence was only 0.07%. This campaign program is still going on by testing neonates before colostrum intake and culling new diagnosed PIs.

A survey on Incidence rate of udder related health disorders in Iranian dairy cows (2007-2008)

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Udder disorders, mastitis in particular, are one of the most important health disorders in a dairy farm. Mastitis is the most prevalent infectious disease of adult dairy cattle that affects herd productivity. We conducted a historical longitudinal study with time-dependent covariates, to investigate the incidence rate of udder related health disorders in dairy herds in Tehran, Iran. A total of 7,067 first- and second- parity Holstein dairy cows that calved from March, 21, 2007 to March, 20, 2008 were followed until the next calving or culling. The annual incidence rate of mastitis and udder injuries were 32.3% (95% CI: 31.1-33.5) and 0.9% (95% CI: 0.5-1.2) respectively. Herd size appeared as an important factor in increasing incidence rate of mastitis and udder injuries. The incidence rate of these health disorders in large herds was significantly higher than small herds ($P < 0.05$). The results presented herein, demonstrate that the incidence rate of these health disorders, principally mastitis, is high in this area.

A knowledge exchange framework for the monitoring and control of paratuberculosis on Scottish farms

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Multiple barriers exist to effective disease control. Among these is a perception that control attempts are futile due to unrealistic or rigid guidelines that may not be feasible or cost effective for all farms. The aim of the PARABAN project is to develop a framework for effective knowledge exchange amongst all stakeholders involved in the reduction of bovine paratuberculosis on Scottish farms and so leave a lasting legacy of best practice for other disease mitigation programmes. Paratuberculosis is an insidious disease of considerable economic impact to Scottish industry. On-farm control is difficult due to its long incubation period and because the disease is frequently spread by subclinically infected animals. Control is best achieved by the removal of infected animals from the herd to prevent further spread yet diagnostic tests may fail to detect early infected cases. Frustration may ensue when infected animals are identified in the herd after years of implementation of gold standard interventions at considerable expense and effort for the farmer. Eight Scottish farms are participating in this longitudinal study. For each farm, the feasibility of the implementation of best practice advice is assessed by all involved in the chain from farm to research (farmers, vets, health scheme providers, laboratories, researchers and recognized experts). Decisions are ultimately made by the farmer and their vet and interventions implemented whilst the prevalence of paratuberculosis on the farms is monitored. Adaptations to control measures are made as necessary whilst the process of knowledge exchange is constantly assessed and refined. The development of a multi-way forum offers a dynamic and adaptable approach to disease control and may be key to the success of disease mitigation programmes.

Outbreak of avian infectious bronchitis (IB) in Finland

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Avian infectious bronchitis (IB) is one of the most important poultry diseases that cause severe economic losses in the poultry industry worldwide. Finland has been free of IB for decades. Last outbreaks were in the 1970'. In 2007 there was one outbreak with a virus that was suspected of originating from a vaccine virus although vaccination for infectious bronchitis virus (IBV) was not allowed at that time. The good situation has been partly due to strict import regulations possible to maintain because of our good *Salmonella* situation and our non-vaccination status of Newcastle disease. In the spring of 2011 IB was confirmed in a layer flock with clinical symptoms. The layer flock had a lot of contacts with hobby flocks. Vigilance combined with follow up studies led to the detection of IB in further flocks. The present epidemiological situation as well as clinical symptoms, both respiratory symptoms and reduced performance, indicate that both broilers and layers have come in contact with IBV. The outbreak in the field is continuing and at the moment we receive samples from new cases weekly. We have found different types of IB viruses and their characterization is in process. The results will be presented in the poster. An epidemiological investigation has been started to find out the origin of the viruses. IB vaccination has not been practiced in Finland although one inactivated vaccine has been on the market. The decision about using a live vaccine is still pending.

Biosecurity measures on Finnish pig farms have become more common

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Two independent questionnaires (in 2002 and 2011) with questions concerning biosecurity on pig farms were analyzed. The first one was sent to 910 pig farmers and the response rate was 24%. The latter one was sent to 1000 pig farmers and the response rate was 42%. Altogether 47 pig farmers answered both questionnaires and their responses were used for this study. Application of six biosecurity measures was studied: (1) protective footwear is provided to and used by visitors; (2) protective clothes are provided to and used by visitors; (3) a separate loading space holding all the animals for loading is in use; (4) the loading space is washed after use; (5) control of rodents and birds on animal premises; (6) control of rodents and birds in feed storage facilities. There were 20 farrowing farms, 13 farrow-to-finish farms and 14 finishing farms in this study. Average farm size had grown significantly (10%) during this nine year period. Two out of six biosecurity measures had become significantly more common: the use of a separate loading space had increased from 45-70% and visitors' use of protective clothing increased from 70-90%. The implementation frequency of other studied biosecurity measures did not change significantly in the study population (McNemar test). In conclusion, these results indicate that the implementation of certain biosecurity measures has become more frequent on Finnish pig farms.

Herd factors associated with pneumonia and pleuritis in slaughter-aged pigs from farrow-to-finish pig farms

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A cross-sectional study was carried out in 143 farrow-to-finish herds to identify noninfectious factors associated with pneumonia and pleuritis in slaughter-aged pigs. Data related to herd characteristics, biosecurity, management and housing conditions were collected by questionnaire during a farm visit. Climatic conditions were measured in the post-weaning and finishing rooms where the slaughter pigs have been raised. A sample of 30 randomly selected finishing pigs per herd was scored for pneumonia and pleuritis at slaughterhouse. Herds were grouped into three categories according to their pneumonia median score (class 1: ≤ 0.5 ; class 2: $0.5 < \text{score} \leq 3.75$; class 3: > 3.75). For pleuritis, a herd was deemed affected if at least one pig had extended pleuritis. Multinomial and binomial logistic regression models were used to identify factors associated with pneumonia and pleuritis, respectively. An interval of less than four weeks between successive batches, large finishing room size and high mean CO₂ concentration in the finishing room significantly increased the odds for a herd to be in class 2 for pneumonia. The same risk factors were found for class 3 and, in addition, a direct fresh air inlet from outside or from the corridor in the post-weaning room versus an appropriate ceiling above the pigs also increased the risk. The odds for a herd to have at least one pig with extended pleuritis was increased when the farrowing facilities were not disinfected, when tail docking was performed later than 1.5 days after birth and if the piglets were castrated when more than 14 days old. A temperature range of less than 5 °C for the ventilation control rate in the farrowing room, a mean temperature in the finishing room below 23 °C and large herd size were also associated with increased risk of pleuritis. All rearing steps from farrowing to finishing should be taken into account in any health programme aimed at controlling pneumonia and pleuritis.

Using educational tools and methods to bridge the gaps between theory and application

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The need for epidemiological skills has never been higher. There is an ongoing need for capacity development and training in epidemiology, at individual, institutional and national levels. This is particularly acute in developing areas of the world. The present day's increasingly widespread access to the internet gives us unparalleled opportunities to collaborate remotely and provide tools, training and support, as well as share information and data. This is facilitated by the establishment of increasingly functional technologies and user-friendly software, which enhance ease of use while reducing development time. The challenge is to make the best use of such opportunities. The EpiCentre has historically had a strong focus on software development. Here, we showcase a number of innovative training and support tools that are currently being used. Since 2010, Massey University has offered a 'One Health' Masters programme which has a focus on epidemiology and is predominantly distance-taught. The online learning environment incorporates innovative features including applied scenario-based learning, tutored small-group activities and use of specific software tools. There is a strong emphasis on communication and collaboration, which has enabled activities such as the synchronous development of cognitive maps, risk assessments and a facilitated expert elicitation workshop. We have also developed a suite of epidemiological calculators for use on iPhone and Android platforms, for individual use. In a decision-making context, we have developed a real-time decision support system to facilitate the entry and analysis of animal health data in Vietnam.

Impact on the productivity of dairy cattle by the subclinical infection to bovine leukemia virus

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Enzootic bovine leucosis is one of the notifiable diseases in Japan. The number of detected cases has increased gradually and exceeded 1000 since 2008. It is known that less than 5% of cattle that were infected to bovine leukemia virus (BLV) develop the clinical manifestation of leukemia. However, potential impact of subclinical infection on productivity is not clear. We investigated Dairy Herd Performance Test's (DHPT's) records of randomly-selected 674 cattle from 43 farms. Among these cattle, 262 (40.5%) were positive to the serum ELISA for BLV. The association between the infection status and the productive performance data including milk yield and other parameters were analyzed using the hierarchical Bayesian model by MCMCglimm package of the statistical computing environment R. In the present analysis, farm was accounted as a random effect, and the parity, calving season, days in lactation and linear score of the somatic cell counts (LSSCC) were considered as possible confounders. As a result, although the mean of the 305-day adjusted milk yield of the infected and uninfected cattle was estimated at 8,753.1 and 8,618.0 kg, respectively, the difference was not significant in the present model ($P=0.91$). Similarly, no other parameters including milk fat, milk protein, solids non fat, milk urea nitrogen and LSSCC were significantly associated with the infection status ($P=0.98, 0.75, 0.25, 0.44$ and 0.40 , respectively). These results imply the subclinical infection to BLV has no apparent impact on the production performance of dairy cattle. However, these influence may also depend on the stages of the subclinical disease progress, further examination will be needed to evaluate the true impact of the BLV infection on dairy production.

EpiCal: an App for Epi geeks

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With the increasing use of tablets and other forms of mobile computing, and in particular the increasing availability and use of iPhones, also by veterinary practitioners, the technology exists to make epidemiologically relevant calculators readily available to the field practitioner and to veterinary students. Here we present an iPhone App that can be distributed through the iTunes App Store (ensuring world-wide accessibility) and enables the mobile calculating of basic epidemiologically important estimates. In its first publicly released version, the App will allow the calculation of, amongst others: (1) measures of association; (2) measures of effect; (3) diagnostic test evaluation and interpretation; (4) sample size calculation. The App will obviate the need for permanent access to the Internet in the field in order to access epidemiological calculators, enable evidence-based decision practice and allow Epi geeks to calculate on the go!

Areas at risk of *Leptospira* exposure among livestock in France, a survey from 2008 to 2011

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Leptospirosis is a worldwide spread disease which affects mammalian species namely cattle and swine, those are main livestock in France. In animal, the clinical signs observed are mainly reproductive disorders, they are not specific. Leptospirosis is usually suspected as part of a reproductive disorder investigation (such as looking for Brucellosis or Infectious Bovine Rhinotracheitis in cattle and virus of respiratory and reproductive disorder syndromes or parvovirus in swine). The aim of our study was to map at-risk areas in France for a surveillance purpose. *Leptospira* survival in the environment is known to rely on temperature and humidity. The exposure of domestic species is expected to be different in different habitats. Consequently, the proportion of exposed livestock should be different from an area to another. The first objective of the study was to assess the frequency of *leptospira* antibodies in swine and cattle with a reproduction disorder. The second objective was to map at risk regions for the main detected serovars. The third objective was to use the geographic distribution of *leptospira* serovars to draw hypothesis on the reservoir species to be implied, in order to plan appropriate surveillance in wildlife. This study was based on *leptospira* serology results with the Micro agglutination test (MAT) carried out at the veterinary reference laboratory for *leptospira* diagnosis (Laboratoire des Leptospires). Results from 2008 to 2011 with whole data were included in the study. Serology test results were considered as tested positive when titer was over a 1:100 in cattle as in swine. Risk map for *leptospira* in livestock and (afterward) in wild animal reservoir should be useful in a public health approach with the further aim to document transmission risk and route of transmission to humans.

Hepatitis E virus infection in domestic swine in Belgium

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Hepatitis E virus (HEV) infection is hyperendemic in developing countries and endemic in developed countries. Many evidences claimed for a zoonotic transmission involving strains from genotypes 3 and 4. The main putative animal reservoirs for HEV in Western Europe are pigs, wild-boars and deers. This survey aimed to investigate HEV apparent seroprevalence in pigs in Belgium. In 2010, the Belgium pig population reached 6,321,055 individuals and HEV could represent a true hazard for the public health. Serum sampling (from an initial randomized sampling) was stratified according to regions and provinces and, within each province, a systematic sampling was realised to select pig farms (n=70). The sampling was performed in sows between September 2010 and October 2011; 6 sera were taken in each farm (n=420). HEV ELISA 4.0v, MP Biomedicals Asia Pacific Pte. Ltd., Singapore, was used and an apparent seroprevalence of 73% was obtained using the cut-off of the kit. Then, a ROC curve was created, adding true negative sera. Finally, randomly selected, positive pig sera (n=50) were tested by Western blotting (modified recomLine HEV IgG/IgM, Mikrogen Diagnostik) in order to validate ELISA specificity and to adapt the cut-off. In conclusion, the high HEV seroprevalence in swine in Belgium raises zoonotic concerns about HEV transmission from pigs to human and the role of pig herds as reservoir of this infection. Research supported by the Belgium Federal Public Service, Health, Food Chain Safety and Environment. We thank Dr Cariolet (Anses-Ploufragan) and Prof van der Poel (Central Veterinary Institute-Lelystad).

Seroprevalence of *Neospora caninum*, paratuberculosis and Q fever in cattle in Belgium

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A large cross-sectional serological survey was conducted between November 2009 and February 2010 to estimate the animal and herd level seroprevalence of *Mycobacterium avium* subspecies *paratuberculosis* (MAP, paratuberculosis or Johne's disease), *Neospora caninum* (neosporosis) and *Coxiella burnetii* (Q fever) in cattle in Belgium. A total of 1,100 cattle herds were randomly selected from the list of all Belgian cattle herds (dairy, beef and mixed herds but excluding veal holdings). Within each herd, blood samples were collected from 10 animals of 12-24 months of age and 20 animals >24 months of age. All serum samples (n=18858, n=957) were tested for *N. caninum* antibodies using a SRS2 sandwich ELISA (Bio K 192, Bio-X Diagnostics). Samples from >24 month old cattle were also tested for MAP antibodies (n=13616, n=937) using an adsorbed indirect ELISA (ID Screen® Paratuberculosis Indirect, ID VET) and for *C. burnetii* antibodies (n=13641, n=942) using an indirect ELISA (LSIVET ruminant milk/serum Q fever, LSI). The true animal level and herd level seroprevalence for *N. caninum* was estimated at 3.5% (95% CI: 2.7-4.4) and 62.5% (95% CI: 59.4-65.5), respectively, with no differences in seroprevalence between production types or according to age. For MAP, a true animal and herd seroprevalence of 2.2% (95% CI: 1.7-2.9) and 21.6% (95% CI: 19.0-24.3), respectively, was found. The animal seroprevalence for MAP was slightly higher in dairy than beef herds. The true animal and herd seroprevalence for Q fever was estimated at 13.3% (95% CI: 12.3-14.6) and 55.1% (95% CI: 51.9-58.3%), respectively. The number of Q fever positive animals increased with age and the animal seroprevalence was higher in dairy and mixed herds than in beef herds. This survey demonstrates that *C. burnetii* and *N. caninum* are widespread in Belgian cattle and confirms that MAP is still endemic in Belgium.

Efficacy of sow washing on the livestock-associated MRSA skin status

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The present study investigated the effect of sow washing, a common Belgian measure, on the skin MRSA status of the sow. A sponge of the back skin of 48 sows, originating from four farrow-to-finish farms (farms A to D; 12 sows sampled per farm) was taken before and after washing. Sow washing included 3 steps: (1) spraying with water; (2) soaping in with product; and (3) rinsing with water. The MRSA skin contamination remained unchanged in 64% of the sows both before and after washing. MRSA was found on the skin of 13% of the sows before washing but not after washing. From the skin of the remaining sows (23%), MRSA was only isolated from the skin samples after washing. Spa types t011 and t034 were observed, which are associated with livestock-associated MRSA. Although hygiene measures are used to diminish the MRSA load on a farm, the present study indicates that sow washing before farrowing has no significant effect on the skin MRSA status of the sow (SAS 9.2, P=0.32). Further research is needed to develop a procedure that reduces the MRSA contamination of the sows.

Distribution of *Haemophilus parasuis* serotypes in several regions of Austria

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Haemophilus parasuis is known as the etiologic agent of Glässer's disease in swine. High morbidity and mortality can occur in naive swine populations. *H. parasuis* can also be isolated from the upper respiratory tract of healthy pigs. 15 different serotypes are known. Although there is no absolute correlation between serotype and virulence, serotypes 1, 5, 10, 12, 13 and 14 are said to be the most virulent. Therefore, the differentiation between the different serotypes can help to improve the control of disease. Aim of the study was to find out which serotypes of *H. parasuis* are common in pig farms in different regions of Austria. A total of 391 serum samples from 146 pig farms in Styria (36 farms), Upper Austria (57 farms), Lower Austria (40 farms), Vorarlberg (7 farms), Burgenland (2 farms), Carinthia (3 farms) and Salzburg (1 farm) were tested with a screening ELISA (Ingenasa) for antibodies against *H. parasuis*. Positive samples were serotyped by indirect haemagglutination test. Antibodies against *H. parasuis* were detected in 176 samples from 74 farms (Styria 33 farms, Upper Austria 29 farms, Lower Austria 10 farms, Vorarlberg 1 farm and Burgenland 1 farm). Serotyping was done in 170 samples. Up to four different serotypes could be found per sample and up to five per farm. Most common serotypes were serotype 9 (65%) – found in all tested parts of Austria, followed by serotype 13 (22%), 14 (12%) and 3 (10%). 13 samples (8%) were non-typable. In Austria, the most common serotypes of *H. parasuis* seem to be 9, 13 and 14. In most farms are two or more serotypes detectable. This should be taken into consideration for interpretation of laboratory results and in therapy and immunoprophylaxis.

Identification of factors at the farm, sow and piglet level associated with the colostrum intake per kg piglet

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Over the last decade, the litter size of sows has substantially increased. This has resulted in a lower birth weight, more variation in birth weight, more stillborn piglets and higher mortality in suckling piglets. As a consequence, sufficient colostrum and milk intake of each single piglet has become a critical issue. This study aimed at identifying factors associated with colostrum intake per kg piglet. Ten randomly selected sows per farm and their offspring from five conveniently selected farms were included in the study. Several farm, sow and piglet factors, potentially associated with colostrum intake per kg piglet were recorded. A linear mixed regression model with farm and sow within a farm as random effects was fit (PROC MIXED, SAS 9.3). Additionally, the contribution of the three different levels to the total variance of colostrum intake per kg piglet was determined. The average colostrum intake per kg piglet during first day of life was 324 gram with a range between 0 and 1554 gram. Most variation in colostrum intake per kg piglet resided at the piglet level (63%). Almost 16% and 21% of the variation occurred at sow and farm level respectively. Parturition duration, birth weight and birth rank were all negatively associated with colostrum intake per kg piglet with a P-value of less than 0.05, 0.001, 0.01, respectively. The average kg colostrum intake per piglet tended to be higher in small litter sizes than in large ones (P=0.06). The average kg colostrum intake per kg piglet also strongly depended on the sow breed (P<0.001). Interestingly, all variation in colostrum intake at farm level was explained by the sow breed.

Bovine tuberculosis in cattle in South Germany between 2007 and 2010

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Bovine tuberculosis has been eradicated in Germany during the 50s and 60s. Since 1997 Germany is recognized as free of bovine tuberculosis. However, from 2000 onwards increasing numbers of animals were found to be infected with tuberculosis during routine slaughter examinations (up to 12 cases in 2007). Therefore, a project was started to test all adult cattle in one part of South Germany between 2007 and 2010, using the intradermal tuberculin skin test. The results of these tests have been collected and stored in a central database. Analysis of the results revealed that nearly 200,000 animals were tested, of which 160 reacted positive in the first skin test. Of these 92 tested negative in the comparative tuberculin test. In total 960 animals tested doubtful in the skin test and were tested again with the comparative test. Of these 16 were positive in the comparative test and 56 also doubtful in the comparative test. Most animals were between four and six years of age. The study also tried to identify summer pasture locations where several cattle were grazed together by looking at the lifetime history of each positive animal, which is stored in the national cattle database (HI-Tier).

Impact of lameness in dairy cows in the visits to an automatic milking system: a case control study

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There is a tendency worldwide for the automation of farms; this involves the introduction of automatic milking systems (AMS). It is known that half of the dairy population per year in the UK suffer of lameness and it has been recognised it as a painful condition. Affected cows show behavioural signs of being ill and in pain such as reduction in mobility, therefore feeding is reduced and attendance to the AMS can also be compromised; these factors potentially affect not only animal welfare, but also farm economy. The aim of our study is to identify the impact of lameness in the milking behaviour and it was conducted as a case-control study. Thirty eight pairs of Holstein-Friesian cows were used in the study, these were selected using a matching criterion that include mobility score, parity, days in milk (DIM) and milk production, and block by pen. Animals had free access to the AMS and feed; feed was provided at 6:00, 8:30, 10:00, 12:00, 14:00, 17:00 and 20:00 hours. Data collected included number of visits in the last 24 hours and time of the visit. Descriptive analysis and logistic regression modelling were performed. Preliminary results show a significant difference in milking visits between the control and case cows, with a tendency for the control cows to visit the robot more frequently than the case animals ($P=0.01$). Differences between control and case cows at each time period were explored. The study suggests that lame cows have reduced attendance to visit the AMS and that therefore it may have an impact on animal welfare and farm economics.

Test accuracy at different cut-offs when plasma concentrations of metabolic indicators are used to detect decreased fertility in dairy cows

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Negative energy balance is a known risk factor for decreased fertility in dairy cows. This study evaluates the accuracy of measuring plasma concentrations of two indicators of negative energy balance, non esterified fatty acids (NEFA) and β -hydroxy butyrate (BHBA), when they are used to predict decreased fertility. For 496 cows in 12 Swedish dairy herds plasma samples were taken 0-21 days in milk and data on breed, parity, calving date, gynecological examinations, and inseminations were collected. The diagnostic sensitivity (Se) and specificity (Sp) at different cut-offs in concentrations of NEFA and BHBA were calculated and compared to each cow's fertility status, measured as anestrus (ANEST) and delayed first AI (DFAI). Positive and negative predictive values (PV+, PV-) were calculated considering different levels of decreased fertility. Strata-specific Se and Sp and associations between test results and fertility parameters were investigated using logistic regression. For this analysis, cut-offs with Sp ~80% was used because a high Sp was considered of interest. This corresponded to a NEFA-cut-off at 400 μ eqv./ml (Se \leq 0.44) and a BHBA-cut-off at 1.8 mM (Se \leq 0.32). Sp was generally higher when the test was used in heifers compared to older cows. With a prevalence of ANEST of 28% PV+ were 0.25 and PV- nearly 0.90. With a DFAI prevalence of 35%, PV+ were <0.38 and PV- nearly 0.90. The results indicate that overall test performance is low when metabolic indicators measured 0-21 days in milk are used to predict decreased fertility in dairy cows. However, the accuracy and the usefulness of the tests could be influenced by cow-level factors as well as the prevalence of decreased fertility.

Prevalence and correlates of influenza-a in piggery workers and pigs in two communities in Lagos, Nigeria

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Worldwide, three Influenza-A virus subtypes (H1N1, H1N2 and H3N2) in swine are major public health issues. In Nigeria, the existence of these subtypes in pigs has not been well studied. This study aimed at determining the prevalence and correlates of Influenza-A viruses circulating in piggery workers and pigs in Oke-aro and Goshen communities in Lagos, Nigeria. Nasal swabs were taken from 197 consenting piggery workers and 281 randomly selected pigs to determine the prevalence of Influenza-A (H1, H3, H5) using Reverse Transcriptase Polymerase Chain Reaction test (gene M). An interviewer administered questionnaire was used to collect information on demography, Influenza-A related symptoms experienced, personal hygiene and management practices from the piggery workers. Descriptive statistics was used and chi square test performed at 5% significant level. All piggery workers and pigs' nasal swabs tested negative for Influenza-A viruses, hence, association could not be tested. Mean age of piggery workers was 41 \pm 13.6 years and 60% were females. Forty two percent were farm attendants, 38.0% were pig farmers and the rest butchers. Nineteen percent had history of headache; 14.0% had catarrh and cough; 4.0% had sore-throat; 5.0% had diarrhea; while 48.0% had muscle pain at the time of data collection. The mean body temperature for the pig workers was 36.5 \pm 0.5 $^{\circ}$ C. A significant difference (P<0.05) existed among piggery workers who had muscle pains. Piggery workers and pigs in study area were free of Influenza-A (H1, H3, H5) viruses. The current practices of the piggery workers should be encouraged.

Risk assessment for the introduction of PRRS via boar semen into Switzerland

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Switzerland, in contrast to other countries, has sustained its pig population free of porcine reproductive and respiratory syndrome virus (PRRSV). No pigs are imported for breeding, but the amount of boar semen imported from EU-countries has substantially increased during the past years. In 2010, the total of more than 24,000 doses originated from five boar studs in Germany, France and Austria. This poses a risk of introducing PRRSV into Switzerland, since transmission via boar semen is one of the known infection routes. In order to estimate the risk of PRRSV introduction into Switzerland via boar semen, a risk assessment was initiated. It included analyzing records on all trans-border shipments of semen available in the TRACES-database. Current import procedures were surveyed in interviews with importing breeding companies and exporting boar studs. Biosecurity measures and monitoring systems certifying the PRRSV status in each boar stud and basic data on sow holdings inseminating with imported semen were documented. Further specific information, such as the infectivity of the virus, etc., was drawn from literature search and expert opinions. This feeds into a release assessment estimating the likelihood of an imported semen dose to contain PRRSV, and an exposure assessment that describes the likelihood of Swiss pig herds to be exposed to PRRSV, using @RISK for a stochastic approach. First results of the release assessment are in line with current knowledge on the spread of PRRSV in pig populations. The risk of PRRSV 'import' rises with the number of imported semen doses per boar stud. They further suggest that testing intervals and techniques of ruling out acute PRRSV infections in boar studs have a considerable impact on the risk. Final results will contribute to the development of science-based guidelines for future imports of boar semen into Switzerland.

Patterns of change in flock *Salmonella* prevalence in broiler production and processing

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The objective of the study was to assess patterns of *Salmonella* prevalence within broiler flocks as they progressed through the production continuum. Presence of *Salmonella* was evaluated in 76 broiler flocks from 38 farms in four states in the southeastern United States. *Salmonella* flock status was determined by sampling a flock upon arrival at the grow-out farm (30 transport tray pads (D1TP) and a gastrointestinal tract (D1GI) sample from a chick from each of the corresponding trays); one-week before processing (whole carcass rinse (GOWC), ceca (GOCA) and crop (GOCP) samples from each of 30 birds); upon arrival at processing plant (PAWC, PACA and PACP samples from each of 30 birds); prior to the chill tank (rinses (PPPR) from 30 carcasses); and post-chill tank (rinses (PPPO) from 30 carcasses). The median flock prevalence varied across sample types and points: D1TP(56.7%), D1GI(0.0%), GOWC(13.3%), GOCA(3.3%), GOCP(0.0%), PAWC(53.3%), PACA(10.0%), PACP(11.7%), PPPR(33.3%), and PPPO(13.3%). The direction and magnitude of changes in prevalence between various sample types and points within each flock were determined. While slightly less than half of the flocks had increased prevalences from grow-out to plant arrival for ceca samples, over 70% of the flocks had increased prevalences from grow-out to plant arrival for crop samples and whole carcass rinses. The prevalence of *Salmonella* decreased from PPPR to PPPO for the majority of the flocks (78.1%). The results of the study provide insight on where to focus interventions to facilitate the control of *Salmonella* in the broiler production continuum.

Association between an index of internal herd growth and welfare indicators

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The objective of this study was to evaluate the association between herd-level welfare indicators and an index of short-term internal herd growth, two tools available to Swedish farmers enrolled in the official milk recording scheme to give an overview of their herd. The index is based on number of inseminations, calvings and heifer calves, number of dead calves, heifers and cows and number of culled cows. The index is calculated per month and, hence, gives an overview of the short-term efficiency in the herd. The welfare indicators are measures of mortality, morbidity and fertility which have been shown to be associated with animal-based welfare measures or production economy. Herds with a continuously high efficiency (CHE) were among the 25% with highest index for at least 4 month and had no month among the 25% with lowest index during 2011 (351 herds). Herds with a continuously low efficiency (HLE) had at least 4 month among the 25% with lowest index and maximum one month among the 25% with highest index (724 herds). The difference between CHE- and HLE-herds was evaluated using Kruskal-Wallis equality-of-populations rank test. The CHE-herds had lower calf and cow mortalities and lower culling rates which was expected since number of deaths and culling are included in the index. More interestingly, CHE-herds also had lower proportion of heifers >17 months of age at first breeding, lower proportion of cows with a calving to first insemination interval >70 days, lower age at first calving and a shorter calving interval. Also, the estimated bulk milk SCC was lower in CHE-herds. HLE-herds had lower disease incidences and lower proportion of cows with a calving to last insemination interval >120 days. In conclusion, CHE-herds also had better values in most welfare indicators, including those associated to farm profitability, which demonstrate the importance of having control over all aspects of the production.

Ecological niche for the establishment of *Oestrus ovis* L. (Diptera:Oestridae) in Cuba

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Oestrus ovis was ever reported in Cuba before 1995 when emerge in the Guantánamo province, coinciding one of the hottest places of the entire country. Guantánamo relief influences three consistently different weather conditions useful to identify ecological niche for the establishment of *O. ovis*. To identify the environmental and climatic variables affecting the distribution of *O. ovis* geographic point data of oestrosis outbreaks were interpolated with layers of: sheep population density, altitude above sea level, mean of humidity, mean of minimum temperature and climate types according to the Thornthwaite classification. According to Pearson correlation, the outbreak density was no related to susceptible animal density nor humidity or altitude above sea level. However X² test demonstrated that arid and semi-arid areas concentrated a significant higher proportion of oestrosis outbreaks. Oestrosis outbreaks mostly coincided (70%) with these types of weather, indicating that its optimal breeding conditions are present in import areas of the territory, as well its importance for fighting against the parasite. The main climatic characteristics of the semi-arid areas in Guantánamo did not differ from those internationally recognized for semi-arid areas of the world. Dry lands were characterized by their dry weather to very dry, and irregular, with herbaceous or shrub and rarely tree vegetation, which is unevenly distributed and offers very little ground cover. The temperature was the climatic variable that better explain outbreaks distribution with an adjusted coefficient of determination of R²>88.63. According to projected climate change *O. ovis* could become endemic in new areas. The currently oestrosis distribution suggests emphasized fighting again its causal agent before its establishment in new areas.

ELISA test as a strategy to detect infected dairy herds with Johne's disease in Uruguay

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Mycobacterium avium subsp. *paratuberculosis* (Map) is the etiologic agent of Johne's disease (JD), which occurs worldwide, affecting many domestic and wild animals including cattle, sheep, and many other ruminants. In 2002 Piaggio J. and Nuñez A (2006) studied the prevalence and risk factors associated to it in Uruguay. In 2008 Nuñez found a seroprevalence lower than 7% at the animal's level. Many control programs recommended for detecting infected herds, testing animals with serological tests, especially ELISA test in serum and / or milk. However, the ELISA for Map has the disadvantage of low sensitivity in animals shedding low concentration of Map in their feces. Authors' has reported the sensitivity of fecal culture test in the range of 23-29% in animals in early stages of infection and 70-74% in advanced stages of disease. The aim of this study was to evaluate the indirect ELISA as strategies to detect infected dairy herds in Uruguay. We select 9 herds with previous history of Johne's disease. Forth hundred fifty one samples were process by fecal sample (Herold with and without mycobactin) and ELISA IDEXX Lab (HerdChek Map). Statistical Software (Stata Corporation) was used to determine the sensitivity, specificity of ELISA tests and herd prevalence with a 95% IC. The fecal sample detects 4 of the nine infected herds. The ELISA test detect 7 of the nine infected herds. The sensitivity (Se) and specificity (Sp) of the ELISA was calculated respect fecal culture which was considered the 'gold standard test'. The Se was 16, 6% and the Sp was 97.0%. The herd sensitivity for the ELISA test was 77.78%.

Diagnostic performance of clinical observations of young lamb welfare

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The objective of this study was to develop valid, reliable and feasible indicators for the on-farm welfare assessment of young lambs (aged ≤6 weeks). A literature review and consensus of expert opinion identified a diverse number of on-farm welfare concerns for young lambs (n=53) including starvation, hypothermia, and the presence of conditions such as lameness and ocular abnormalities. Consequently, 4 non-invasive welfare indicators: demeanour, lameness, body condition and eye condition were assessed according to the behaviour and physical appearance of individual lambs. Indicator assessments were performed by 2 trained veterinary surgeons (A and C) and 2 trained animal-science students (B and D) on 966 young lambs from 17 farms. Inter-observer reliability was examined using Fleiss's κ and graphical distributions of observer scoring differences. Latent Class Analysis (LCA) estimated the diagnostic sensitivity (Se) and specificity (Sp) of each observer and predicted the test performance of unknown, random observers who may perform indicator assessments in the future. Demeanour assessments produced a κ 0.55, Se of 0.75-0.85 and Sp 0.98-1.00. Eye condition assessments were also consistent (κ 0.72, Se 0.86-0.89, Sp ≥0.99). Lameness assessments achieved a κ 0.68, Se ≥0.7 and Sp 1.00. Body condition produced κ 0.71 and observers A, B and D achieved higher test performance (Se ≥0.80, Sp ≥0.99) than observer C (Se 0.38, Sp 0.98). Overall, few scoring disagreements occurred and future observers were predicted to have good diagnostic ability for all indicators (Se ≥0.76, Sp ≥0.98). Results suggest that demeanour, lameness, body condition and eye condition appear to be valid, reliable and feasible indicators of young lamb welfare that could be included in on-farm assessments applied by trained assessors.

Efficiency of different on-farm biosecurity measures in Switzerland

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On-farm biosecurity is a collective term for all measures implemented on farms to reduce the risk of introduction and spread of infectious agents. The European Union currently discusses the replacement of the existing system (a combination of national and on-farm biosecurity measures) for maintaining a good animal health status, by an on-farm biosecurity concept only. This will be a challenge for Switzerland, as the currently very high standard of animal health is mainly achieved through national measures such as import restrictions. Thus, this project aims to assess the efficiency of various on-farm biosecurity measures in Swiss livestock. Due to sparse scientific data on the efficiency of individual biosecurity measures, the required knowledge will be extracted by means of an expert elicitation using a modified Delphi method. Through one-on-one interviews, Swiss and international experts will be asked to give their opinion on the effectiveness and importance of various biosecurity measures. Following the completion of all interviews, experts will be given the opportunity to reevaluate their answers as compared to the response of the group. Based on these results, a model will be created, allowing us to estimate the degree of protection following the implementation of biosecurity measures. Through a risk assessment for selected diseases we intend to evaluate the probability of disease introduction under different combinations of biosecurity measures. These results will be used to elaborate recommendations for biosecurity measures that can be implemented under Swiss animal husbandry conditions, while ensuring a good health status of livestock.

Capacity building and training program in animal health in Peru

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US Agency of International Development and US Department of Agriculture entered into a 3-year Participating Agency Service Agreement (PASA) in support of the US-Peru Trade Promotion Agreement that went into effect in 2009. This agreement fosters commerce between the 2 countries through the liberalization of trade in goods and services. Activities implemented under the PASA agreement address sanitary and phytosanitary issues that result in technical barriers to trade of agricultural products. The PASA supports the development and implementation of sector-specific programming in the areas of animal health, plant health, food safety, education and research. The University of Florida (UF) is collaborating with USDA Foreign Agricultural Services and the Peruvian Ministry of Agriculture's National Agricultural Health Service (SENASA) by providing technical expertise and training in targeted areas of the animal health system in Peru. The main objective is to enhance SENASA's surveillance systems for, and response to, priority diseases of economic importance to animal agriculture. To accomplish this objective, this project considers (a) delivery of workshops in the areas of: (1) epidemiology and health policy; (2) trans-boundary diseases; (3) laboratory biosafety and biosecurity; and (b) delivery of a mentoring program in epidemiology and health policy to SENASA veterinarians. In each workshop, participants complete a pre and post evaluation instrument to assess learning objectives. In the mentoring program, each participant is given a project assignment that requires the use of epidemiologic methods to generate scientific data as the basis for formulation of health policy. The participant is assigned a mentor who provides guidance and assistance. The project is expected to produce results, conclusions, and recommendations to animal health policy makers on the need (yes, no) to update or implement new uniform methods and rules for disease control and eradication in animal populations in Peru. Project outputs and outcomes will be presented at the Symposium.

Evidence-based veterinary medicine survey of veterinarians in the United Kingdom

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Finding relevant evidence, critically appraising it, and using it to help make decisions about patients is a key part of practising evidence-based veterinary medicine (EVM). Currently little is known about what veterinarians perceive EVM to be, or what published or online resources they use. Additionally, little is known about what conditions are commonly seen in veterinary practice, which could further assist in identifying relevant areas for researchers. Therefore the aim of this study was to conduct a survey of UK veterinarians to determine the awareness of EVM and to identify where veterinarians obtain information relating to veterinary issues. Additionally, the aim was to establish which species and conditions/diseases are commonly nominated as being seen by veterinary practitioners. All veterinarians registered with the Royal College of Veterinary Surgeons (n=14,531) were invited to participate in the survey via a postal questionnaire. Participants were given the option of completing the questionnaire online or on paper. Approximately 35% of vets (n=5,053) completed the questionnaire. Most respondents (69%) were practicing veterinarians. A large proportion of respondents had heard of EVM (87%), and the majority were interested in finding out more about it (66%). Veterinarians read the *Veterinary Times* (15%), and accessed Google (15%) most frequently from a list of resources. Dogs were the most common species nominated (26%), and skin problems were the most commonly cited for all species (24%). An awareness of the resources used by veterinarians could assist in determining how best to inform practitioners of research findings relevant to the common species and conditions they see. This is an important step towards facilitating the further practise of EVM within the veterinary profession.

Factors influencing On-Farm-Biosecurity measures: steps towards On-Farm-Biosecurity management

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In veterinary science it is a basic assumption that farms with high level of biosecurity contribute less to the spread of contagious animal diseases and to zoonotic pathogen load in the food chain. Within the last decade the terms 'Biosecurity' and 'On-Farm-Biosecurity' became more and more popular. On-Farm-Biosecurity is regarded as an essential part of concepts like compartmentalization or food defense and it is explicitly named in the third pillar of the EU animal health strategy. In contrast, there is not yet a commonly accepted definition of the term On-Farm-Biosecurity for science, veterinary administration and farming practice. And most concepts of On-Farm-Biosecurity miss soft factors like compliance, feasibility, necessity of special skills and necessity of coordination. As part of a general trend towards evidence based policy and towards private food safety management systems livestock policy makers, researchers and private actors of the food chain need concepts to assess and evaluate On-Farm-Biosecurity measures. Hence, our study had two research aim: First, to find a definition of the term On-Farm-Biosecurity and second to elaborate on factors that mainly influence the applicability and feasibility of On-Farm-Biosecurity measures. Within the framework of the cross-border research project SAFEGUARD we conducted desk research, expert elicitation and on-farm surveys on that topic. The main outcome of our study is a proposal for a definition of On-Farm-Biosecurity that can be used by scientists, veterinary authorities and private actors within the food chain and a model explaining the main factors influencing On-Farm-Biosecurity measures. As an outlook, our results might be a first step towards a strategy of On-Farm-Biosecurity management.

The epidemiological characterization of the surroundings of a pork compartment in Chile and its uses in front of an exotic disease event

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Recently the first pork compartment in Chile, based on OIE standards, was approved. This includes Foot and Mouth Disease, Classical Swine Fever, African Swine Fever, and Aujeszky's Disease, all of them exotic for the country. High standard risk management, including bio-security and surveillance, has been applied for all the possible introduction routes of those diseases to the compartment if the country faces an exotic disease event outside of it. The knowledge and management of physical or spatial factors that could affect the compartment bio-security is one of the key elements to successfully overcome the management of a sanitary emergency. The herds, wildlife, pests, and routes of the compartment surrounding based on different administrative zones, were carefully identified and epidemiologically characterized. Herd information was generated through direct visits and semi-structured interviews: location, distance to compartment site, number of animals and species, health practices, origin of inputs and destiny of outputs, movements, slaughtering and official surveillance results were included. Wildlife species and habitats and other free-movement animals were also characterized. Risk herds, wildlife and pests were qualified according the threat they represent to the compartment, assuming the presence of an exotic diseases in any of the administrative zones defined. The results of this epidemiological characterization were used for the construction of the private and official contingency plans to be applied in case of an exotic disease event. This product involves target surveillance of herds, wildlife sites and compartment units, movement restriction, and the activation of an official preventive zoning to strengthen bio-security.

Risk factors for African swine fever and the effect of biosecurity

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ASF is economically devastating for the pig industry. Data on risks of ASF are lacking from West Africa. Evaluation of risk factors supporting infection of pig farms in this region remains the key to the development of a risk-based approach to the epidemiology of ASF and control. In Nigeria, perpetual infections of certain localities with intermittent infection of contiguous areas makes it an ideal setting for a matched case-control study for risk factors and biosecurity practices in pig farms. Subsets of farms located in high-density-high-risk pig areas for ASF infection were randomly selected for this analysis. Although, routine purchase and introduction of untested pigs, infected neighbourhood, keeping of other livestock, presence of abattoir/slaughter slab within pig communities, indiscriminate disposal of visceral content of slaughtered pigs, entrance of wild birds into pig pens, and free access to feed store by rats were all associated risk factors, only the presence of abattoir within a pig farming community and the presence of an infected pig farm in the neighborhood were significant. There was a marginally significant negative association (protective) between risk of ASF infection and sharing of farm tools and equipment. Of the 28 biosecurity measures evaluated, food and water control, separation of sick pigs and washing and disinfection of farm equipment and tools were negatively associated (protective) with ASF infection. Consultation and visits of veterinarian or paraveterinarians when animals were sick, and pest and rodent control were positively associated with ASF infection of farms in Nigeria. Region-based approach to control ASF in addition to farm-based biosecurity is important as such an approach will benefit ASF control and cover other infectious diseases in Nigeria and West Africa.

African swine fever in the Russian Federation: geo-spatial analysis and evaluation of the economic impact

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African swine fever (ASF) is a viral disease of domestic and wild pigs which leads to almost total mortality among the affected animals. Due to the absence of the vaccine the only measure to prevent spread of the disease is total slaughter of livestock population in the focus of infection and depopulation within the risk zone. The necessary measure is restriction of transportation and trading of animals and pork products. More than 280 ASF outbreaks have been reported from private holdings, large pig-breeding farms and in wild boars population in the territory of the Russian Federation since 2007. The analysis of spatial distribution of ASF cases performed by means of GIS-technologies demonstrates a correlation between the disease spread and direction of primary transportation links, domestic swine population density and human population density. This allows us to make a conclusion about predominately anthropogenic nature of the virus transmission by transportation and trade of live animals and contaminated agricultural products. MaxEnt software modeling with regard to detected risk factors allowed us to create a risk map which indicates the probability of emergence and spread of the disease in different regions of the European part of the country. The evaluation of economic losses caused by ASF in 2010-2011 was performed using the methodology adopted by the OIE considering both direct impact to livestock sector (costs of animal slaughter in the focus of infection and depopulation in the risk zone, losses of processing industry, indemnity payments to owners) and indirect losses associated with transportation and touristic restrictions, feed and grain trading bans, etc. According to experts' opinion the total economic damage was 2271 million Rubles (about 57 million Euros) in 2010.

Patterns of contacts in the network of pig movement in the Philippines

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The aim of this study was to describe the traceability system used in the Philippines for slaughtered pigs using social network analysis. The following information were collected prior to finisher pigs arrival for slaughter: 1) date of slaughter; 2) livestock trader name, address and contact details; 3) livestock transporter name, address and contact details; 4) animal source farm details; 5) date of purchase; and 6) number of pigs bought and intended for slaughter. Records of movement events between pig farms, traders, and slaughterhouses allowed us to construct a network of named contacts. The following parameters were calculated for each node of the network: 1) edge weight 2) out-degree; 3) out-degree centralization; and 4) betweenness centrality. The farm to slaughterhouse network consists of different types of farms (commercial, n=84; backyard n=56) together with specific links between them and their traders (n=169) and slaughterhouses (n=22). Of the total possible number of ties in this network (n=109,230) 412 were actually present. The proportion of possible ties that were present was 0.004, indicative of a network of relatively low density. The out-degree centralisation index for this network was 0.02, indicating a low organisation of off-farm and off-trader movement of pigs around main focal nodes. Modification of an existing slaughterhouse information system was effective in allowing the development of a system that could trace back slaughtered animals to source farms and thus allow the construction of a network of animal movement. The network structure for node-to-node movement of pigs was characterised by a very small number of network hubs that were influential in movement of pigs through this network. Identifying those nodes is of great importance for controlled animal movement programmes.

Salmonella infection in pigs: case-control study

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In 2007, a national *Salmonella* surveillance and control program was implemented in Belgian fattening pigs. Its purpose is to sensitize the farmers starting by identifying the farms with the highest levels of *Salmonella*-specific antibodies (high risk farms). The high risk farms are required to take part in a *Salmonella* specific action plan (SSAP) which consists of a checklist and control measures designated to reduce the risk of *Salmonella* infection. The checklist foreseen in the SSAP was a great opportunity to perform a case-control study on a number of explanatory variables and identify critical on-farm risk factors for being a *Salmonella* high risk farm in Belgium. The checklist consisted of about 70 questions and was submitted to both case and control farms. Risk factors were analysed individually and simultaneously using a multivariable logistic regression model. The results of the logistic regression showed an association between the physical form of feed (OR=0.22 (0.1-0.48) for flour versus pelleted) and the risk of *Salmonella* infection. Frequent concomitant respiratory diseases (OR=3.95 (1.85-8.44)) and bird proof housing (OR=4.37(2.68-7.11)) were identified as risk factors. The study demonstrated that the disinfection of boots (OR=0.46 (0.28-0.76)) and the separation of poor-doers (OR=0.33 (0.19-0.56)) were significant protective factors. A negative association was found between the size of the herd and the risk of *Salmonella* infection (OR=0.99(0.99-0.99)). This study identified mainly type of feed, hygiene, and the control of concomitant diseases especially respiratory diseases as on-farm risk factors and therefore acting on those parameters may help control *Salmonella* on the farm.

Effect of influenza A(H1N1)pdm09 virus on live weight of Duroc boars during growth phase (100-140 days)

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This study presents the impact of influenza A(H1N1)pdm09 virus infection has on Duroc boars during the growth phase between 100 and 140 days of age at a boar testing station. Data are obtained from an outbreak investigation at a boar testing station after clinical signs were reported in early April 2011. The station receives young boars (70-85 days old) and monitors their performance including daily feed intake and daily weight. Cohorts of 72 boars are kept in groups of 12 in 6 equal sized pens (14.0 m²) in the same room for an average of 72 days until they reach a bodyweight of 100 kg. Serological and virological tests were performed on 375 boars from all 16 rooms on 8 occasions from April to July 2011. A synopsis of the results is presented based on results from one room where 18 boars (8 were Duroc boars) were tested positive on 14 April 2011. A control group of a previous cohort of 23 Duroc boars that occupied the same room admitted in November 2010 was selected. Surveillance results confirmed that the station was not infected at that time. The growth curves of the average means of live weights of the two groups (infected vs uninfected) were compared. Student t-test was used to test significance in the differences between the two group means of the live weights. The growth curves of uninfected and infected pigs appear to diverge just before 100 days of age. This coincides with the detection of A(H1N1)pdm09 virus infection in the 8 Duroc boars on 14 April 2011. Even though the divergence in the growth curves indicated a possible negative impact of A(H1N1)pdm09 virus has on the growth rates of the Duroc boars, the one-tail t tests on group mean differences did not show consistently that the negative impact on live weight of Duroc boars were significant at the 95% confidence level.

Outbreak investigation of progressive atrophic rhinitis in an SPF pig population

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Progressive atrophic rhinitis (PAR) in pigs is caused by an infection with strains of capsule type A or D *Pasteurella multocida*. These are able to produce a dermonecrotic toxin encoded by the *toxA* gene. This induces necrosis and atrophy of the conchae resulting in deformity of the upper jaw. Suffering pigs have a reduced productivity. In Switzerland this disease was not observed in herds monitored by the Swiss Pig Health Service (90% of Swiss breeding herds) in recent years. Disease freedom is monitored by annual examination of 10 nasal swabs per herd in multiplying herds, cultural and by *toxA*-PCR. In August 2011, an outbreak of PAR was detected on a multiplying farm. A tracing back and forward was initiated focusing on (1) source of the pathogen on the index herd; and (2) spread of the disease via gilts sold during latency period. In 38 herds that had received gilts from the index herd since beginning of 2010, 20 nasal swabs were obtained for examination in culture and PCR. 17 herds were tested positive. Analysing the trading history revealed the most likely time period for infection of case 0 to be between August and November 2010. During this time and the preceding years, no animals had been introduced into this herd. The most likely sources were introduction from neighbouring fattening farms or by a seasonal worker from a country with endemic PAR infection who might have been a carrier of toxigenic *P. multocida*. Fattening farms in Switzerland are not free from infection; a transmission via vectors (cats, dogs, foxes, etc.) seems possible. The 3 closest fattening herds were tested negative during investigation but this does not surprise considering the time since infection and their all-in-all-out stocking system.

The development of a pork compartment in Chile

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Chile is one of the main pork export country in the world, based on high productivity and quality performance plus an extraordinary national animal health status. In order to offer a new sanitary guaranty to main import markets, a first compartment of pork, as OIE terrestrial code stated, has been developed by the main agribusiness company in Chile. The objective of this preventive compartment is to maintain regularity in exportation of pork products if an exotic disease event occurred in any other part of the country. The compartment is an integrated unit of 50,000 sows located in Atacama region in the north of Chile, representing the biggest pork farm in the nation. This includes local port, feed plant, reproduction, grow and fattening sites, and processing plant. Four diseases were included: Food and mouth disease, Aujeszky's disease, Classical swine fever and African swine fever. The epidemiological independence of the animal sub-population of the compartment and the rest of the national territory, were demonstrated based on OIE standards. Qualitative risk introduction and dissemination assessment were carried out to identify animal health issues to be managed by the company. An epidemiological characterization of the compartment surroundings was overcome to facilitate risk assessment. The risk management measures required, based on risk assessment findings, was identified in the company protocols already implemented. It was checked that bio-security, traceability, surveillance and contingency plan components were documented and applied as OIE guided, otherwise new measures were created. Main management measures were defined as critical control point (CCP) for private and official auditing and management purposes. The compartment was approved by the veterinary service according to the new official legislation and complementary it has been supported by OIE.

Anthelmintic resistance in Ontario sheep flocks

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Anthelmintic resistance (AR) has been reported in all major sheep-raising areas in the world, yet little is known about the AR status in Canada. This study was conducted to determine the frequency of AR for gastrointestinal nematodes (GIN) in Ontario sheep flocks. Forty-seven sheep flocks were enrolled in the study, and their level of GIN parasitism was monitored monthly by analyzing owner-acquired fecal samples from 15 grazing lambs per flock. When the average GIN fecal egg count (FEC) reached a threshold of 200 eggs/g, Ivomec™ was supplied to producers for the purpose of performing a drench check, and the reduction in average FEC 14 days after ivermectin treatment was calculated. 'Drench failure' was defined as a reduction in average FEC of $\leq 95\%$. In those flocks with drench failure, researchers performed a FEC reduction test (FECRT), enrolling 15 lambs in each of four treatment groups: control, ivermectin, fenbendazole and levamisole. The reduction in average FEC post-treatment for each treatment group was calculated using arithmetic means, and AR was defined as a reduction in average FEC of $< 95\%$ and a lower CI $< 90\%$. Approximately 85% (40/47) of farms reached the FEC threshold and subsequently performed an ivermectin drench check; 87.5% (35/40) of these farms had drench failure. FECRT was performed on 29 of the 35 farms. Ivermectin, fenbendazole and levamisole resistance was demonstrated on 93% (27/29), 100% (20/20) and 6% (1/17) of the farms tested, respectively. Geometric means, Bayesian analysis and regression techniques are being examined as alternative methods of AR identification. On these 29 tested farms, fenbendazole and ivermectin AR were common. Therefore, veterinarians and sheep producers should exercise judicious use of anthelmintics and incorporate alternative strategies of GIN control.

Scottish sheep movements and their potential for disease transmission

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Animal movements play a major role in the spread of livestock diseases. Identifying and targeting farms that are pivotal to the network of livestock movements would act to curb disease transmission. In addition, if it were possible to integrate the control of livestock infections such that a single control measure could target multiple diseases, the result would be an economical and efficient way to ease the burden of farm animal disease. Different diseases spread via different mechanisms, and therefore different types of contact are important in their spread. Thus the relevant movement network underlying the spread of one disease between farms may be very different from that involved in the spread of another. Here, we describe work to assess the possibility of targeting a subset of Scottish hill sheep farms that are 'important' in terms of the types of movements involved in both a rapidly-transmitting and a slowly-transmitting sheep disease. Importance is calculated as the product of the movements on to the farm (proportional to the probability of becoming infected) and the movements off the farm (proportional to the probability of spreading that infection). All movements could potentially spread a rapidly-transmitting disease, whereas only movements resulting in long residence times would be relevant to a slowly-transmitting disease. Farms important in terms of both types of movements were identified. Disease simulations were then used to assess the effect that removing this one subset of farms could have on reducing the spread of both rapidly-transmitting and slowly-transmitting diseases. This work raises the possibility that targeting controls at a single group of sheep farms may enable the holistic control of multiple infectious diseases within the national flock.

Actualization of strategies for national project on pest des petits ruminants control in Liberia

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Under the African Union (AU) Vaccines for the Control of Neglected Animal Diseases in Africa (VACNADA) programme, the Republic of Liberia instituted a nationwide mass vaccination project against Pest des Petits Ruminants (PPR), a killer disease of small ruminants that is enzootic in West Africa. An estimated 80% of sheep and goats population in the country was targeted for primary vaccination and booster in 2011 to attain antibody level above threshold immunity against PPR. Serological evaluation of sheep and goats' response to mass vaccination against PPR was subsequently carried out at the Central Veterinary Laboratory, Fendal, Liberia as part of the VACNADA-Liberia 2011 project. The aim was to evaluate outcome of the nationwide vaccination exercise and conduct real-time hands on training of Laboratory Technicians in the evaluation of mass vaccination exercises in-country. This paper presents the epidemiological strategies and achievements of the project. The authors present developments in the infrastructure for veterinary services in Liberia, with emphases on field epidemiology and technical manpower capacity development in the use of c-ELISA test in monitoring seroconversion among vaccinated animals. This project has made significant impact on reducing morbidity and mortality losses associated with PPR outbreaks in sheep and goats in the county. The 2011 mass vaccination against Pest des Petits Ruminants was mainly supported by the European Union and has contributed significantly to national capacity building for improving food security and animal health in Liberia.

Diagnostic tools to monitor udder health in dairy goats

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Disease monitoring is important to diagnose problems in health status of individual animals or an entire herd. To assess the udder health status of dairy animals, somatic cell count (SCC) and bacteriological culture (BC) are important diagnostic tools. This paper presents an overview of the practical application of these two tools in dairy goats and goat herds. In multiple recently published papers, we studied diagnostic aspects of SCC and BC in dairy goats. Bulk milk SCC and BC of bulk milk were studied in a large number of Dutch dairy goat herds. Seasonal fluctuations in SCC were studied over a three years period, and associations with risk factors were identified. At goat level, SCC and BC were studied in a longitudinal study, comprising about 500 goats in 5 herds, and test characteristics of SCC and BC were estimated using latent class models. These studies showed that SCC as well as BC are valuable tools for assessment of the udder health status of an individual goat and of a herd. However, both tests should be interpreted with caution. We observed a strong effect of stage of lactation and an effect of extended lactations on SCC. Therefore, the most optimal timing of SCC measurement in goats appeared to be around peak lactation and the interpretation of the results should account for the number of extended lactations. At goat-level, an SCC of $>1.5 \times 10^6$ cells/ml was indicative of *Staphylococcus aureus* infection. Bacterial culture of milk samples of individual goats was shown to be a specific, but insensitive test, which hampers its use as a confirmatory test of high SCC animals. BC of the bulk milk had low repeatability, but bulk milk SCC was positively related to the count of staphylococci. We will present practical guidelines to utilize and interpret these diagnostic tools at goat and herd level, taking into account the goat specific epidemiological background.

Monitoring of endemic goat's diseases using farms' health assessments done by private veterinarians
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As part of a dairy goat's disease surveillance network developing in Poitou-Charentes, France, veterinarians are participating to the monitoring of priority diseases at the regional scale. Since 2007, every farmer has to implement every year a health assessment of his herd with a veterinarian in order to be allowed to treat his animals on his own against specific diseases, respecting a precise protocol. In 2011, the health assessments done by seven practitioners in 144 dairy goat farms were used to identify and describe the priority diseases of each farm. The data standardization was made possible thanks to the conception of a specific form including a user-guide and 61 diseases case-definitions. Priority diseases identified in three age groups (pre-weaning, replacement herd and adults) were described by the main symptom observed, the main etiology suspected or confirmed, the estimates of the disease morbidity and mortality rates, the age class concerned and some free comments of the veterinarians. Annual mortality and culling rates were also recorded, as well as farms' characteristics (feeding, annual milk production...). The first results obtained have proven the functionality of this surveillance system. Actually, the results from 3 veterinarians, who provided more than 20 forms, show similar frequencies of priority diseases. Practitioners specialized in goats medicine consider that these first results are consistent with their own beliefs. Besides, most veterinarians recognize the simplicity and rapidity of the form filling. Despite the subjectivity of veterinarians in their choice of the farms priority diseases and the lack of precision of some results, this tool turns out to be adapted for the identification of priority diseases using veterinarians' expertise. Adaptations of this system are still required to encompass a larger number of veterinarians and maintain their participation on the long run.

Sharp decline in scrapie prevalence in The Netherlands after breeding for resistance: are we close to achieving eradication?

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In the Netherlands an ambitious programme to control scrapie in sheep was started in 1998, based on genetic selection of animals for breeding. From 2002 onwards EU regulations required intensive active scrapie surveillance as well as certain control measures in affected flocks. Here we use standard statistical methods as well as mathematical modelling to analyse: (1) data on genotype frequencies and scrapie prevalence in the Dutch sheep population obtained from both surveillance and affected flocks; (2) data on genotype frequencies in a random sample of flocks; and (3) postal survey results on between-flock differences in breeding strategy and flock management. Analysing the data (1) we find that the breeding programme has produced a steady increase in the level of genetic scrapie resistance in the Dutch sheep population. We also find that a few years later this was followed by a sharp decline in the prevalence of classical scrapie in tested animals. Notably, the estimated classical scrapie prevalence level per head of susceptible genotype declined significantly as well. This indicates that selective breeding has a disproportionate effect on infection prevalence, reminiscent of the well-known population effect of vaccination against a transmissible disease. The overall recent decline in classical scrapie prevalence in Dutch sheep suggests that eradication of the disease in The Netherlands may be within reach. However, a subset of farms may still continue to act as a core group for scrapie transmission for some time, as we show by analyzing between-flock heterogeneities using the data (2) and (3). In addition, genetic resistance levels may decline again in future as participation to the selective breeding programme has recently become voluntary.

Impact of farm management and premises on studies intending to develop housing systems for laying hens

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As farm management is a comprehensive issue innumerable hen environmenting factors have to be considered when intending to improve the housing conditions. Embedded within a network project on laying hens in German enriched colony housing systems this study was to assess the differences between onsite production conditions for laying hens in similar housing systems. Five experimental field stations were compared as conditions there were considered most similar and controllable. Questionnaire data was analysed performing hierarchical agglomerative cluster analyses for an overall dataset and different contextual subsets. A high degree of heterogeneity between the field stations was detected, which varied between different contextual subsets. In the contextual subset light, only the field stations FS 2 and FS 4 were similar according to the chosen criteria of similarity. In the subset climate the field stations FS 1 and FS 5 showed similarity. In the contextual subsets facility structure, nutrition, health/hygiene and workforce, the field stations FS 3 and FS 5 displayed similarity according to the preassigned criteria. The system itself hardly influenced the cluster structure, whereas the superordinate hierarchical levels, hen house and facility in general, had the strongest influence on cluster structures. The description of distance and similarity in general as well as within the contextual subsets provides a basis for analysis and interpretation of our network project's results. Analyses of specific influences on the welfare and health of laying hens should always consider the not investigated however significant influences from the contextual subset of farm management and farm premises related to the study question.

Infectious diseases and survival of Ethiopian village chickens

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The majority of chicken production in Ethiopia is in backyard flocks, where they are important to the livelihoods of rural smallholders, who identify infectious disease as a major production constraint. Epidemics during the rainy season are usually assumed to be Newcastle disease; however information on pathogens responsible or risk factors for infection is limited. We sampled 400 birds in the Ethiopian highlands before the rainy season, using stratified random sampling at 4 levels (Household, Village, Market shed and Region). Plasma and faecal samples were collected and birds were examined for ectoparasites. After the rainy season, farmers were re-interviewed to determine the fate of sampled birds. Plasma was tested for antibodies to Newcastle disease, Marek's disease, infectious bursal disease and *Salmonella enterica* O9 serotypes; all were prevalent in both regions. The most prevalent enteric parasites were *Eimeria* and ascarids. The most common ectoparasites were *Cnemidocoptes mutans* (scaly-leg mite) and lice. At follow-up, 202 survivors were identified (50.5%). Owners reported one in five birds had died of disease, and described various symptoms. Differences between regions and villages were evident, both in the amount of disease, and the degree of clustering at household level. Birds reported to have died of disease were compared to survivors, using mixed-effects models. Univariable analysis suggests a strong effect of region; other risk factors, including previous infections, may also be important. Multivariable analyses are underway to investigate these factors further. In conclusion, multiple diseases may be of importance in village chickens in Ethiopia, with differences at regional and more local levels in patterns of disease occurrence. Improving surveillance through increasing the use of diagnostic facilities is important to develop control strategies tailored to local needs.

Social network analyses of Bali live bird markets

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This paper presents the results of a survey of live-bird markets in Bali during September 2010, analysed using Social network analyses. The objective of the study was to describe contact structures within the live-bird marketing system across Bali to identify important sources and destinations of live-birds as a means to identify areas at higher risk of HPAI incursion or transmission. Within markets, vendors, drivers and market authorities were interviewed. Eighty-four out of 86 (response rate of 97.6%) officially listed live bird markets were visited. The study identified a number of districts as important sources of live birds at markets during the study period. These districts should therefore be targeted as part of a surveillance/prevention programme for poultry diseases. Contact were made across all districts in Bali, implying a potential for rapid disease or information spread through markets across the island. A small number of markets in four districts had relatively high betweenness scores indicating their role in controlling the flow of live-birds across Bali. The movement of birds to markets did not appear to have a seasonal influence which may be a reflection of the large number of festivals which occur throughout the year in Bali. A number of markets were identified as riskier in terms of their potential role in the spread of disease based on a number of criteria. To better identify risky markets it may be necessary to have a group of experts from Bali rank each market in terms of risk. This then would provide a more informed categorization of market risk for disease transmission or spread.

The efficiency of wire nets as a means of enhancing the biosecurity of poultry in Brazil

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The aim of this study was to evaluate the efficiency of wire nets of different mesh sizes as a means to enhance biosecurity of the poultry industry in Brazil by preventing other bird species from entering chicken houses. The Brazilian poultry industry is technically advanced and employs updated technology. A recent agricultural Act, Normative Instruction (IN) No. 59, recommends 25.40 mm mesh. However, scientific proof regarding the efficiency of this measure is lacking. In this study, a bird biometric methodology was developed for evaluating bird species. The methodology was based on a few body dimensions, and it used a new statistical design for analysis of the data. Three groups of bird species were formed according to a criterion of importance. The value of this criterion was estimated in terms of the ability of birds to pass through the net. The paradigm was used to study 23 wild avian species naturally occurring in Brazil. The best results were observed for nets with mesh ≤ 19.11 mm. This mesh size was efficient for restraining all species studied. However, the net mesh (25.40 mm) recommended by Act IN No. 59 could not restrain some of the bird species examined and was therefore considered inefficient as a means of ensuring the biosecurity of poultry houses.

Risk factors for *Campylobacter* infection in Danish broiler production

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Data from the Quality Assurance system in Danish Broiler Production (KIK system) were analysed to identify within farm biosecurity and management related risk factors for *Campylobacter* infection in Danish broiler flocks. In the study, data from 2835 flocks originating from 187 farms reared from December 2009 to November 2010 were included. The PCR test results of fecal samples collected on socks revealed that 14% of the Danish broiler flocks were positive for *Campylobacter* during the study period. Fifty five percent of the flocks were positive during the summer, and related to areas where clustering of infected farms was identified in previous conducted studies. The median number of people working in, or with an access for entering, broiler houses was 2 (from 1 to 7). For 311 flocks (12%), the previous flock in the house had a positive status. Median slaughter age of the birds was 35 days (from 31 to 61 days). A multivariable logistic regression model with a random effect of farm was performed. The analysis revealed a higher risk for positive infection status during summer time: OR=13.30, (95% CI: 6.56-26.90) and a higher risk if more than one person had access to the house: OR=2.16, (95% CI: 1.25-3.72). Furthermore, a higher risk was seen if the test result for the previous flock from the same house was positive: OR=1.67, (95% CI: 1.10-2.52) and if the average slaughter age of the birds was more than 35 days: OR=1.50, (95% CI: 1.07-2.09). The continuous variable 'establishment year of the house' was found significantly associated with the infection status of the flock with a P=0.02 and an OR=0.98, (95% CI: 0.97-0.99).

What promotes the circulation of HPAI H5N1 in Indonesia: a descriptive analysis of a network of moving duck farmers, rice paddy owners, duck transporters and hatcheries

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Ducks can harbour HPAI H5N1 virus, thereby promoting its spread in the field. HPAI H5N1 endemicity in Indonesia is likely associated with the high density of ducks in that country. Consequently previous investigations focussed on identifying hazards related to the management of duck flocks by their owners, but various other occupations are also associated with duck production. For example, moving duck flock farmers are part of a network that also comprises rice paddy owners who provide paddies for scavenging, duck transporters who move ducks to and from scavenging locations and hatcheries which purchase eggs and sell ducklings to the farmers. Therefore, in 2009 we conducted cross-sectional surveys and interviewed total of 121 rice paddy owners, 30 transporters and 75 hatchery owners in Indonesia. We used descriptive statistics, descriptive social network analysis and descriptive spatial analysis to identify interrelationships of members of this network, movement patterns of duck flocks and bio-security factors possibly influencing the dissemination of HPAI virus. For example, the number and frequency of duck flocks allowed scavenging per paddy and the disposal practices of carcasses found by rice field owners were identified as important risk factors for HPAI spread. Furthermore, the cost-reducing practice of combining flocks from different farms or the mixture of duck flocks with other poultry types and poultry feed during transport as well as a lack of disinfection in both, transport vehicles and hatcheries, presented further high-risk management practices. The complexity of the duck production network was further highlighted in the identified spatial travel patterns of moving duck flocks. Based on our results, we highlight recommendations for HPAI control that go beyond the management of ducks on farms and also consider other members of the community involved in duck production.

Online survey of health prophylaxis and management practices on Swiss dairy farms

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Health prophylaxis and management practices play a major role in the success of dairy herd health programs. Many prophylactic measures have been described and advised, however, there is little data available on how these or other measures are valued and implemented in the field. The aims of this study were to gather information regarding the most important and frequently used dairy farm prophylactic measures, and to identify links between such measures and certain disease outcomes. A trilingual online questionnaire was designed that contained 75 questions divided into 5 sections (general farm management, feeding practices, reproductive management, udder health and demographic information). The questionnaire was sent by email in March 2011 to a stratified random sample of 2,285 Swiss dairy farmers, of which more than 50% responded. Management practices varied considerably between dairy farms; 51% used homeopathy, 57% herbal medicine, 50% prophylactic antihelminthic treatments, 93% antimicrobial dry-cow treatments, 77% post-milking teat disinfection, 55% propylenglycol supplements before or after calving, 88% calcium supplements at calving and 79% magnesium supplements. Herd size, regional variation and barn type played an important role in the implementation of different prophylactic measures. Currently, negative binomial regression models are being used to identify factors associated with (1) incidence of clinical mastitis; and (2) monthly somatic cell counts >200,000 cells/ml for tie-stalls and free-stalls separately. These results will be presented during the conference.

Epidemiological investigations of bovine enzootic haematuria in Bhutan

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A chronic, debilitating disease of grazed cattle known as bovine enzootic haematuria (BEH), characterised by either continuous or intermittent passage of red urine was formally recognised in Bhutan in the early 1990s however it is likely that the condition has been present in the country well before that time. Given that bracken fern (*Pteridium revolutum*) grows in abundance in most areas of the country and the consistency of the clinical signs and *post mortem* findings from cases with literature reports of bracken fern toxicity, it can be assumed that bracken fern toxicity is the primary cause of BEH in the Bhutanese cattle population. In September 2011 the authors of this paper took part in an intensive one-month project to develop a strategy to minimise the impact of BEH on the health and productivity of Bhutanese cattle. Two field studies designed to better understand the epidemiological features of BEH in the Bhutanese context were the key recommendations from the strategy development project. The first was a cross-sectional survey to determine the demographic features of the cattle population, with an outcome being an estimate of the total years of productive life lost attributable to BEH. The second was a case-control study to identify risk factors for BEH operating at: (1) the individual cow; (2) the household; and (3) environmental level. In February 2012 field work commenced to collect data for the cross-sectional and case-control studies. This talk will discuss aspects of the design and implementation of the two studies in particular issues related to case definition, selection of controls for the case-control study and sample size considerations that needed to be taken into account when the prevalence of exposure was expected to be relatively high.

Mastitis control in Swedish dairy herds

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Mastitis remains a major issue in dairy production despite research efforts and control programs. The aim of this study was to investigate the degree to which recommended control practices are being implemented. Data on herd characteristics and applied preventive measures were collected through a postal questionnaire, and 428 usable answers were obtained (response rate 48%). Cleaning of stalls at least 2 times daily and replacement of teatcup liners according to recommendations were performed in over 90% of the herds. In more than 80% of the herds, cows were treated with a postmilking teat disinfectant and feeding plans were continuously gone through and revised. Herds with tiestalls grouped lactating cows according to udder health status twice as often as herds with freestalls and milking parlour (70% and 35%, respectively). Herds with automatic milking systems rarely considered udder health status when grouping their lactating cows (7%). Very few herds (7%) grouped dry cows according to udder health status. Half of the herds allowed cows to calve in single pens that were cleaned between animals, this was however implemented in only 27% of the tiestall herds. A milking order based on udder health status was applied in over 80% of the tiestall herds, whereas two thirds of the herds with freestalls and milking parlour and almost all of the herds with automatic milking systems ignored the udder health status of cows during milkings. Freestall herds with milking parlour more frequently used milkers' gloves, washed dirty udders with water, stimulated hardmilking cows manually, and rinsed clusters with warm water after milking cows with clinical mastitis or high somatic cell count as compared with tiestall herds. It was concluded that advisors must emphasize the importance of grouping of cows according to udder health status and calving hygiene. Furthermore, special attention should be paid to tiestall herds and herds with automatic milking systems where the implementation rates are lower than in freestall herds with milking parlour.

Effect of different dry period lengths on milk production in subsequent lactation

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In recent years, growing interest has developed toward a shorter dry period (DP) as a management strategy which could be more appropriate for today's high-producing dairy cows. Several options exist in applying this management strategy, like complete omission of the DP for all cows in the herd, or cow-specific DP lengths. The aim of this study is to determine the effect of both DP management strategies on subsequent milk production. In the Netherlands, five commercial farms started in the beginning of 2011 with a complete omission of the DP for all cows. From these herds, information on 333 cows (1,514 monthly test-day records) was available. Test days of the year before applying complete omission of the DP are used as control (386 cows, 2,126 test days). Six other commercial farms decide, based on milk yield and somatic cell count, for each individual cow for no DP (59 cows, 246 test days), a short DP (<30 days) (77 cows, 555 test days) or a conventional DP (>30 days) (209 cows, 1,386 test days). A non-linear regression model incorporating an autoregressive covariance structure accounting for repeated test-day yields within cow was developed to estimate the daily yield (milk, fat and protein) of all cows. For day 1 till 300 d of lactation, average daily milk yield was significantly lower for cows without a DP (23.0 kg) compared with control cows (29.7 kg). On farms with cow-specific DP lengths, daily milk yields were 25.3, 29.4 and 32.2 kg (P <0.05) for the three DP length groups. Research is ongoing to study precalving milk yields and effects of different DP strategies on milk yield during subsequent lactations.

Risk factors for *Staphylococcus aureus* in bulk tank milk samples from Swiss dairy herds

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Mastitis is a frequent problem in Swiss dairy herds and it has a significant economic impact. One of the main pathogens causing subclinical and clinical mastitis is *Staphylococcus aureus*. The aim of this study was to identify risk factors for the presence of *S. aureus* in bulk tank milk (BTM) samples from Swiss dairy herds. One hundred herds with a theoretical BTM somatic cell count between 200,000 and 300,000 cells/ml in 2010 were recruited and visited once during milking time in 2011. A standardized protocol investigating farm specific data, milking equipment, milking routine and hygiene was filled out. A sample of BTM was taken and tested by quantitative PCR for the presence of the *S. aureus*-specific nuc gene. This resulted in a *S. aureus*-prevalence of 48% (farms with single-visit positive bulk milk samples). Multivariable logistic regression models are currently being developed to identify risk factors for presence of *S. aureus* in BTM samples. This is the first study identifying risk factors for *S. aureus* in BTM from a nation-wide sample of mastitis problem herds. Detection of risk factors will help defining possible intervention strategies to improve udder health in *S. aureus* positive herds.

Are treatment decisions regarding mild clinical mastitis in dairy cows influenced by farmer and herd characteristics?

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In the Nordic countries, i.e. Denmark, Finland, Norway and Sweden, the legal requirement is that a cow has to be examined by a veterinarian before antibiotics can be prescribed. Consequently the farmer's perceived needs for antibiotic treatment of the cow with mastitis will affect whether a veterinarian is contacted or not. As disease recording is based on veterinary registrations, the incidence of treated and recorded mastitis cases is influenced by the behaviour of the farmer when detecting a case of mild clinical mastitis (MCM). Nordic dairy farmers have previously been shown to differ regarding this behaviour. The study used a questionnaire based on the Theory of Planned Behaviour (TPB). According to TPB a person's behavioural intention is a proxy for the actual behaviour and is decided by three psychological constructs; attitude, subjective norm and perceived behavioural control of the behaviour. It was shown that the behavioural intention to contact a veterinarian for a visit to the herd the same day as detecting a case of MCM was significantly lower in Sweden compared to the other Nordic countries. It was further demonstrated that several demographic parameters, e.g. the milking system and the farmer's own rating of the mastitis incidence in the herd, were associated with the farmers' behavioural intention to contact a veterinarian. It was also found that in all four Nordic countries, the attitude of the farmers was the most influential predictor of behavioural intention in the TPB model. Therefore, the objective of the present study was to further explore how the attitudes to mild clinical mastitis are influenced by the farmer and herd characteristics. This study will include the responses from the Swedish farmers (n=199, 52% of distributed questionnaires). Results from linear model analyses of the associations will be presented.

Relationships between milk urea and somatic cell counts using a large database

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Relationships between high nitrogen diets and somatic cell counts (SCC) are ambiguous. A positive association is evocated by practitioners, but ex-vivo trials showed various effects of high nitrogen diets on neutrophils, depending on the nature of the excess (acute or chronic). The aim of this study is to evaluate the relationship between milk urea (MU) (as indicator of diet nitrogen level) and SCC. 35 million cow-test results and 120,000 test-day herd MU means were used. MU values <50 mg/l were excluded. Static and dynamic panel models were used to test the within farm association of the monthly herd composite mean SCC (CMSCC) and the monthly MU of the current or previous months, including milk production, herd size and lactation stage (...) in the models. A normal distribution of MU was noticed, and the average cow-test and herd test-day MU were both 260 mg/l (SD=80 mg/l). The correlation between MU and SCC, MU and milk production and SCC and milk production were -0.08, +0.05 and -0.10 (cow-test) and -0.07, +0.07 and -0.20 (herd-level test-day), respectively. The results of the static and dynamic panel models showed a positive association between MU and SCC of the same month: a 10 mg/l increase in MU was associated with up to a 5% increase in CMSCC. The dynamic analysis showed a negative association between CMSCC of one month and the urea of the previous month. For both models, CMSCC was also associated negatively with the milk production. The negative correlation of MU and SCC could come from the dilution effect of the milk production on SCC (negative correlation), as suggested by the positive correlation of milk production and MU. The panel model showed that CMSCC was positively associated with the current MU, when the milk production was taken into account. The negative association occurs for the urea of the previous month. This is in agreement with results of our lab showing opposite effects of chronic and acute nitrogen excesses on neutrophils.

Evaluation of udder health based on real-time PCR on bulk tank milk

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Since 2009 bulk tank milk from all Danish dairy herds has been tested once per year by a single bulk tank milk sample using a real-time PCR kit (PathoProof Mastitis PCR Assay, Thermo Fisher Scientific, Vantaa, Finland). To evaluate the variation over time of the PCR results 30 herds which had previously tested positive with low Ct values (strong reaction) for *Staphylococcus aureus* or *Streptococcus agalactiae* were sampled repeatedly once per month in 12 months, once per milk delivery for one month (typically every second day) and within that month all cows in the herds were sampled once on the same day. Sampling was finished in December 2011. Results from all Danish herds sampled in both 2009, 2010 and 2011 (n=3,828) was also available for analysis of variation between years. The presentations will evaluate the variation in PCR results over time (year, month, day) and discuss the value of single samples compared to repeated sampling. Furthermore the relation between bulk tank PCR and herd prevalence of different major mastitis pathogens will be discussed.

Impact of coagulase-negative staphylococci on 305-days milk production in dairy cattle

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Coagulase-negative staphylococci (CNS) are a large group of organisms that are considered as minor udder pathogens. As in most other developed dairy countries, they are the most frequently isolated bacteria from udder quarters of Canadian dairy cows. In a Belgian study, heifers infected with CNS in early lactation had a higher milk yield during their first 285 days in milk compared to their non-infected herd mates or heifers infected with a major pathogen. However, no data are available on adult cows. There is a lack of information about the impact of CNS intramammary infections (IMI) on udder health and production in Canadian dairy herds, and consequently, the present study was conducted on 89 dairy farms of the Canadian Bovine Mastitis Research Network (CBMRN) in four regions of Canada. In total, 137,316 milk samples were collected and recorded in the CBMRN database over a period of two years (January 2007-December 2008). Bacterial culturing and identification was done as per NMC guidelines. Cows were classified as culture-negative (CNEG) (all 4 quarters), major pathogen (MP) positive (at least 1 quarter), CNS-positive (at least 1 quarter, no major pathogen), or other minor pathogen (OMP) positive (at least 1 quarter, no major pathogen). 305-days milk yield data were extracted from the DHI milk production database. Generalized linear regression model will be built to determine the impact of CNS IMI on 305-days milk production. Mean 305-days milk yield (kg) of cows in different parities was as under: Parity 1: CNEG (10,311) > CNS (10,082) > MP (9,785) > OMP (9,648) Parity 2: CNEG (10,629) > CNS (10,566) > OMP (10,363) > MP (10,136) Parity 3: CNEG (10,963) > CNS (10,817) > OMP (10,733) > MP (10,688) Preliminary results indicate that cows with CNS IMI had higher 305-days milk production than cows infected with major pathogens or other minor pathogens. The results suggest a protective role of CNS in udder health.

Lameness in dairy cows: using gait score as a predictor for claw lesions

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Early detection of lameness is critical for optimizing treatment plans and reducing economic loss. It is commonly thought that lameness relates directly to the occurrence of either infectious or non-infectious claw lesions. The intent of our study was to evaluate the use of gait scoring as a tool to identify cows with claw lesions. Materials and Data were collected on 80 free stall dairy farms. It included video recordings to assess gait score by trained observers of 40 Holstein cows from each herd. Limping (L), asymmetric steps (A) and head bob (H) were the 3 clinical signs recorded. To categorize a cow as lame, the clinical sign L had to be present. Claw lesions were identified by 7 trained hoof trimmers and recorded using a computerised system (Hoof Supervisor®). Gait scores were recorded within 4 weeks before the hoof trimmer's visit. Not all gait scored cows were trimmed. Association between lameness and the presence of claw lesions was analyzed using Chi-square statistics. Sensitivity and specificity were calculated to demonstrate the ability of gait score to identify the presence of claw lesions. Preliminary analysis of 1,370 cows showed that 18.6% were clinically lame. Overall, no lesions were found on 63% of the trimmed cows, 24% had one and 13% had more than one claw lesion. Digital dermatitis was the most prevalent claw lesion (35%), followed by sole ulcers (16%), white line lesion (16%) and sole haemorrhage (9%). A alone detected 49%, L alone 43%, and H alone 41% of the cows with claw lesions. However, by combining the clinical signs A+L+H a sensitivity of 70% and a specificity of 60% were achieved. There is limited value in the use of gait scoring as a tool for early identification of claw lesions.

Effect of access to pasture on claw health in Swedish dairy cows

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Our objective was to study the effect of access to pasture on claw health in dairy cows. Factors of interest were the length of the pasture period, hours per day with access to pasture and cow density at pasture. Information on housing and pasture management in 2010 were collected from farmers by phone interviews. Information on individual cows, such as claw-trimmings and parity, were retrieved from the Swedish Dairy Association. The risk of having a claw disorder at claw trimming after the pasture period was analyzed at the individual level using multilevel logistic regression and including claw trimmer and herd as random effects. The diagnoses analyzed were; dermatitis (mild), digital dermatitis (severe dermatitis, DD), sole ulcer (also including severe sole haemorrhage) and heel horn erosion. Information from 174 herds and 16,364 cows were used in the analyses (76 and 41 herds for dermatitis and DD). The median (10th/ 90th percentile) length of the pasture period was 123 days (92/ 153), hours per day with access to pasture was 11 hours (6/ 20) and cow density was 4.6 cows per ha pasture (1.9/ 15.2). Significant associations were found between the length of the pasture period and the risk of sole ulcer and between the amount of daily access to pasture and DD. However, the risk for either of these disorders did not decrease linearly with a longer pasture period or with a higher daily access to pasture. Cow density at pasture was significantly associated with the risk of sole ulcer, dermatitis and DD. The risk of dermatitis and sole ulcer were highest in herds with the highest cow density but the risk of DD did not decrease with lower cow density. In conclusion, in our study most cows had access to pasture to a larger extent than the law stipulates. The amount of pasture was associated to sole ulcer, dermatitis and DD but not to heel horn erosion. We expected a decreased risk of claw disorders with increasing access to pasture but this pattern was not seen.

Factors affecting the incidence of calf diarrhea in Iranian Holstein dairy herds

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Neonatal calf diarrhea is one of the most important causes of economic loss in dairy herds. The objective of this study was to identify risk factors associated with the incidence of calf diarrhea in large dairy herds in Iran. 3214 calves which were born in eight dairy herds between 21 March 2009 and 20 March 2010, were followed for 90 days after birth. For each live birth, the sex of calf, the parity of the dam, the type of parturition and season of birth were retrieved. Also, occurrence of diarrhea before 90 days of age was recorded. Logistic regression model was used to evaluate the effects of explanatory variables on occurrence of calf diarrhea. 1550 (48.2%) of calves were affected with diarrhea. Incidence risk of calf diarrhea was 22 per 100 animal-month at risk. Calves born in the summer had a significantly higher risk of diarrhea [OR: 1.73 (95% CI: 1.42-2.10)] than winter-born calves. Calves born from a difficult calving had an odds ratio of 1.43 (95% CI: 1.13-1.80) of diarrhea compared with those born from a normal calving. Also, probability of occurrence of calf diarrhea for calves born from multiparous dairy cows were 1.39 (95% CI: 1.20-1.62) times greater than those born from primiparous dairy cows. The results showed that high proportion of calves are affected with diarrhea during the preweaning period in Iranian dairy herds indicating economic importance and that environmental and management factors affect the incidence risk of calf diarrhea.

Risk factors for recurrent TB infection in New Zealand: an investigation using time dependent covariates in a Cox proportional hazards regression model

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Recurrence of infection with bovine tuberculosis (TB) in cattle and deer herds that have previously tested to a clear status is a problem that has recently become more apparent in New Zealand. Uncontrolled movements from these herds pose a risk to the TB eradication strategy. A retrospective cohort study was conducted to identify herd-level risk factors for TB recurrence. Data were collected from 356 New Zealand cattle and deer herds that met the following criteria: (1) a culture positive case of TB had been identified on or after 1 June 2006 (the 'first' TB episode); (2) the herd status had been cleared by testing that was completed by 1 November 2010; and (3) the clear status was not achieved by destocking. A Cox proportional hazards model was developed to quantify factors influencing the outcome. There was a positive relationship between (1) the monthly hazard of recurrence and the number of TB episodes in a herd prior to the first episode (HR 3.2 for two prior episodes, 95% CI 1.2-8.5; HR 86.7 for five prior episodes, 95% CI 13.3-564.9); and (2) the presence of more than one lesioned animal at the first TB episode (HR 2.3: 95% CI 1.2-4.3). The time dependent covariate showed that the monthly hazard of recurrence during the first 2 years after clearance was significantly increased in herds with one or more reactors at the final test (HR 2.8: 95% CI 1.2-6.4), but this effect was not observed more than 2 years after clearance (HR 1.5: 95% CI 0.6-3.6). We conclude that the presence of unresolved infection in a herd is a contributor to further TB breakdowns in the first two years after clearance. The Animal Health Board is reviewing policies to increase the sensitivity of detecting residual infection before clearance and to intensify post clearance testing and movement tracking in herds with risk factors.

Comparison of management characteristics between *Mycobacterium avium* subspecies *paratuberculosis* positive and negative herds

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The between-herd and within-herd prevalence of *Mycobacterium avium* subspecies *paratuberculosis* (MAP) infection on dairy farms is influenced by specific management practices. The Alberta Johne's Disease Initiative (AJDI) assesses farm-specific best management practices (BMPs) using a 34-question risk assessment. The associated MAP status of the herd is determined with six environmental fecal samples. The objective of this study is to compare BMPs between MAP-positive and negative herds. The AJDI goal is to have 80% (480 herds) of Alberta dairy farms participating in the program by December 31, 2012. As of January 1, 2012, uniformly trained veterinarians have collected environmental samples and completed risk assessments at 201 (35%) participating farms. Preliminary results analysing 159 matched risk assessments and fecal sample sets indicate that MAP-environmental sample positive herds (n=34) were significantly more likely to spread manure on pastures where heifers graze in the same year than MAP-negative herds (n=125). Water troughs and food bunks of MAP-negative herds were less frequently contaminated with manure. Herd size was higher in MAP-positive herds compared to MAP-negative herds. In MAP-positive herds, the number of positive environmental samples increased with an increasing herd size. Based on the first set of farms, we have detected a difference in management between positive and negative herds, which indicates that best management practices are effective tools to control MAP on dairy farms. As the sample size increases, confounding effects of farm characteristics on the relationship between MAP infection status and management practices will be determined. Also, potential differences in evaluating management practices between participating veterinarians will be analysed and presented.

Can information derived from the analysis of farm-to-farm movement events be used as a predictor of bovine tuberculosis breakdown risk?

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Since 1995 the national milk recording authority in New Zealand, Livestock Improvement Corporation (LIC), has provided facilities to allow herd managers to record details of movements of individual dairy cows from one farm to another. While the main purpose of this service is to allow production records to be transferred when animals are sold to another herd for milking, it is likely that information derived from the analysis of farm-to-farm movement events should also be able to be used as a predictor of herd level tuberculosis (TB) breakdown risk. This was a retrospective cohort study of New Zealand dairy enterprises that used the herd recording facilities of LIC during the period 1 July 1995 to 30 June 2010. Social network analyses were carried out on herds that recorded farm-to-farm movements of dairy cattle during each of the 15, 12-month intervals during this time frame. Herds included in each of the social network analyses were matched with TB information kept by the Animal Health Board. Data was used that defined historical disease status and areas with differential risk of infection transfer from wildlife. Our hypothesis was that a herd breaking down due to movement risk in a given year depended on network characteristics accumulated during the previous five years. The number of dairy cow movement events ranged from 6.5 to 13.5 million per year. For the majority of herds network parameters were relatively constant from one year to the next. In a small number of herds network parameters were more variable: presumably due to a change in ownership or due to a management decision to increase or decrease herd size. TB breakdown risk was associated with herd in-degree and the TB status of areas supplying incoming movement events.

Risk analysis approach applied to the development of compartment for BTB control

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Chile has become a net exporter of milk and dairy products in recent years with nearly 20 thousand farms and a half million milking cows. For over 25 years, the country has developed a voluntary free bovine tuberculosis (BTB) certification scheme and still herd prevalence are high, between 24% and 2,6% in central and south of country respectively. In 2011 started the National Control and Eradication of BTB, using a strategy based on the development of compartment for farms suppliers to dairy industry, as OIE terrestrial code oriented. In order to deal with epidemiological variability among farms and to facilitate the development of compartments, a method to assess and monitor BTB risk in dairy BTB farms has been designated. Risk of introduction, exposure and dissemination of BTB in farms that are part of a dairy compartment were carried out. Semi quantitative risk analysis guided by OIE and HACCP approach has been used in the methods. Possible routes of entry to domestic animals, wildlife and human as well as equipment and transportation vehicles, food and water sources were assessed. Possible routes of exposure and dissemination of BTB were considered like contact between farm animals, diagnosis and elimination of infected, shared facilities and equipment, food, water use and working staff. Special consideration was taken to the neighboring properties, characterizing them according to their level of risk. Critical control points were established for main bio-security measures for their control. Finally, a pilot study of compartment to control BTB in central Chile was conducted to test the methodology proposed, estimating the risk of BTB compartment.

Milk quality assurance programme for paratuberculosis results in increasing proportion of test-negative dairy herds

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In 2006, a milk quality assurance program (MQAP) for paratuberculosis in Dutch dairy herds was initiated. The aim of the MQAP is to reduce the concentration of *Mycobacterium avium* subsp. *paratuberculosis* in milk delivered to the milk factories. Herds participating in the MQAP are assigned a herd status based on the results of herd examinations by individual milk-ELISA. Farmers are entitled to confirm positive ELISA results by faecal culture. Test-negative herds are assigned status 'A'. Test-positive herds are assigned status 'B' (if all test-positive cattle have been removed from the herd) or status 'C' (if any test-positive cattle are retained in the herd). The MQAP promotes preventive management measures and culling of test-positive cattle to reduce the spread of Map. On the herd-level, these measures increase the probability to obtain and maintain status A. On the national level, these measures taken by individual farmers increase the milk quality of the national dairy herd. The aim of this paper is to present results obtained over a six-year period (2006-2011) in the first cohort of 711 herds that voluntarily entered the MQAP in 2006-2007 without prior participation in a paratuberculosis programme. To date, 30% of the 711 herds have consistently had status A, 15% of the herds have consistently had status B or C, and 54% of the herds had transitions between status A and status B or C. At all, the proportion of status A herds increased from 45% upon the initial assessment to 75% at five years after the initial assessment. It is concluded that the programme results in an increase of the proportion of status A (test-negative) herds over time. Based on the results achieved in the programme, the Dutch dairy processing industries are requiring all dairy herds delivering milk to their factories to have at least status 'B' since January 2011.

Herd-level risk factors for bovine brucellosis in Brazil

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Brazil launched a new and ambitious nationwide programme to control and eradicate bovine brucellosis in 2001. Between 2001 and 2004, studies of prevalence and risk factors associated with this disease were carried out to characterize the epidemiological situation of 14 Brazilian states and 65 regions within them. The published results revealed important differences in prevalence of brucellosis among several regions. Data from 17100 herds were consolidated and statistically analyzed for the investigation of risk factors at the herd-level. After an exploratory analysis of variables by the chi-square test, all variables with a $P \leq 0.20$, were included in a multiple logistic regression model. The result revealed that the herd traits associated with the presence of brucellosis were the herd size, measured by the number of females, and the purchase of breeding cattle. The risk of infection, indirectly estimated by the odds ratio (OR), was 1.25 higher [95% CI: 1.12-1.40] at farms that purchase breeding cattle. Compared with the baseline category, i.e. herds with less than 30 females, the Odds Ratio for herd size was 1.94 [1.68-2.23] for herds with 31 to 100 females, 2.98 [2.55-3.49] for those with 101 to 400 females, and 5.56 [4.53-6.82] for herds with more than 400 females. These results show that open herds, as well as larger herds, which are mostly dedicated to extensive beef production, have higher probability of introduction and maintenance of bovine brucellosis. This is consistent with the geographical distribution observed in prevalence studies and is likely to account for the high herd prevalence found in the states of the Midwest and neighbouring regions.

Herd-level risk factors associated with seropositivity for antileptospiral agglutinins in dairy cattle: Minas Gerais, Brazil, 2010

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Our objective was to determine herd-level risk factors associated with seropositivity for *Leptospira* spp. in a large number of randomly selected Brazilian dairy herds. Serum samples were obtained from 2,915 randomly selected cows from 151 herds in eleven municipalities located in the Sete Lagoas microregion, a large dairy cattle region. The technique used was the microscopic agglutination test (MAT) for leptospirosis agglutinins. All herd-level predictors were obtained through personal interviews with questionnaires administered to each farm manager. A logistic-regression model was built using *Leptospira* spp. serostatus at the herd-level as the outcome variable. All variables were first subjected to univariate analysis, where those with a significance level ($P < 0.20$) were subsequently used for the development of multivariate models ($P < 0.05$), which were divided into two categories: animal's management and biosecurity. In the category of animal's management, the use of rotational grazing for dairy cows (OR=3.52) was set up as a risk factor. The protection factors were shelter for calves in individual houses (OR=0.17), the bull does not stay in a paddock collective (OR=0.05) and provide milk replacer for calves (OR=0.25). In the questions relating to biosafety, the presence of a Medical Veterinarian in the property was a protective factor (OR=0.20) and the factors controlling ectoparasites by injection (OR=2.82), using the same equipment for cleaning up the environment for feeding animals (OR=3.58) and the request for serological tests of the animals before purchasing (OR=4.46), due to examination of leptospirosis is not part of this routine, are risk factors for the disease. Funding: CNPq, FAPEMIG and INCT-Pecuária.

Factors associated with morbidity, mortality, and growth of dairy heifer calves up to 3 months of age

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Calfhood diseases and mortality have substantial impacts on many dairy operations. The objective of this observational study was to investigate risk factors associated with enzootic calf diarrhea (scours), bovine respiratory disease (BRD), mortality, and growth in young dairy heifers. A total of 2,874 heifer calves from 19 commercial dairy farms in Minnesota, USA and Ontario, Canada were enrolled at 1 to 7 d of age and followed for 3 months. The incidence of failure of passive transfer (FPT) was 11 and 32%, using cut-points of serum total protein of 5.2 and 5.7 g/dl, respectively. Over 23% of calves were treated for scours and risk factors were herd incidence of scours, season of birth, receiving a colostrum replacement product, not being fed colostrum by bottle, and weight at enrollment. Almost 22% of calves were treated for BRD and risk factors included FPT, herd incidence of BRD, season of birth, navel dipping, and being treated for diseases other than diarrhea or dullness. Supplemental antibody products were associated with a reduced incidence. Mortality risk was 3.5% and was increased by herd-level incidence of BRD, and calf-level treatment for BRD and other diseases. The mean average daily gain was 0.95 kg/day and was influenced by twinning status, FTP, and treatment for diarrhea or dullness. This study identified several important factors associated with morbidity, mortality, and reduced growth. It reinforces the interconnectedness of multiple diseases and the importance of good colostrum management. This study also highlights the significant effects of calfhood disease, adding further evidence that improving calf health can improve growth and survival.

The interaction between *Theileria parva* and *Theileria mutans* and the association with clinical outcomes

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East Coast Fever (the clinical disease associated with the tick borne parasite, *Theileria parva*) is a major restriction on cattle production in East and Southern Africa. Fatal to most European breed cattle, there is believed to be a tolerance to the disease in the indigenous short horn zebu (SHZ) cattle breed. However, indigenous breed calves also experience mortality from ECF with reported rates varying from 3 to 25%. A cohort of 548 SHZ calves was followed from birth until 1 year old. They were examined and sampled frequently, with longitudinal data available for growth, blood parameters, antibody levels, and for intestinal worm burden. Autopsies and extensive testing was carried on dead animals to establish cause of death. This data has offered an opportunity to examine the interactions between infections in a non-experimental setting. 72% of the calves were exposed to *T. parva* before they left the study, but only 35 of the 548 calves died from ECF. The aim of this work was to explore the differences between those calves that died and those that survived following exposure to *T. parva*. Each of the 35 ECF deaths was matched by proximity to 2 controls that survived but were exposed to *T. parva* during their time in the study. The most significant association with survival was being infected with *T. mutans* prior to exposure to *T. parva*. This very significantly reduced the odds of being a case. This work offers an interesting example of how pathogens can interact to change clinical outcome.

Uptake and use of cattle vaccines in the UK

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The aim of this study was to investigate current uptake and use of vaccines available to the dairy and beef industry in the UK. The existing evidence indicates a lack of compliance from farmers with regards to correct application of a vaccine. A questionnaire was distributed to dairy and beef farmers between September and October 2011. The questionnaire collected information on which vaccines were used and how and why farmers were using these vaccines. The majority of respondents administered vaccines within the timeframe recommended on the datasheet. This was carried out correctly more often for first vaccinations (87% of farmers carried this out correctly) than for the second dose within a primary course (46% of farmers carried this out correctly). The proportion of farmers vaccinating earlier than the youngest recommended age varied between vaccines, with higher levels (18-20%) of incorrect use seen for vaccines against respiratory and clostridial diseases. The efficacy of disease control may be improved with correct use of vaccines; only 34% of farmers indicated that they excluded certain animals. When asked to specify which animals were excluded from vaccination, 23% indicated that they excluded sick and injured animals. This suggests that more farmers need to be made aware that immunocompromised animals will not produce the most effective immune response after vaccination and there is a risk that vaccinating these animals may worsen their disease. This survey indicated that vaccination is heavily relied upon to control disease. It was noted that farmers consider vaccines to be highly effective, to the extent where other disease control measures may be compromised. The research was confined to the UK; however conclusions from the study are expected to be relevant in countries where vaccination of cattle is common. Although excellent research continuous to develop novel methods to control disease, results of this study support that successful disease control by vaccination is dependent on more than the quality aspects of the vaccine alone.

Necessity of a strict biosecurity to maintain BVDV-free status in artificial insemination centers

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In Belgium artificial insemination (AI) is commonly used for the breeding of cattle. Sperm mostly originates from artificial insemination centers (AIC). AI bulls are required to be free of Bovine Viral Diarrhea Virus (BVDV). We report the introduction and spread of BVDV in an AIC despite repeatedly BVDV testing before and after entrance of bulls in the AIC followed by the quick recovery of the BVDV-free status by enhanced analyses and biosecurity measures. Between June and September 2011 BVDV seroconversion was detected in five out of the 43 bulls of an AIC. Subsequently all potentially contaminated semen batches were tested by real-time RT-PCR. BVDV infected batches were detected from two bulls and destroyed before any infected semen was used for AI. The circulating strain was characterized and identified as a BVDV type 1b strain. BVDV seronegative and seropositive bulls were separated to prevent further virus transmission. Follow-up tests of the bulls showed semen became BVDV-free after seroconversion. So far no other bulls have BVDV seroconverted. Three hypotheses could explain the origin of infection. A first one is the introduction of a bull persistently BVDV infected in the testes despite testing of the first produced semen batch. Another hypothesis is the introduction of a bull with an acute BVDV infection not detected by the performed tests. A third one is the contact with a BVDV infected wild ruminant as a deer was observed in the AIC pastures shortly before detection of BVDV seroconversion. BVDV transmission between deer and cattle has been described. This BVDV episode caused direct and indirect economic losses for the AIC and illustrates the epidemiological importance of horizontal BVDV transmission and the necessity of a strict biosecurity to prevent BVDV infection.

Herd-level prevalence and risk factors associated with herds infected with bovine viral diarrhoea virus (BVDV) infection, in dairy herds of Chile

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The aims of this study were to assess the Prevalence of Herds with Active BVDV Infection (PHAI) on bulk tank milk (BTM) samples collected from dairy herds and individuals, and to estimate associations between management practices of the farm and the status of infection. A cross-sectional study was performed and it was obtained a stratified (by herd size) random sample of 150 dairy herds in the main dairy area of Chile. A RT-PCR on BTM or at least 1 positive animal to ELISA for antigen from a sample of cows within-herd (proportional to herd size) was used to assess the infection status of the herd. In addition, at the day of sampling, a survey was completed on each farm, that is aimed to collect information from the farm that could be associated as herd-level risk factors for the disease, assessed by a logistic regression analysis. The overall PHAI was 81.2% (95% CI 74.1; 88.3). The PHAI for Large herds was 100.0% (100.0; 100.0), for medium herds 89.7% (78.6; 100.0) and for small 75.9 (66.5; 85.4) and the differences were statistically not significant (P<0.05). The final model included; Calves shared springs with other cattle within-farm (Yes vs No) OR=3.2 (1.1; 9.3); Young stock contact with animals GT 1 Yr from neighbors through fences (Yes vs No) OR=2.4 (0.9; 6.6); Presence of fox in the farm (Yes vs No) OR=0.4 (0.1; 1.0); Young stock contact with animals GT 1 Yr by paddocks rotation (Yes vs No) OR=0.3 (0.1; 0.9). The prevalence of infected herds is high and it was identified management practices associated with infection status of the herds that could help to control the transmission. Study funded by FONDECYT # 1101020.

Bovine neonatal pancytopenia (BNP) in young calves in Germany on high and low incidence farms
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BNP is a new emerging calf disease, characterized by multiple haemorrhages, thrombocytopenia and leucocytopenia as a result of bone marrow depletion. It occurred sporadically before 2006, but an increase in incidence was observed in 2006 in Bavaria, Germany, and the disease has been seen in many European countries thereafter. Several studies reported an interaction between colostral-derived alloantibodies affecting neonatal blood cells. However, some farms have multiple cases, even in one year, while others only have one or two cases over several years. The present study compared farms (n=40) with high and farms (n=40) with low incidence of BNP in their calves in Germany. All farms have been randomly selected from the database containing over 250 farms with BNP in Germany. All 250 farms had been asked by telephone interview about the number of BNP cases they had experienced since 2006. The farms were then categorized as 'high' or 'low' incidence farms and study farms selected randomly of these. An extensive questionnaire was used to collect data about hypothesized risk factors, such as colostrum management and vaccinations, including different schemes of vaccinations against BVDV. In total 1,178 BNP cases had been mentioned by the farmers of the 250 case farms. Only about 60% of the cases were confirmed. Due to the bad prognosis of the cases, many farmers did only report the first one or two cases. Incidence on farms ranged between 0.3% and 20% of cows affected within the years, in which BNP was observed on the farm. Data collection using the questionnaire is finished, and analysis comparing the frequency of risk factor occurrence between the two groups of farms will focus on colostrum management and vaccinations. Results of this analysis will be presented at the conference.

Lack of monitoring and biosecurity measures to maintain a BVDV-free status in cattle herds
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Bovine Viral Diarrhea Virus (BVDV) is still endemically present in Belgium, nevertheless many herds attempt to eradicate BVDV at herd level. Once persistently infected (PI) animals have been eliminated from the herd a strict monitoring and biosecurity should be applied to maintain the BVDV-free status. In a descriptive study we report the lack of biosecurity measures and BVDV monitoring in 40 Belgian cattle herds after having eliminated all PI animals. Data on farm infrastructure, herd management and BVDV control were collected during a face to face interview. In 30% (12/40) of the herds the BVDV-free status was not annually monitored. In all herds, contact with neighboring cattle, often non certified BVDV-free, over pastures fences was possible. In only 24% (6/25) of the herds purchasing cattle, a quarantine period of at least three weeks was applied. Moreover, 88% (22/25) of the farmers kept purchased cattle in quarantine in the same stable as the rest of the herd. Visitors had direct access to the stables at 88% (35/40) of the herds. The herd veterinarian and inseminator wore farm-specific protective clothing at respectively 33% (13/40) and 10% (3/29) of the herds. A disinfectant footbath was present in 70% (28/40) of the herds. Yet only half (35% of the herds) was filled with an appropriate disinfectant and in 15% (6/40) of the herds the footbath was always used by all visitors. The lack of implementation of these basic biosecurity measures is remarkable since the studied herds all have suffered from BVDV related problems in the past and invested time and money to eradicate the disease from their herd. The absence of these preventive measures is exposing these herds to a high risk of reintroduction of the virus.

Influence of temperature on BTV-8 transmission in NW-Europe in 2007

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A temperature limit for bluetongue virus (BTV) transmission has been established from the data of the 2006 BTV-8 epidemic. That analysis showed that the temperature threshold required for transmission between livestock herds was about 15 °C. This result was considered to be specific for the situation in NW-Europe in 2006, and it remained unknown, whether and how these results can be extrapolated to different conditions. We analysed the 2007 BTV-8 epidemic data with the same method, and compared the results from the two years, to derive more insight into the impact of some of the more uncertain variables. We established that the method needed to be extended with a correction, for the fact that the advancing epidemic could no longer be evaluated as a starting epidemic. Especially in Belgium, many farms were already infected in 2006, which causes reduced transmission levels, due to dilution of susceptible farms. After correcting for the fraction of remaining susceptible farms, we found that the threshold temperature at which the infection spreads between herds again lies at 15 °C. So we have validated the previous results as being far more general than expected, and not only relevant for the specific situation in 2006. The consistency of both results, despite being derived from a different year, a different temperature profile during the year and a larger area of concern, proves that this conclusion is quite robust. In conclusion, these results can be used for extrapolation to other years and regions, while considering that a similar type of animal husbandry, similar host density and similar *Culicoides* species involved are probably still a requirement for a valid extrapolation.

Identifying sources of heteroskedasticity of average daily weight gain in commercial feedlot cattle using a hierarchical Bayesian approach

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The objectives of the present study were to assess the heterogeneity of variance in average daily weight gain (ADG) in commercial feedlot cattle cohorts, and to identify demographic factors as potential sources of cohort- and feedlot-level heteroskedasticity in ADG. An operational dataset compiled from 25 U.S. commercial feedlots containing 24,050 cohorts from 2005 and 2006 was utilized for this study. Inference was based on a hierarchical Bayesian model implemented with Markov Chain Monte Carlo, whereby cohorts were modeled at the residual level and feedlot-years were modeled as clustering random effects. Forward model selection based on Deviance Information Criterion was used to screen potentially important explanatory variables for cohort- and feedlot-level heteroskedasticity. The Bayesian modeling framework was preferred as it naturally accommodates the inherently hierarchical structure of feedlot data whereby cohorts are nested within feedlot-year clusters. Heterogeneity of variance was primarily concentrated at the cohort-level. Feedlot-year specific effects were, by far, the greatest contributors to ADG heteroskedasticity amongst cohorts. In addition, identifiable demographic factors associated with between-cohort variances included cohort size, arrival season, days on feed and mean arrival weight. These results indicate the need for further investigation of sources of heteroskedasticity in feedlot performance in order to increase consistency of beef production outcomes as well as enhance efficiency of statistical inference on treatment effects.

Use of epidemiologic approaches and operational data to elucidate feedlot cattle health issues

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Veterinarians and feedlot managers often have access to large amounts of health and production data routinely collected within the production systems. However, epidemiologic concepts and tools must be appropriately applied for these data to be utilized for accurate evidence-based decisions. We will demonstrate how our research team utilized a robust dataset compiled from U.S. commercial feedlots and applied core epidemiologic principles and methods to enhance the practical understanding of real-world cattle health problems. Our research allowed us to demonstrate how comprehensive, multivariable assessments with analytical control of potential extraneous variables enabled us to identify significant associations between weather conditions, cattle demographic factors, and daily respiratory disease incidence risk. In addition, we have generated unique results illustrating important interactions among cohort-level demographic factors associated with feedlot mortality and culling risks in heterogeneous populations of cattle from multiple feedlots monitored across several years. We also have utilized hierarchical and temporal data and multivariable mixed models to more thoroughly quantify the performance and economic impacts associated with the timing and number of respiratory disease treatments. We believe that researchers and veterinary practitioners can benefit from the use of existing data if appropriate epidemiologic concepts and analytical tools are applied. Alternatively, we can demonstrate with operational data how issues like confounding and effect modification need to be considered in order to make robust inferences that support appropriate health and economic risk management programs.

Latent class growth analysis of the effect of individually tailored biosecurity advice on the presence of endemic pathogens in British beef suckler herds

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Farm biosecurity is considered integral to the avoidance of pathogen incursion, yet the effect of biosecurity measures is rarely studied. This study investigated the effect of individually tailored biosecurity advice on the presence of bovine viral diarrhoea virus (BVDV), bovine herpesvirus 1 (BHV1), *Leptospira interrogans hardjo* (L.hardjo), and *Mycobacterium avium paratuberculosis* (Map) in English and Welsh beef suckler herds. 116 farms were randomly assigned to 'intervention' and 'control' groups. Vets visited these farms annually for three years to blood sample 50 cattle and assign a numerical 'risk score' for each pathogen. At least three pieces of biosecurity advice were given to intervention farms and advice was given to control farms if requested. Bayesian methodology was used to identify seropositive farms (amongst youngstock for BVDV, BHV1 or L.hardjo; and adults for Map), and latent class growth analysis (LCGA) was used to identify classification of farms according to patterns of pathogen experience and risk score over time. The effect of intervention status on pathogen presence and risk score within these groups was then studied. Three risk score groups (low, medium and high) and two pathogen presence groups (low and high odds) were identified for each pathogen. Medium risk score groups showed a gradual decrease over time, with other groups remaining static. A decrease in odds of BVDV presence was observed amongst farms with low initial odds of presence, but pathogen presence was otherwise static. Intervention farms with medium risk scores had lower BHV1, L.hardjo, and Map scores than control farms, but pathogen experience remained similar to controls. Farms in high risk score groups were more likely to be in high pathogen presence groups for all pathogens except Map, where the opposite was observed. Based on these results, LCGA may provide a useful tool for capturing complex heterogeneity in longitudinal data.

In search of clusters of Wisconsin dairy farms to determine the compatibility between high standards of animal health, well-being and milk production

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A random selection of production variables from more than 1000 Wisconsin dairy herds ranging from small to large facilities with a low to high range of annual average milk production and a variety of management systems have been selected for the year 2010. The aim of the study is to cluster the herds for their herd characteristics with regards to animal health, genetics, management (herd size and milking frequency) and milk production without preconceived choices regarding the variables used for the clustering process. Methods such as concordance analysis and principal component analysis will be used to identify the most suitable subset of clustering variables from Dairy Herd Improvement Association (DHIA) stored data (AgSource Cooperative Services, Verona, WI). The resulting clusters will be subjected to a questionnaire in order to gain knowledge regarding herd management and facility design characteristics, and a sample of individual farms will be visited to objectively determine levels of well-being (including scores for locomotion, hygiene, hock and other injuries). Ultimately, the information will be used to determine whether high milk production is compatible with excellent standards of animal well-being. The proposed presentation will focus on the process and results for the selection of clustering variables, the outcome of the clustering analysis and its implications for the development of the questionnaires presented to the farmers.

In-depth interview-based study of farmer perceptions of and attitudes towards biosecurity on English and Welsh beef suckler farms

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A qualitative study was undertaken to investigate English and Welsh beef farmers' perceptions of and attitudes towards infectious disease biosecurity. A semi-structured interview schedule was designed to explore barriers and motivators to adopting new biosecurity practices, as well as farmers' opinions of advice given by the veterinary profession and attitudes to research. Forty farmers who were willing to be interviewed were purposively selected from those who had participated in a larger intervention study of the effect of tailored farm-level biosecurity strategies. The sample included 20 'intervention' farms, to which a specifically tailored biosecurity advice package had been provided, and 20 'control' farms, to which more general advice had been provided. In-depth one-to-one interviews were conducted with each farmer and the resulting textual data were explored using established thematic methods. The findings were triangulated with quantitative data on how the same farmers responded to advice given over the course of the four-year intervention study. Preliminary findings will be presented and discussed in the context of the potential benefits of a mixed-methods approach to the investigation and development of realistic biosecurity practices.

Trajectories in multidimensional pathogen space of indigenous calves reared in a smallholder farming system in western Kenya: the IDEAL calf cohort

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Epidemiological studies often focus on single or dual co-infections, however, in real settings animals are assaulted by a range of parasites at different times and stages of their life and in different combinations. These co-infections and their timings have potentially additive or multiplicative detrimental or beneficial effects. Understanding the natural ecology of the pathogen space calves occupy can provide new insights and understanding of pathogen interactions and their impact on key parameters such as growth rates, morbidity and mortality. This study is the first to attempt to describe and quantify the full range of pathogens infecting a naturally reared indigenous cattle population in its first year of life. The IDEAL calf cohort consists of 548 newborn calves sampled using a stratified two-stage cluster sampling design in Western Kenya. Calves were recruited in the first week of life and visited at 5 weekly intervals until 12 months of age or death (or were censored). A range of clinical and laboratory techniques were used to identify as many pathogens as possible at each visit. For some diseases only serological evidence was available from screening at 12 months. This analysis examines patterns and associations in the calves' infection profiles through time. These are represented as trajectories through a multivariate 'pathogen space'. Our analysis identifies calves with similarities in their infection sequences and patterns. These will be related to clinical episodes and ultimately to correlated with clinical signs. This may then help improve disease profiling and clinical diagnosis and can be used to improve decision support tools for use in the field.

Herd-level risk factors associated with seropositivity for *Neospora caninum* in dairy cattle: Minas Gerais, Brazil, 2010

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Our objective was to determine herd-level risk factors associated with seropositivity for *Neospora caninum* in a large number of randomly selected Brazilian dairy herds. Serum samples were obtained from 2,915 randomly selected cows from 151 herds in eleven municipalities located in the Sete Lagoas microregion, a large dairy cattle region. Indirect ELISA Test (IDEXX) was used in serological diagnostic. All herd-level predictors were obtained through personal interviews with questionnaires administered to each farm manager. A poisson model was developed using number of seropositive cows in each herd. The poisson model was chosen due to the high frequency of positive-herds. All variables were first subjected to univariate analysis, where those with a significance level ($P < 0.20$) were subsequently used for the development of multivariate models ($P < 0.05$). Protection factors such as embryo transfer (Incidence Rate Ratio (IRR)=0.61), use of natural colostrum (IRR=0.71) and presence bull used in cows with pregnancy failure using artificial insemination (IRR=0.83) were found in the final model. A Risk factors found in the final model was the presence of abortion as a major reproductive problem in the farm (IRR=1.23). Presence of dogs birth at the barn, at the farmer house and at an unknown place by the farmer were found as a risk factor (IRR=1.38; 1.30; 1.21, respectively). Presence of veterinary services on farm was found as risk factor (IRR=1.26) and it was considered as a possible confounder. Funding: CNPq, FAPEMIG and INCT-Pecuária.

Cross-sectional study of Johne's disease in dairy farms and cattle of Uruguay

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Cross-sectional study of Johne's disease in dairy farms and cattle of Uruguay. Johne's disease is a chronic enteric disease caused by *Mycobacterium avium* subsp. *paratuberculosis* (Map). A cross-sectional serological study was conducted in 92 randomly selected dairy farms in which 25 cows were sampled in each farm or all the cattle was sampled when the number of cows was lower. 2,224 cattle samples of Uruguay's largest dairy region were tested by ELISA test for antibody detection. The sampling results show $5.65 \pm 1.3\%$ cattle seroprevalence and the estimated projection show that 70.27% of dairy farms have at least one serologically positive animal. In 35% of farms, more than 10% of the animals tested seropositive. These results are consistent with other studies in dairy herds, but with other calf rearing and herds management, where intensive rearing creates good conditions for the spread of the disease. Collins *et al.*, found a slightly higher seroprevalence, 7.2%, but less spreading between herds (50%). Similar results were found by Johnson-Ifearulundu *et al.* in 1998 in Michigan State. These reports are higher than reported in the NAHMS Dairy '96 (3.4% cattle seroprevalence and 21% of herd level prevalence). Farm stratification according to animal level prevalence shows that 29.72% of the farms are negative, 35.88% have less than 10% of seropositive animals, 22.29% have 10% to 15%, 3.4% have a seroprevalence between 15% and 20%, 8.07% between 20% and 25%, and 0.64% of farms have more than 25% seroprevalence. In conclusion, 35% of Uruguayan farms have a prevalence above 10% which means that a high number of fecal Map shedders increase the spread of the disease, making it present in 70% of dairy farms. Statistical analysis was performed using the software routines of Intercooler Stata 12.0. These data indicates that preventative measures should be taken to avoid the spread of *M. avium* subsp. *paratuberculosis* in Uruguayan dairy herds

Modelling the effectiveness of cleaner fish for the biological control of sea lice in farmed salmon

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Wrasse (cleaner fish) have been stocked commercially with farmed salmon since 1989 as part of an integrated pest management approach. Such biological control is attractive because it reduces the need for the use of chemical treatments. Results of commercial trials reported in the literature have largely been positive, however the degree of biological control during these trials is unclear. This is because it can be difficult to establish appropriate reference populations and because there is rarely opportunity for experimental replication in commercial operations. Furthermore there is incomplete understanding of how conditions on farms can influence cleaning behaviour by wrasse, and how conditions might be manipulated to promote cleaning behaviour. This work uses an individual based modelling (IBM) approach to explore the effectiveness of using wrasse for controlling sea lice on salmon farms. An advantage of using an IBM compared to a deterministic model is the ability to represent stochastic variation in cleaner fish feeding behaviour. Model estimates for some parameters are available from the literature, such as the proportion of the wrasse population that exhibits cleaning behaviour. Other aspects of the system that are less clear include the optimum ratio of wrasse to salmon. Sensitivity of the model is being tested to determine these parameters for most effective treatment management.

Stochastic simulation model: proportions of pregnant salmon lice

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The effect of lice distribution on proportions of pregnant salmon lice (*Lepeophtheirus salmonis*), was modelled in a stochastic simulation model. An overall fit of the data to the Poisson distribution was found in two separate datasets, and thus was used as the base of the stochastic model. In dataset one all lice stages followed a true Poisson distribution. Examining the variance-mean ratio (VMR) of adult female lice in dataset two showed a pattern where most cages (n=125) had a VMR above 1, indicating degrees of over-dispersion, while a few (n=7) showed under-dispersion. Of the 146 samples in the final dataset, 139 showed a dispersion within ± 0.5 of the mean adult females, conforming reasonably to the Poisson distribution. We constructed a model in @Risk which generated the number of fish carrying both adult female and adult male lice, being a necessity for lice reproduction, from a range of expected mean numbers of adult lice (λ). A variation of the same model with added extra variance was also generated in the @Risk software for the same λ values. The model was run first with an additional variance giving a VMR of 1.3, which was the VMR of adult females observed in data set two, and secondly with a VMR of two, being the outermost limit of acceptable variance of a Poisson distribution. The model showed that at an estimated adult female lice count of 0.5 adult lice per fish only 40% of the female lice are effectively reproducing. Sea lice reproduction is not linear with female abundance and the proportion of pregnant females will be lower at low lice levels and go towards 100% as the abundance increases. Our findings should have implications for routines for lice counts and decisions on when and how to establish intervention regimes against lice.

Identifying best management practices associated with reduced white spot disease prevalence on smallholder shrimp farms in the North Western Province of Sri Lanka

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Having recently emerged from a prolonged civil war, Sri Lanka is turning to brackish-water shrimp (*Penaeus monodon*) farming to help stimulate its economy and improve the livelihoods of its rural poor. Outbreaks of white spot disease (WSD), in part due to unsustainable farming practices, have historically led to production losses, abandonment of farms, and unemployment among smallholder shrimp farmers. One way to promote sustainable farming is by implementing best management practices (BMPs), which are developed by industry experts to increase sustainability and minimize disease outbreaks. We examined associations between 35 BMPs and WSD prevalence in order to generate hypotheses as to which practices have the greatest impact on WSD reduction. Practices included those related to pond preparation and filling, seed selection and stocking, water quality management, and disease outbreak control. A cross-sectional study was conducted in June-August 2011 in the North Western Province, where WSD has historically been a problem, with 127 smallholder shrimp farmers (representing 32% of known farms) interviewed regarding implementation of BMPs and WSD history. The prevalence of WSD was 54%. Preliminary candidate logistic regression models have identified two BMPs associated ($P < 0.05$) with reduced WSD occurrence (presence of a water reservoir and appropriate water treatment during disease outbreaks) and one BMP associated with increased WSD occurrence (deposition of sludge away from ponds). We are currently generating hypotheses as to why the BMP of depositing sludge away from ponds was associated with increased disease.

Epizootic haematopoietic necrosis virus (EHNV) (Family *Iridoviridae*) has not spread in south eastern Australia

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Outbreaks of disease in Redfin perch (*Perca fluviatilis*) and farmed Rainbow trout (*Onchorhynchus mykiss*) due to Epizootic Haematopoietic Necrosis Virus (EHNV) have been recorded since 1985 from some parts of south eastern Australia. Most infected fish are believed to quickly succumb and die. Experiments performed more than 20 years ago showed that EHNV also can kill native freshwater fish species, including species of high conservation value. EHNV is listed by the OIE but despite its significance, very little is known about its natural distribution as no formal surveys have been conducted. Consequently a wide scale survey was undertaken over 1 million km sq. in the Murray-Darling Basin with power to detect 10% prevalence. EHNV remains endemic in the upper Murrumbidgee River catchment and may have an annual cycle of infection in juvenile fish which is observed only intermittently. Not all parts of the upper Murrumbidgee catchment are infected. Sufficient data were obtained from some regions to be 95% confident that EHNV was present in <10% of the population and in some cases <5%, <2% or <1% were infected. This provided a high level of confidence that EHNV was absent. It is possible that the virus has not entered the middle and lower regions of the southern part of the Murray-Darling Basin, nor the western and northern parts of the Basin. Given the lengthy history of EHNV in the endemic region it would appear that long distance spread of EHNV downstream via water flow in rivers is not important. There is evidence of other means of spread including anthropogenic factors. This study was funded by the Murray-Darling Basin Authority and the University of Sydney.

Spatio-temporal analysis for the distribution of delousing treatments in marine fish farms in Norway

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Emamectine benzoate (EmBZ) is the preferred delousing agent for control of sea lice infections in Norway. EmBZ is an oral administered and highly effective treatment for the prevention and control of sea lice. In this paper, we have assessed spatio-temporal changes in the volume of EmBZ treatments and its relation with EmBZ effectiveness in Norway. Data included more than 1,800 EmBZ treatments in all active sites from January 2004 to December 2009. Clusters of high density and volume of EmBZ treatments were consistently detected in the southern and central regions of Norway between 2004 and 2008. However, use of EmBZ markedly declined in 2009, as it was replaced by other delousing agents. This decline occurred in regions with high biomass of fish and was preceded by a reduction in the effectiveness of EmBZ. Results presented here are critical for the development of focused strategies to prevent and mitigate the spread of resistance to old and new drugs.

Modelling pathogen spread through the live cyprinid movement network in England & Wales

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In England and Wales, the ornamental fish trade imports large quantities of fish from overseas, and when these are released into the wild, infections can be seeded in the sport fishing sector. In 2003, a serious pathogen of cyprinids, koi herpesvirus (KHV), emerged in sport fisheries, thought to have been introduced via imported ornamental fish released into fisheries and spread between fisheries via live fish movements (LFM). Taylor *et al.* modelled the spread of KHV through the sport fishery network assuming that all sites are fully connected. This study uses LFM data to construct a network of connections between farm and fishery sites, i.e. social network analysis (SNA). The structure of the network was analysed and seasonality in movements was examined. Pathogen spread simulations were run to quantify the amount of spread likely to occur from a single introduction of a pathogen to the network, and test the conclusions drawn by Taylor *et al.* Analysis revealed that the network is heterogeneous in structure; it is dominated by a small number of 'supersources' (farms that supply fish to many other sites), while most sites receive fish from one other and do not supply any other sites. A pathogen seeded in one of these fisheries would be unlikely to spread, while infection of a supersource could spread to a large portion of the network. The number of movements made is highest in spring and autumn. As KHV can persist in a sub-clinical state, and disease only occurs at above 15 °C, it is likely that KHV is spread between sites by sub-clinically infected fish when conditions are outside the permissive range for the disease. Our analysis identifies high risk sites and connections that can be used to target both surveillance efforts and control in the face of an outbreak.

Factors associated with changing efficacy of emamectin benzoate against sea lice (*Lepeophtheirus salmonis*) on farmed Atlantic salmon (*Salmo salar*) in the Bay of Fundy, Canada, 2004-2008

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Emamectin benzoate (EMB) (an avermectin product administered to fish as an in-feed treatment) has been used to treat sea lice infestations on farmed Atlantic salmon in the Bay of Fundy, Canada since 1999. This retrospective study examined the efficacy of 114 EMB treatment episodes from 2004 to 2008 across 54 farms. Study objectives were to investigate changes in the effectiveness of EMB over this period, to examine factors associated with treatment outcome, and to determine variables which influence differences in post-treatment lice abundance. The analysis was carried out in two parts: first, treatment efficacy and trends in sea lice abundance were explored, and second, linear and logistic regression models examined the effects of multiple variables on post-treatment sea lice abundance and treatment outcome. To account for the hierarchical data structure with repeated measures, a linear mixed model was used with treatment episodes as random effects and follow-up weeks were nested within treatment episodes. Post-treatment lice abundance was found to increase in the later years examined. Mean abundance was found to differ between locations, with higher lice numbers on farms closer to the mainland and lower levels around Grand Manan Island. Significant variables associated with higher post-treatment lice quantities were location, year, pre-treatment abundance, and an interaction between age of fish and season of transfer. Not all treatments were observed to be effective with an increased risk for unsuccessful treatments being identified for 2008. Treatments applied during autumn were more likely to be ineffective than those applied during summer.

Cross-sectional study for the detection of the salmon pancreas disease virus (SPDV) in wild and feral fish populations, Los Lagos Region, Chile

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The salmon pancreas disease virus (SPDV) is the causal agent of pancreas disease (PD). This disease presents an economic impact in countries of the northern hemisphere with a developed salmon industry. This is why the disease becomes listed as compulsory notification to the local sanitary authority. In response to the potential danger of entrance of this highly pathogenic agent and because of the detection of antibodies in saithe near salmon farms in Ireland, we seek to detect the presence of the virus in populations of wild and feral fishes from ten lakes in Los Lagos Region, Chile, with concessions for salmon farming. An epidemiological study was conducted during the year 2009 to demonstrate the presence of a specific pathogen agent. With a minimum estimated prevalence of 1%, a confidence level of 95%, considering the diagnostic test as perfect, this yield a sample size of 297 fishes per lake, ADL Diagnostic Chile run all the qRT-PCR. On the six lakes where the indicated sample size was fulfilled by the study, there was no detection of any positive individual, which leads to the conclusion that if the agent is present the prevalence could be less than 1% or the virus is not present in these lakes; a total number of individuals sampled of 2.098, leads to the same conclusion (95% confidence), even if the diagnostic test was not perfect. Results can be influenced by the lack of knowledge of the parameters of the selected test allowing the occurrence of false negatives (even when it is highly sensitive and specific), as well as the possible temporary effect of the sampling time, performed during the winter when the development of the virus is less probable. Finally, it proposes future areas of research that allows for the accurate detection of this agent and to know the role of wild fish populations.

The operational sensitivity and specificity of diagnostic testing procedures for aquatic animal infections

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There are a wide variety of diagnostic testing procedures and the World Organisation for Animal Health has defined several purposes for their application; a knowledge of their strengths and limitations is necessary to evaluate their suitability for each purpose. There are, however, very few assessments of the field performance of test procedures used to detect aquatic animal pathogens. We have recently estimated the operational sensitivity (Se) and specificity (Sp) of the diagnostic test procedures used in our laboratory for *Renibacterium salmoninarum* (causing bacterial kidney disease) in rainbow trout, infectious salmon anaemia virus (causing infectious salmon anaemia) in Atlantic salmon and salmonid alphavirus (causing pancreas disease) in Atlantic salmon at the individual fish level. These incorporate bacteria culture, virus isolation, ELISA and/or qPCR. Estimates of Sp are high (approximately 99%) although estimates of Se vary widely. For example the Se of the bacteria culture test procedure used to detect *R. salmoninarum* is low (approximately 10%) for individuals experiencing a sub-clinical infection, and while the method may still be appropriate for confirming clinical cases it is not be suitable for demonstrating freedom from infection. In contrast the Se for qPCR-based test procedures used to detect infectious salmon anaemia virus and *R. salmoninarum* are high ($\geq 90\%$). This has led to the adoption of qPCR for testing farms with suspected *R. salmoninarum* infections rather than the previously used ELISA. The use of qPCR is not however a guarantee of high Se; for example the Se of the qPCR-based diagnostic test procedure for salmonid alphavirus was estimated to be only 40% and this informed a change to the tissue samples we use for testing. We present estimates of Se and Sp for the test procedures evaluated in our laboratory and compare these with the other published estimates available.

Shellfish disease incursions into England and Wales: routes of introduction

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In recent years three exotic shellfish diseases have been detected in England: the new variant of Ostreid herpesvirus-1 (OsHV1- μ Var) in the Pacific oyster (*Crassostrea gigas*), *Bonamia exitiosa* in native oysters (*Ostrea edulis*) and *Marteilla refringens* in mussels (*Mytilus edulis*). In this paper we discuss the most likely routes and introduction and possible risk mitigation. OsHV1- μ Var emerged in France in 2008 and spread within and outside the country mainly with the movement of live animals. At the time of detection of OsHV1- μ Var in Whitstable, England no imports of live oysters for relaying had taken place for some months. The most likely routes of introduction were contamination of imported equipment (trestle and bags) from France or the reimmersion of oysters imported for human consumption. Similarly the detection of *B. exitiosa* in the Fal estuary could not be linked to introductions of live animals. The most likely route of introduction was through international shipping (biofouling or ballast water). Uniquely in the UK the Fal has deep water mooring for container ships in close proximity to shellfish beds. The investigation of *M. refringens* did identified the usual potential routes of introduction (anthropogenic introductions, natural movements, discharge from restaurants, etc., and vessels) but none could highlighted as most likely. The possibility remained that *M. refringens* had been present for a considerable period. Investigations of exotic disease incursions rarely definitively identify the route of introduction. However, we were able to highlight weaknesses in biosecurity related to live shellfish imported for human consumption, the import of equipment and shipping. The site where an exotic parasite is first detected is not necessarily the site of introduction. *M. refringens* and *B. exitiosa* may cause low level effects which may go undetected for months or longer allowing spread before detection and making the identification of routes of first introduction problematic.

Potential for invasive diseases to impact Scottish shellfish aquaculture

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Scottish shellfish production consists mostly of mussels (*Mytilus edulis*), with Pacific and native oysters (*Crassostrea gigas* and *Ostrea edulis*). Production of *C. gigas* depends on hatcheries and translocation (including, from England, Ireland and the Channel Islands), the other species use wild spat and are transported only locally in Scotland. Disease might threaten production and we review risk from *Bonamia*, *Marteilia* and oyster herpesvirus (OsHV-1). *Bonamia* affects *O. edulis*, while OsHV-1 affects both kinds of oyster and *Marteilia* all three shellfish. Isolated *Bonamia* is already in Scotland. *Bonamia* and OsHV-1 are in Ireland and England, while *Marteilia* has a foothold in southwest England. All are widespread in Continental Europe. We identify translocation of *C. gigas* from hatcheries as a key risk route for introductions. Other anthropogenic activity, e.g. shipping, are also risk factors, as is natural spread over shorter distances. *Marteilia* introduction would require a long-distance vector. *Bonamia* already survives in Scotland and as OsHV-1 is present in Ireland it is very likely to be able to do so. *Marteilia* requires >17 °C to sporulate, which would restrict it to southern and shallow coastal areas in Scotland. Existing *Bonamia* infection is localised, so it does not spread easily within Scotland. OsHV-1 might spread more easily owing to extensive translocation of *C. gigas*. The large farmed and wild beds of mussels might ease natural spread of *Marteilia*. *Bonamia* outbreaks in France occur in winter, so lower water temperature in Scotland is unlikely to prevent clinical disease. *Marteilia* and OsHV-1 cause most disease at warmer temperatures that are rare in Scotland. However OsHV-1 does cause mortality in Ireland, so disease is possible at lower temperatures in naïve host populations. In conclusion: the risk in declining order is from *Bonamia*, OsHV-1 and *Marteilia*, although the consequences of each are in the reverse order.

Assessing sea lice transmission within Loch Linnhe, Scotland

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Atlantic salmon aquaculture contributes over £0.5bn to the Scottish economy. It is Scotland's largest food export by value providing employment in remote regions. Sea lice, *Lepeophtheirus salmonis* and *Caligus elongatus*, are ubiquitous ectoparasites that are a concern to farming and wild fish industries. Scottish farms spend ~£35 m/y controlling lice, which is the highest across the salmon farming nations per kg produced. There are 10 stages in the lifecycle with non-infective nauplii hydrodynamically dispersed during which they mature into infective copepodids and require a salmonid host to develop into later stages. Maturation is temperature determined, whilst salinity effects survival. As part of integrated pest management (IPM) for lice control, farms are structured into farm management areas (FMAs) where synchronized practices e.g. treatment and production cycles occur. Loch Linnhe is Scotland's largest sea loch system containing 10 active salmon farms managed in two FMAs, which account for 10% of Scotland's consented production. A coupled biological-physical model is used to assess lice transmission and distribution within the system which can inform IPM. A hydrodynamic model, forced by wind, freshwater input and tides, is run for Loch Linnhe for different time periods. The model outputs (surface currents) are combined with a biological particle tracking model representing lice which age and die. Lice transport is modeled from a range of wild and farmed inputs to determine distributions within the system. Hydrographic measurements are obtained to validate the physical components of the model, whilst nauplii distributions are assessed using planktonic tows, and copepodid distributions using sentinel caged fish. 2011 data shows some consistency between recorded sampling and simulated lice distributions and conditions. Initial model simulations indicate that lice are potentially spread at varying densities throughout the system and could be able to be transmitted across FMA boundaries.

Modelling management strategies for bacterial kidney disease in Scottish salmonid aquaculture

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Bacterial kidney disease (BKD) is a disease affecting both salmon and trout farms in Scotland. Its causal agent, *Renibacterium salmoninarum*, can also exist subclinically and this makes detection, and hence management, of infection problematic. The principle management strategy is through the use of movement controls on known infected site. We present a susceptible-infected (SI) model in which the infected farms are sub-divided into diseased (D) and subclinically infected; these latter are in turn subdivided between those whose infection is known (K) or unknown (U) to the authorities. Prevalence data are derived from these official records. The model is parameterised to fit observed $T = \Delta \text{prevalence}$ assuming steady-state and using an arbitrary time step (time giving infection 20% chance of spreading from an infected site). Under these conditions the model parameters can be well constrained for a given level of undetected infection, to which they are sensitive. The model is used to investigate effectiveness of BKD control scenarios, including retention of movement controls on infected sites (D+K), movement controls only on sites with disease (D), lifting movement controls, intensive surveillance, and vaccination. Model results indicate that lifting controls leads to a relatively small increase of BKD in trout but a large increase in salmon farms. Conversely tightened controls gives a small trout but large salmon decrease in BKD, with eradication from salmon a common outcome. Improved fallowing is the most effective control, while vaccination can under some conditions actually increase BKD. Modelling results on the numbers of sites suffering disease and under official controls are used to provide input to economic modelling.

Pacific oysters aquaculture diseases: surveillance considerations

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Increased mortality events in Pacific oysters were detected in 2008-2009 in mollusc farming areas throughout the whole French coastline, Ireland and the UK. According to the reports the increased mortality events affected mostly juveniles. The mortality rate varied from 40% to 95% of the affected stock. EFSA was requested to assess the impact of the increased mortality events. The assessment required a description of the surveillance approaches in place in European member states and a collection and analysis of the available information on mortality events during the period of 2008-2010. The European legislation on aquatic animals' health require that a risk-based animal health surveillance scheme in all farms and mollusc farming areas is implemented. The scheme aim at the detection of the listed diseases and of any abnormal increase in mortality, 'increased mortality' meaning unexplained mortalities significantly above the level of what is considered to be normal for the farm or mollusc farming area in question under the prevailing conditions. Baseline mortality levels vary and a harmonized approach for its estimation does not exist. When abnormal mortality occurs it must be notified but without an established threshold different countries, regions, farming area or individual farmers have different policies to implement notification system. The current passive surveillance system does not allow for an accurate estimate of increased mortality. A full description of the production systems and numbers of animals is not available at European level. Incomplete knowledge of the health status of incoming oyster stock to production areas, insufficient traceability of movements between production areas and production methods of low biosecurity standards such as mixing of different stocks and age groups were other problems identified. The paper describes the difficulties and limitations in providing a comprehensive and useful epidemiological description of the outbreaks of increased mortality of Pacific oyster in Europe providing recommendations for improvement.

Risk factors for red mark syndrome in UK rainbow trout farms

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Red Mark Syndrome (RMS; also known as cold-water strawberry disease) is a skin disease of rainbow trout that has been identified in the UK since 2004 and has since been reported in other European countries. The disease affects farmed rainbow trout as they approach market size; affected fish are downgraded at processing or are not marketable. The disease is thought to be transmissible, but an aetiological agent still remains to be confirmed. A questionnaire was used to ask about history of the disease on site, environmental data, live fish movements onto site, management practices, etc. Data were collected at farm and pond level. Answers were obtained from 37 case and 26 control sites in England, Scotland and Wales using the questionnaire during site visits. Initial analysis suggests that farms that use fish pumps to move fish between units were at increased risk of RMS, whereas farms employing netting were at a reduced risk of the disease. Farms applying bath treatments (usually employed to control infections with ectoparasites) were at reduced risk of RMS. Presence of an infected farm upstream appeared to increase the risk of RMS. Results of multivariate analysis of the dataset will be presented.

Developing indices for identifying obstacles to achieving sustainability on smallholder Sri Lankan shrimp farms

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Having recently emerged from a prolonged civil war, Sri Lanka is turning to brackish-water shrimp (*Penaeus monodon*) farming to help stimulate its economy and improve the livelihoods of its rural poor. Disease outbreaks, however, in part due to unsustainable farming practices, have historically led to production losses, abandonment of farms, and unemployment among smallholder shrimp farmers. While the necessity for promoting sustainable growth of this industry has been noted in the literature, little has been done to determine and measure practical indicators that may affect sustainability at the farm level. We developed a list of 18 farm-level indicators for the shrimp aquaculture sector in Sri Lanka on the basis of industry best management practices, relevant indicators described in the agricultural literature, and suggested indicators for shrimp aquaculture, with particular attention to disease prevention. This list was modified based on input from local stakeholders and researchers at Wayamba University of Sri Lanka, and used to develop a comprehensive questionnaire consisting of approximately 200 questions for assessing shrimp farm status. The questionnaire was administered to 187 smallholder shrimp farmers in communities throughout the North Western and Eastern provinces of Sri Lanka in June-August 2011. The results of the questionnaire will be compiled into indices for each of the 18 indicators identified at the beginning of the study. These indices will be verified using factor analysis, and will then be used to identify potential obstacles to sustainable shrimp farming at both the national and regional scales. A composite index will also be created to facilitate further analysis and to highlight farms/regions which may be particularly unsustainable.

Risk Assessment for introduction and spread of epizootic ulcerative syndrome (EUS) in Europe

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Epizootic ulcerative syndrome (EUS) is an epidemic disease in wild and farmed freshwater and estuarine fish caused by *Aphanomyces* Invadans. Severe outbreaks have been observed in various parts of the world. The disease has never been reported in Europe. A structured qualitative pathway model was constructed with the aim to determine the factors that can influence the introduction of EUS into Europe. The risk of entry was linked to the probability of infection of imported fish and the frequency of imports. The key components were the certification of EUS freedom by exporters and the capacity for detection of infection at the European border inspection point. The large majority of live fish (>99%) imported into Europe is ornamental fish. It is likely that EUS has repeatedly entered into the EU via ornamental fish importation. Release can occur with the movement or sale of live fish or insufficient effluent treatment or unintentional contact with natural waters. Assuming regular entry and release lack of reporting is contradictory, the following hypothetical scenarios (1 to 4) could explain it: 1. Despite entry and release of the pathogen, fish in EU have never been exposed 2. Fish in EU are exposed to the pathogen but EUS does not establish; 3. EUS epidemics repeatedly establish and spread unnoticed in the EU because conditions are not favourable for disease expression; 4. EUS is endemic in the EU and regularly misdiagnosed. It was concluded that the impact of EUS on EU aquaculture would range from no impact (scenarios 1 and 2, if no spread) to low impact (scenarios 3 and 4, no disease response or low incidence or weak disease patterns). However, if EUS is endemic (scenario 4) the impact may change in future if conditions such as climate, water quality or availability of susceptible species, either in aquaculture or in natural water bodies, become favourable for initiating epidemics and disease expression.

The risk of introduction and establishment of white spot syndrome virus into England and Wales via import of non-viable commodities for human consumption

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A qualitative risk assessment was carried out to investigate the likelihood of introduction and establishment of White Spot Syndrome Virus (WSSV) in England and Wales through imports of non-viable, raw crustacea for human consumption. The pathogen is not known to occur in England and Wales. The five main routes of release of the pathogen considered in the risk assessment were (1) via waste generated by processing plants; (2) restaurants and similar establishments; (3) end-consumers; (4) disposal of product no longer fit for consumption; and (5) diversion of product to use as fishing bait. Import data were obtained from Her Majesties Revenue & Customs. Taking into account the annual level of trade, it was concluded that the overall risk of introduction and establishment of WSSV via these pathways was low for waste generated by restaurants or endusers and low for diversion of crustacea in use for bait. The risk was assessed to be very low for waste generated by processing plants and product disposed of because it is no longer fit for human consumption. There was a considerable level of uncertainty associated with several of the steps in the pathways assessed, including the quantities of raw crustacea being imported into the UK, the extent of use of raw crustacea as bait, the extent of processing of raw crustacea occurring in the UK, the frequency of disposal of untreated waste into the environment, and the several more. Several other potential routes of introduction were identified, such as live crustacea imported for human consumption, and crustacea imported as bait. The import of aquatic animals for purposes such as use as bait should be given more attention. This is an area not covered by current aquatic animal health legislation, while potentially associated with a considerable level of risk.

A study on risk factors of white spot disease outbreaks in shrimp in Khuzestan province by using logistic regression model

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White spot, as one of the infectious viral diseases, has made severe losses in shrimp ponds all over the world. Despite extensive efforts made to deal with and control the disease, white spot continues to be a major health problem in shrimp farms across Iran. In this research, the significance of the risk factors of white spot disease epidemic occurred in shrimp ponds of Choubdeh farming site in Khuzestan province of Iran is determined. A cross sectional study was conducted from June 1, 2010, to September 22, 2010 in 223 shrimp ponds of the site. Data was collected on 17 variables, hypothesized to be associated with the occurrence and epidemic of white spot, with the aid of the shrimp ponds owners and fisheries and veterinary organizations. The occurrence of white spot disease in the farming site was determined by clinical symptoms and the results of conventional PCR tests. Multiple regression and Chi square methods were used for analysis of the data and the effectiveness of the risk factors was established by odds ratio (OR). It is found that poor management of birds fighting (OR=3.72), less educated farm head worker (OR=3.29) and poor filtration of the intake water (OR=3.43) are significantly affected the occurrence of the disease while little changes in the salinity of shrimp ponds (OR=0.16) decreases the odds of the disease. The most important risk factors of white spot disease in shrimp farming sites were identified in Khuzestan province and the share of each risk factor was determined. These findings help better develop shrimp farming across Iran, especially in Khuzestan province.

Aquaculture, food security, and gender roles in Sri Lanka

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Aquaculture has emerged as a key agricultural sector and is the fastest expanding animal production industry worldwide. A benefit to households is increased income, which contributes to improvements in food security and poverty. The government of Sri Lanka seeks to determine if shrimp farming has the potential to provide sustainable livelihoods, especially for female headed households. A cross-sectional survey to assess food security status and gender roles of smallholder shrimp farming households was undertaken from June to August, 2011. Men and women within a household were interviewed individually. Approximately 60 farms were identified in the Eastern Province (EP), and 600 in the North Western Province (NWP). For the EP, all farms were approached. For the NWP, a sample size of 195 was calculated based on anticipated frequencies from a pilot study and 5% confidence intervals. A randomized list of all farms that fit the inclusion criteria (farms with <6 ponds and actively worked by the owner) were then stratified by geographical regions and the first 33% of farms within each region were selected. To further elucidate enablers and barriers to women entering the shrimp farming industry, qualitative interviews were conducted with female shrimp farm owners. These women were identified by triangulating knowledge from local shrimp farming associations, universities and government experts. A total of 220 farms were surveyed by community researchers. The data collected is currently being translated and analyzed. Preliminary results indicate perceptions of food security differ between men and women within households. Only five women were identified as owners of shrimp farms. These women faced various problems, from sabotage to stealing. This project will provide key information for government stakeholders concerning growth of the shrimp farming sector, to inform policy and identify key factors, including gender, associated with food security.

Implementation of epidemiology into a national program for aquatic animal diseases in Brazil

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Given the socioeconomic importance of aquatic animal production related activities and their increased investments, Brazil's Ministry of Fisheries and Aquaculture has established a partnership with the veterinary epidemiology research groups of the Universities of São Paulo and Brasília aiming at implementing epidemiology into a national program for aquatic animal diseases. The strengthening of the Brazilian fisheries and aquaculture production market is related to high quality and sanitary standards. Therefore the application of epidemiological concepts and tools become fundamental to the development of a sustainable production process which might guide the achievement of a world class healthy products. The range of activities of this agreement involves the proposition of a national active surveillance system; the development of specific sampling methodologies for bivalve molluscs; the design of prevalence studies for crustaceans; the assessment of import risk analysis; and the development of epidemiology courses to the Ministry of Fisheries and Aquaculture' staff. The successful implementation of such program is expected to address the specific needs of a decision making process based on objective and scientific criteria, which is essential to any country wishing to protect their internal supply chain against the entry of existing diseases found in exporting countries. It is also relevant to structure effective control programs and surveillance systems based on quantified disease impacts, as well as to spread the use of veterinary epidemiology to aquatic animal health professionals.

Description of the morbidity caused by *Piscirickettsia salmonis* (SRS) in salmonid production sites in Chile

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The aims of this study were to describe epidemiological evolution of the outbreaks of SRS from 2005 to 2010 and to analyse the use of the antibiotics for treating it. It was used a dataset that included information of outbreaks from 18 salmon companies located in the main two productive regions of Chile (X y XI Regions). It included data from 126 sites that produced atlantic salmon (AS), 54 of rainbow trout (RT) and 24 of coho salmon (CS). From this, it was analysed only those companies that provided complete data from January 2005 to December 2010. Out of the sites affected for any outbreak, 85.7% of them were diagnosed by SRS and 70% of them affected AS. The distribution of affected sites increased until year 2008 (ISAv outbreak) and then declined, with no significant changes in the year pattern for the other species. For AS there was seasonality in the frequency of outbreaks, with peaks in summer and autumn. For CS, peaks were reached during summer, autumn and spring seasons. Finally for RT, there was a cyclic bimonthly pattern with a small peak of outbreaks. Considering the production cycle, for all species most outbreaks occurred in fish up to 1 kg., thereafter, for AS, declined the occurrence. For RT and CS it reached a plateau until 2 kg., after all declined as well. There was a strong decreasing pattern (74% less) in the antibiotic use except for year 2009. In 2005, it was used 887.2 kg in average per site against 233.6 kg., in 2010. In addition, AS was the most treated species, it was followed by CS and then RT. The average length of the treatments by drug type was 7.7 days for oxytetracycline, the half of this for flumequine and oxolinic acid and 13.7 days for florfenicol (the antibiotic most frequently used as treatment). These preliminary findings support the need of a better understanding of the epidemiology of the transmission and risk factors given that currently, the industry relies on vaccines and treatments to deal with this agent.

Epidemiological factors and VNTR typing of seven cases of seal tuberculosis (*M. pinnipedii*) found in domestic beef cattle from coastal properties in New Zealand

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The New Zealand fur seal is abundant in the coastal areas and is known to harbour several zoonotic pathogens, including tuberculosis. Members of the *Mycobacterium tuberculosis* complex includes bacteria such as *M. tuberculosis*, *M. bovis*, *M. africanum* and *M. pinnipedii*. The latter has been found in fur seals and sea lions in Argentina, Australia and New Zealand. This paper describes epidemiological factors associated with cases of *M. pinnipedii* infection documented in beef cattle from 1991-2011 and delineates the DNA strain-typing using analysis of tandem repeat segments (VNTR) sequence of these isolates and their major deviations from the more common *M. bovis* isolates in New Zealand cattle. Epidemiological factors were analyzed by examination of the case reports and a telephone survey of 35 neighbouring farms. VNTR testing was performed on all case isolates and the results were compared to 470 isolates of the *M. bovis*. In all *M. pinnipedii* outbreaks in cattle, only a single animal within the herd was found to be infected. In 6 of 7 cases, lesions were identified within the chest, indicating a likely aerosol pathway. The lack of multiple cases within a herd suggests that cow to cow transmission does not commonly occur. The only apparent epidemiological differences between case farms and neighbouring farms was that in ALL case farms, seals had access to cattle either by beach grazing or access to cattle grazing areas via creeks and tributaries that were less than a km from the sea. Many of the neighbouring farms had similar topography and grazing patterns. Seal sightings were not uncommon on pasture and in waterways both on case and neighbouring farms. The VNTR suggested that there is some variation in the strains identified. Two isolates were identical but all were similar and distinguishable from *M. bovis* strains.

Diagnostic and recording accuracy for distal limb fractures in Thoroughbred racehorses in the U.K
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Musculoskeletal injuries have been recognized as the major cause of days lost from training and wastage in Thoroughbred racehorses, whilst limb fractures are the most common cause of euthanasia in racehorses in the United Kingdom (U.K.). Accurate injury diagnosis and recording at the racecourse is essential to ensure correct treatment and provide reliable data for epidemiological studies. Methods to improve the U.K. racecourse veterinary records have been employed, with the introduction of a computerised recording system in 2004. *Post mortems* of all fatal distal limb fractures from U.K. racecourses were performed between 01/02/99 and 31/07/05. During the same period, racetrack veterinary diagnosis was recorded. Different criteria were used to assess racetrack diagnostic accuracy. A comparison was made between the accuracy of diagnosis before and after the introduction of a computerised recording database in January 2004. National Hunt Flat races carried the highest risk of fatal distal limb fracture, whilst flat racing on turf carried the lowest risk, which is similar to previous findings. There were 366 *post mortem* examinations performed in the study period. The percentage of suspect fractures submitted for PM was excellent (97%) and racecourse veterinarian identification of the presence of a fracture was very good (94%). The ability of racecourse veterinarians to accurately identify all fractured bones in the affected limb was poor (53%), with some improvement since the introduction of a computerised recording system. Fracture diagnosis at the racetrack could be improved; either through further training or provision of x-ray units at the racecourse. The quality of data recording has improved since the introduction of a computerised system, but is not yet perfect.

Analysis of enquiries to a South African radio programme on animal matters

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Over a period of six years a total of 2,385 letters and e-mail messages were submitted for veterinary advice to a weekly veterinary information programme on a South African national radio station (Radio Sonder Grense (RSG)), in the native Afrikaans language. A total of 1,839 (77%) of this correspondence contained one or more questions on veterinary and animal matters. This concerned mostly companion animals within the canine (68%), feline (13%), avian (14%) and equine (1%) species. A total of 892 (48.5%) of these enquiries were answered during a period of five and a half years. The most common enquiries involved issues of behaviour (45%) and skin conditions (11.5%). The most common behavioural correspondence was regarding social interaction (55%), followed by normal but unacceptable behaviour (15%) and elimination behaviour (14%). The most common reported skin complaint was pruritus (32%), followed closely by alopecia / feather loss (29%). 18% of dog breeds were not specified, but where the breed was indicated the Jack Russell Terrier was the highest represented breed (9%), followed by the Dachshund (7%) and the South African Boerboel (6%). In contrast 90% of cat breed type was not specified in the enquiries. Although a bias toward the interest of the veterinary presenter can influence the perceived need for information and the listener population requiring veterinary advice is skewed compared to the client base in general veterinary practice, the extent and distribution of the most common and general information needs were expected to be very similar. This is benchmarked against published data and compared with accurate listener figures, which were obtained from the broadcaster. The mode of communication is also explored as ease of access to the presenter was vastly improved by internet radio (audio streaming). The facility of allowing listeners to send e-mails directly to the studio during broadcastings significantly increased the enquiry rate since its introduction during 2007.

Small animal consultations: is a diagnosis always reached?

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A diagnosis has been defined as ‘the label given to a disease with certain clinical or pathologic characteristics applicable to a particular case’. However in first opinion practice a definitive diagnosis may not always be reached, yet decisions on how to proceed still have to be made. The aim of this study was to determine the types and frequency of diagnoses made during small animal consultations in 8 practices. For each consultation, data were collected on all complaints discussed, the body system affected and the type of diagnoses made. Definitions including Definitive, Previous and Open diagnoses were developed to allow consistent categorisation across consultations. Data were collected over 9 weeks by direct observation of consultations. In total 1,015 consultations were observed involving 2,589 problems in 1,132 animals. For presenting problems, Previous diagnosis (27.3%) and No Diagnosis Required (38.4%) were most frequently recorded. Definitive diagnosis (7.0%) was rarely made. Diagnosis type varied with the body system affected, Definitive diagnoses were made for 67.5% of dental problems (n=160) but never reached during renal (n=17), endocrine (n=49) or neurological consultations (n=41). Open diagnoses were made most frequently for behavioural (71.2%; n=59) and least frequently for haemopoietic problems (0%; n=8). The high number of cases assigned to Previous diagnosis or No Diagnosis Required likely reflects the large proportion of caseload involving ongoing cases and preventive medicine. The low numbers of Definitive diagnoses suggests decisions are often made before a final diagnosis is reached, and it appeared that type of diagnosis varied with body system affected. Future work will examine the influence of other factors on the type of diagnosis made, and on the outcome of the consultation.

Epidemiology of *Streptococcus zooepidemicus* infection in dogs in New Zealand

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Streptococcus zooepidemicus infections have been reported increasingly in dogs worldwide, with fatal haemorrhagic pneumonia in intensively housed dogs as the most important clinical manifestation. The organism belongs to the Lancefield group C streptococci with *S. equi* and *S. equisimilis*, and is commonly isolated from horses. *S. zooepidemicus* is not considered commensal in dogs but prevalence studies are lacking. This study had two aims; firstly to estimate the prevalence of *S. zooepidemicus* in healthy dogs and horses in New Zealand and secondly to test the hypothesis that contact with horses is associated with Lancefield group C streptococci infection in dogs. A prospective study with a convenience sample of Massey University Teaching Hospital client animals was performed. A total of 149 dogs were sampled using oropharyngeal swabbing and 97 horses using nasopharyngeal swabbing, visited on 37 separate holdings. Dogs or horses were not always present at each holding and not all animals present at each holding were always swabbed. Given the small sample sizes, the small number of positives detected and the use of an imperfect test, Bayesian methodology was used to give more robust estimates of apparent prevalence. Four of 149 dogs had *S. zooepidemicus* and 20/149 had *S. equisimilis*; 9/97 horses had *S. zooepidemicus* and 22/97 had *S. equisimilis* positive isolates confirmed. The estimated prevalence of *S. zooepidemicus* in dogs was 3.1% (95% CI=1.0-6.5%) and in horses was 19.4% (95% CI=10.7-32.3%). Collapsing the data over both Lancefield group C isolates, the odds ratio for the association between horses and dogs was 11.6 (95% CI 2.8-38.7) and the probability that a dog with a Lancefield group C isolate has had contact with horses is almost 100%. This study reveals that *S. zooepidemicus* can be isolated from oropharyngeal swabs in healthy dogs, and contact with horses and subclinically infected dogs may be important in the epidemiology of *S. zooepidemicus* infections.

A disease outbreak investigation into unexplained causes of equine deaths in western Queensland in 2010

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Western Queensland is a predominantly cattle and sheep grazing area where horses are kept for the purpose of work and competition. In the first six months of 2010, a disease outbreak on five properties led to the death of 36 horses from a population of 133. A stepwise disease outbreak investigation was carried out, using a conventional epidemiological approach. A high morbidity, fatality and case fatality rate led investigators to suspect a toxin as the primary determinant. Deaths occurred more-or-less simultaneously on all five properties, which was consistent with a point epidemic, but temporal patterns on each property were sporadic suggesting an accumulating toxin. Although properties were spatially clustered, only two conjoined, and there was no movement of horses between properties, nor was there over-the-fence contact making a direct contact infectious disease cause unlikely. Further spatial patterns indicated an unusual weather pattern in the area of the outbreak in 2009. This coupled to the evidence for an accumulating toxin led to the hypothesis that above average rainfall during the wet season from December 2008 to March 2009 led to an increased biomass of a local variety of *Crotalaria medicaginea*, the dry remnants of which were preferentially grazed during a prolonged dry period at the end of 2009 causing pyrrolizidine alkaloid toxicity and death of horses. The paper covers the outbreak investigation and illustrates the strength of applying a sound epidemiological approach to a complicated outbreak investigation.

Knowledge, awareness on rabies and attitude to dog bite among students and residents at the university of Ibadan, Nigeria

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Globally, about 55,000 human deaths are recorded yearly of which 24,000 are cases from Africa. Past studies have shown that effective rabies education and regular vaccination of dogs can help prevent new infection. This study aimed at assessing the knowledge and awareness on rabies and attitude to dog bite among students and residents at the University of Ibadan, Nigeria. Review of University hospital records for dog bite cases from 2005 to 2010 was done. A structured questionnaire was used to obtain information on demography, dog bite history, management and vaccination of dogs, awareness and knowledge of rabies from 326 purposively sampled students and residents. Incomplete entries were removed and the remaining 315 entries analyzed using Epi-Info 3.5.1 version. Knowledge on rabies was scored using appropriate grade point. Statistical significance ($P < 0.05$) was determined using chi square test at 95% confidence interval. Review of hospital record revealed a total of 10 dog bite cases were reported from 2005 to 2010. Eighty seven dog bite cases were reported among respondents and their family members; most (46%) reported to have had bite on the legs. Most (67%) of the dog bite victims were between the ages of 13-18 years. Of 315 respondents, 79% were aware of rabies. Majority (43%) reported to have heard from friends. There is a significant difference ($P < 0.05$) in the awareness level among various age groups, educational levels, dog ownership and regular vaccination of dogs. There is also a significant difference ($P < 0.05$) among the residents and various categories of students on their knowledge of etiology, mode of transmission, clinical signs, prevention of rabies and what to do in case of a bite. Majority of the respondents have poor knowledge on rabies despite high awareness level. Dog bite cases are under reported and friends can serve as good source of information dissemination.

A retrospective serological survey on pandemic H1N1 influenza virus in the canine population of Northern and Central Italy

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Since its global emergence in April 2009, pandemic H1N1 [A(H1N1)pdm09] influenza A infection in humans has peaked twice in Italy (November 2009 and January 2011). We recently reported serological evidence for infection of pet dogs in Italy by A(H1N1)pdm09 during the first peak in 2009. To further investigate the A(H1N1)pdm09 situation in dogs we undertook a second serological study on samples originating from dogs residing in Central and Northern Italy between January 2010 and February 2011. The sample size was calculated using a hypergeometric exact probability formula in order to achieve a 0.95 probability of detecting at least one positive case assuming a low minimum expected prevalence of 2% and specificity and sensitivity values as per screening test characteristics. The sample selection approach adopted in this study attempted to ensure an unbiased geographical and temporal representation of the samples available. Based on a proportional allocation scheme, we randomly selected 642 sera weighting the selection on the influence of each region in terms of sample submission. The screening of the serum collected from 642 dogs identified nine positive samples in cELISA, five of which (0.77%, 95% C.I. 0.25-1.8) were confirmed by haemagglutination inhibition test. Our findings indicate that the virus was circulating to some extent in the domestic dog populations from which the samples originated. It appears, at least in our study group, that all the positives identified are associated with the first 2009 influenza peak as no positives were identified in dogs born in 2010 or in the period from April 2010 to February 2011. However, to clarify this observation and to determine whether A(H1N1)pdm09 infection in dogs continues, further epidemiological studies are required.

Dogslife: a web-based study of canine health

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Dogslife is a web-based, longitudinal study of the health of Labrador Retrievers. Participants are requested to complete an online questionnaire at defined intervals which captures phenotypic data and owner-reported information on the dog's environment, diet, exercise levels and health/illness. The platform is ideally suited to maintaining the cohort as participant retention is facilitated via automatic email reminders and ongoing costs can be minimised. Recruitment began in July 2010 and to date 2,170 dogs have been registered. The recruitment rate is 2.2% of the (available) Kennel Club registered Labrador Retriever population. Recruitment rate was highest for those directly targeted by email and/or postal advertising (5.9%). After 18 months 2.6% of the registered dogs were permanently lost to follow-up either due to re-homing (1.5%) or death (1.1%). Continuous evaluation indicates that the cohort is geographically representative of UK-based, Kennel Club-registered, Labrador Retrievers. Rarer coat colours are slightly over-represented and the owner cohort comprises fewer smokers than the wider UK population. In the first year of life, illness or clinical signs were reported for 86% of dogs and at 18 months into the project, over 2,700 illnesses or clinical signs had been recorded. Of these reported signs, 1,510 were not associated with veterinary visits and would therefore not be detected in more traditional studies of canine health based on veterinary presentations. Current work includes validation of the data collected. Veterinary records are being requested for a random cohort subsample to verify illness reports. Random visits will also be undertaken to verify owners' measurement of height and weight and assess the ongoing validity of the questionnaire. Once validated, the breadth of illness data captured by Dogslife will offer a unique opportunity to seek relationships between the environment, early minor illness and subsequent ill health in a companion canine population.

Impact assessment of a charity training programme on health of working horses in Lesotho

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To assess impact of an equine charity's farriery, saddlery and nutrition training programme in Lesotho on horse health and owners' knowledge and husbandry practices. One survey (S1) was undertaken before the first training programme began (April-June 2007) and one (S2) 20 months after its completion (August-October 2009). Randomly selected horses (S1: n=312 vs. S2: n=245) underwent structured clinical examination; blood and faeces were sampled for haematology, biochemistry and worm egg count. Tack was assessed for condition, cleanliness and fit. Owners were interviewed using a pre-tested local language face-to-face questionnaire. Differences between surveys were assessed using Chi-squared and t-tests. Most horses provided ridden transport (S1:79% vs. S2:91%). Forefoot shoeing frequency increased (S1:14% vs. S2:29%, P=0.02) but overgrown forefoot horn frequency was unchanged (S1:45% vs. S2:42%). Owners noted trained farriers' enhanced skills but poor shoeing affordability. Tack availability, condition and cleanliness remained suboptimal but bridle fit improved. Tack-associated injuries (S1:58% vs. S2:78%) and pain on spinal palpation (S1:53% vs. S2:72%) persisted. Mean body condition score remained suboptimal (S1:2.5 vs. S2:2.1), although many owners (S1:62% vs. S2:41%) recognised their animal's diet was unbalanced. A minority of horses had low red blood cell count (S1:21% vs. S2:17%). Strongyle infestation was endemic (S1:88% vs. S2:89%) and most horses had ticks (S1:59% vs. S2:76%). While some positive impact was achieved, key horse health issues remain and sustained intervention may be required before improvements are seen. Results could aid in selecting community-based intervention topics. Acknowledgements: World Horse Welfare; Lesotho Department of Livestock.

Recruiting a representative sample of British veterinary practices for conducting a generalisable epidemiological study of equine laminitis, 2009-2011

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Equine epidemiological studies frequently use convenience rather than random sampling, recruiting horses under the care of volunteering veterinary practices. This study aimed to recruit a representative, sample of compliant veterinary practices to study the epidemiology of equine laminitis in Great Britain. As no complete data on the British horse population exist, analyses were undertaken to establish if the recruited sample represented the underlying veterinary population with results applicable to the general horse population. Initially, 1169 Royal College of Veterinary Surgeons-registered practices dealing with horses were contacted to make them aware of the study. Those willing to help further were sent more information and invited to submit answers to 8 questions on requirements for study data collection, with practices asked to provide data on cases of equine laminitis and the population of horses seen by them over a 24-month period between 2009 and 2011. Initially, 175 (15.0%) of 1,169 veterinary practices responded and of these 148 (84.6%) expressed interest in co-operating with the study. Sixty five (43.9%) practices were willing to provide data with 28 (18.9%) practices finally recruited on the basis of their eligibility responses. Of the 28 recruited practices, 2(7.1%) were in Wales, 4 (14.3%) were in Scotland and 22 (78.6%) were in England. Spatial analysis suggested the 28 practices were geographically representative of the underlying British veterinary practice population. Epidemiological data exceeding required sample size estimations were collected over the planned 24-month study period from the participating veterinary practices. The methods adopted facilitated recruitment of a geographically representative sample of veterinary practices, which provided generalisable epidemiological data on equine laminitis in GB between 2009-2011.

Estimating the frequency of veterinary attended equine laminitis in Great Britain, 2009-2011

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Although laminitis is recognised as an important disease among equids, a recent systematic review assessing quality of published evidence highlighted a paucity of quality studies estimating the frequency of laminitis worldwide. This study aimed to estimate both the prevalence and incidence of veterinary-attended laminitis in the general British horse population. A prospective study followed a cohort of horses attended by a representative but compliant convenience sample of British veterinary practices for 24 months from May 2009. A custom-designed reporting form was used to collate numerator data on active laminitis cases diagnosed by practitioners. Denominator data comprised figures supplied by practices on animals visited by ('visits') and registered with them ('registered') each month. Prevalence based on denominators of horse visits and registered horses and incidence measures based on incident only and recurrent cases were estimated from available data. The overall 'visits' laminitis prevalence estimate was 0.47% (95% CI 0.42-0.52%) based on 297 reported cases among 63,054 horse visits. The overall 'registered' laminitis prevalence estimate was 0.49% (95% CI 0.43-0.55%) based on 235 reported cases among an average of 48,082 registered horses. Laminitis incidences based on incident only and recurrent cases were estimated as 0.50 cases/100 horse-years at risk (95% CI 0.44-0.57) based on 235 cases in 46,814 horse-years and 0.53 cases/100 horse-years at risk (95% CI 0.47-0.60) based on 241 cases in 46,970 horse-years, respectively. Laminitis prevalence and incidence were lower than previous published estimates, probably due to differences in geographical setting (nationally representative of Great Britain), study period (May 2009 for 24 months), case definition (veterinary confirmed), study design and population studied (prospective veterinary-attended cohort).

Crude incidence rate of malignant tumours in pet dogs: city of Rome

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In 2009, it was launched a three-year project for the monitoring of tumours in pet dogs living in a pilot area covering 4 boroughs of Rome: the project was coordinated by the Istituto Zooprofilattico Sperimentale Lazio e Toscana (IZSLT), in collaboration with the Local Health Unit 'Roma B' and 29 veterinary practitioners. In 2011, the dog population of this area was estimated as 26,345 (95% CI:24,247-28,443) dogs. The aim of the present study was to provide a reliable estimate of the annual crude incidence rate (IR) of primary malignant tumours (PMT) in pet dogs. From 2009 to 2011, practitioners submitted to the IZSLT tissue samples of dogs with suspected tumour for histology testing free of charge. Tumours were coded according to the ICD-O. In 2012, 4 of the practitioners provided the full list of dogs seen at least once at the respective practice over the study period, independently of the reason for medical examination. Because records from these lists and those from laboratory results had a field for the owner's address, it was possible to geocode and keep those falling into the pilot area. Assuming an open population in steady-state, the resulting number of dogs from the lists was taken as a representative sample of the entire dog population at risk, while the resulting number of dogs with PMT from the 4 practitioners was taken as the corresponding number of new cases: the IR was estimated accordingly. 102 PMT from as many dogs were submitted by the 4 practitioners. The average population at risk was 2,585 dogs: the IR of PMT was 1,315 (95% CI:1245-1388) per 100,000 dogs. The most common tumour was the mammary carcinoma. The IR appears greater than values commonly reported in literature. An accurate definition of the parameters was obtained by geocoding. It cannot be excluded the effect of selection bias, especially because data come from dogs that received veterinary care and the 4 practitioners were not selected randomly.

Fate of Thoroughbred horses in New Zealand after the yearling sales

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A previous analysis of the supply chain in New Zealand Thoroughbred racing highlighted the loss of horses from the industry, estimating 57% of horses failed to reach their full potential; 27% of racehorses were never registered with a trainer. As part of a wider longitudinal study, there was an opportunity to describe the fate of yearlings after the sales and the loss of horses that occurred at each stage from the stud farm to racing as a 2-year-old. As part of a larger prospective study, Thoroughbred horses born in 2007 were followed from the stud farm to the end of their 2-year-old racing season (31st July 2010). Official data extracts containing sales and racing data of all the horses in the 2007 foal crop were linked to the horses followed in the study population. To describe the fate of the yearlings after the sales, horses were categorised into five groups: (1) registered with a trainer at two years of age; (2) registered with a trainer at three, but not at two; (3) exported at two; (4) died; and (5) unknown. After the sales, the fate of most (53%; 333/627) horses in the study population was 'registered with a trainer at two years of age', 24% (151/627) were exported and the fate of 8% (49/627) was 'unknown'. The most common country of export was Australia (87%; 131/151), followed by 3% each going to Hong Kong, Korea and Singapore. Of the sales horses, 28% were exported compared to 9% of store horses, whilst 40% (92/231), 21% (39/189) and 10% (7/71) of horses catalogued for Premier, Select and Festival sales, respectively, were exported. The fate was 'unknown' was for 16% (22/137) of store horses and 13% (9/71) of horses catalogued in the Festival sale. The predominant fate of yearlings after the sales was registered with a trainer at two years of age. The fate of a group of horses remained 'unknown' at the end of the 2-year-old season, indicating that these horses had not entered the cohort of horses trialling or racing in that year.

Analysis of risk factors of canine diabetes mellitus: a matched case-control study

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Canine diabetes mellitus (CDM) is a multifactorial disease with a high incidence secondary to autoimmune insulinitis, pancreatitis or Cushing's syndrome. However, many environment factors have been associated with CDM, such as unbalanced diet, overweight, lack of physical activity, and diestrus in bitches. The aim of this study was to identify possible risk factors for diabetes in dogs throughout a matched case-control study in southern Brazil. The sample comprised 110 diabetic dogs diagnosed between 2004 and 2011 at the University Veterinary Hospital and by a private veterinary endocrinology consulting, which were paired by breed, age and sex with 136 dogs (case-control ratio of 1:1.2). The owners were contacted by phone and interviews performed by three blinded trained interviewers. A previous validated questionnaire was used to assess exposure to several risk factors. Univariate conditional logistic regression was performed in order to select potential risk factors associated with CDM. Only variables with a $P < 0.20$ were offered to the multivariable model. The multivariate model was built using forward selection starting with the variables with the lowest AIC values from the univariate analysis and backward elimination of variables with a $P \geq 0.05$. Two variables were significantly associated with CDM in the final model ($P \leq 0.01$): unbalanced diet (OR=4.85; IC 95%: 2.2-10.7) and overweight (OR=3.5; IC 95%: 1.6-7.5). This result is similar with previous European studies. A correlation matrix analysis showed that both variables were independent, and both factors are known as insulin resistance inductors. By conclusion we assume that feed with an unbalanced diet and keeping the dog overweight can predispose to diabetes development.

Preliminary quantification of the prevalence of angular and flexural limb deformities in a population of Standardbred and Thoroughbred foals in New Zealand

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This study aimed to describe the quantification of the prevalence of angular and flexural limb deformities in a population of Standardbred and Thoroughbred foals in New Zealand in their first week after birth. Furthermore, it aimed to describe the influence of several risk factors such as gender, breed, size, condition score, gestation length, season and parity of the mare on the prevalence of limb deformities. Two Standardbred stud farms and two Thoroughbred stud farms were selected using a convenience sample. Data on limb deformities were collected on all foals that were on the farms during the 2010/2011 breeding season. Observational assessments were used to score foals from their first week after birth to fifteen months of age. Descriptive statistics, univariable logistic regression and multivariable logistic regression models were used to evaluate data. The majority of the foals (253/313, 80.83%) had one or more limb deformities recorded in their first week after birth. Of these, 196 had more than one problem recorded (196/253, 77.47%). Carpal valgus was recorded in the majority of the foals (162/313, 51.8%), with 84/162 (51.85%) being unilateral and 78/162 (48.15%) being bilateral. Most of the problems recorded (628/807, 77.82%) in this study were slight deformities that required no veterinary attention. The risk factors that showed a significant association with 3 of the limb deformities investigated were: breed, gender, size, condition score and season. This study provides preliminary work where future studies could build on and it could provide a reference point for the New Zealand industry. Furthermore, it could provide an opportunity to examine if angular and flexural deformities are associated with racing and sale performances.

Polo: an epidemiological study of the whole

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Polo, one of the world's oldest sports, offers an unrivalled opportunity for medical, dental and veterinary scientists to work together in a non-infectious disease arena. Prevention of injuries to these modern day centaurs is neither a veterinary nor medical problem; it is both. A cross sectional study and structured telephone questionnaire were used to collect data on falls, injuries, preseason training and attitudes towards risk from a random sample of 112 UK polo players. Injuries to riders and horses were defined as those requiring a hospital or veterinary visit respectively. Risk factors for falls and pony injuries were estimated using multivariable logistic regression. The median number of falls in the previous season was one (IQR 0-2). 2.5% (90%CI 0.4-5.4) of players fell off 10 or more times. 17.3% (90%CI 10.4-24.2) of riders reported polo related injuries, requiring hospitalization, in the previous season. 48.1% (90%CI 39-57.2) of participants owned at least one horse that sustained a polo related injury requiring veterinary treatment. Overall 10.6% (90%CI 5-16.2) of horses experienced an injury requiring a veterinary examination. Women were at quarter of the risk of falling compared to men (OR 0.27). Players expecting to improve their handicap were eight times at risk of falling compared to players expecting to maintain their handicap (OR 8.36). Players exercising their ponies for a mean of 51.1 (SD 12.2) days prior to the first chukka of the season were less likely to fall than players with ponies exercised for a mean of 43.5 (SD 10.9) days. When adjusted for confounding falls were associated with increased risk of injury (OR 6.57) as was higher self-assessed fitness score (OR 1.68). In contrast, players who used a gym were less likely to be injured (OR 0.14). Wearing wrist protectors also reduced the risk of injury (OR 0.17) (RR 0.32 0.08-1.31 P=0.07). Goggles and face protectors had no effect. This is the first population based study of falls and injuries to horses and riders during the game of polo.

Stray dog population dynamics at university of Sao Paulo Campus, Brazil

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A longitudinal study was carried out to describe the stray dog population dynamics in University of Sao Paulo Campus, Brazil from November 2010 and November 2011. The Campus is located inside the urban area of Sao Paulo, the biggest city of Brazil, with a human population over 11 million. Its 4.2 square km are walled, with 10 access gates, allowing stray dogs to move in and out of the campus freely. Over 100,000 people and 50,000 vehicles circulate in the campus daily. Five observations were made during the study period, using a two-sample method. The same route was made in all observations, being traveled twice each day. Observed animals were photographed and the sight coordinates were obtained using a GPS device. The stray population showed seasonality associated with class periods and holidays, varying from 55 (44; 76) to 32 (23; 56) individuals. The stray population also showed susceptibility to difference between inward and outward dog movements and to the proportion of females in the population during the study period. Overlapping home ranges were observed in areas where most of people circulate, corresponding to the docile dogs. A feral group was observed close to two forest areas, and no overlapping with other dog's home range was observed for this group. A spatial correlation between dog sights and food sale point distributions was observed, rather than trash bins. A kernel density map showed that high stray dog density is associated with larger organic matter generators, such as university restaurants. One can conclude that preferred food source is the leftover food offered by the restaurant users and bad waste conditioning.

Characteristics of a UK pet cat cohort

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UK pet cats aged 8-16 weeks are being recruited to a (lifelong) longitudinal study (1st June 2010-31st December 2012). The aim of the study is to use prospectively collected data to study a range of outcomes, including feline unwanted behaviours, obesity and specific diseases. Following 20 months of recruitment, initial analysis of the data was conducted to provide descriptive data on the cohort. Characteristics of cats and owners recruited through different methods were compared with data collected from UK households in 2007 using telephone interviews. Questionnaires had been completed for 898 eligible (8-16 week old UK) cats. Cats were recruited through internet sites (including Cats Protection website, facebook and pet forums) (33%), veterinary practices (30%), 'word-of-mouth' (12%) and through rescue centres (7%). Most cats (49%) had been obtained from friends, relatives, colleagues or via advertisements for non-pedigree cats, whilst 21% came from rescue centres, 15% were from pedigree breeders, 7% had been bred by the owner (accidentally or deliberately) and 6% had been stray cats. Cats recruited to the cohort were significantly more likely ($P<0.001$) than the 2007 telephone sample to be pedigree cats (21% vs 8%). Further analysis of breed differences revealed that the proportion of pedigree cats varied according to how the owner had heard about the cohort study (6% via rescue centres, 13% via vets and 26% of owners had had been browsing feline-related websites. One-third (33%) of the cohort had been obtained at no cost to the owner and a further 14% cost only £1-£29. Most owners planned to have their cats neutered; 10% when the cat was aged <4 months, 23% at 5 months, 44% at 6 months of age and 9% at 7 months or older. The results of this analysis will be used to direct future recruitment efforts to increase the external validity of the study through recruiting a sample that is as representative of the UK pet cat population as possible.

Prevalence and factors associated with *Leptospira* spp infection in dogs and cats in the regions of Los Ríos and Los Lagos, South of Chile

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A cross-sectional study was conducted in Los Ríos and Los Lagos regions to determine the Apparent prevalence (AP) and True Prevalence (TP) of *Leptospira* spp exposure, antibody titers, individual characteristics and risk factors associated with samples taken from 390 dogs and 104 cats. Positiveness was detected via Microscopic Agglutination Test with a panel of 6 serovars. For dogs, the AP was 6.2% (95% CI=3.8; 8.5) and TP was 2.7% (95% CI=1.1; 4.3). Positivity was detected for serogroups Sejroe, Pomona, Canicola, Ballum and Icterohaemorrhagiae with titers ranging from 1:100 to 1:1,600; the most frequent serovar was *L. interrogans* serovar Pomona (29.2%). Positive animals were mixed breed (37.5%), males (54.2%), between 1 to 3 years old (41.7%), living outside the home (66.7%), without clinical signs of leptospirosis (87.5%) and from urban areas (62.5%). Contact with cattle, sheep, goats, pigs and/or horses was a risk factor, but not statistically significant (OR=1.9; 95% CI=0.8; 4.5). In cats, AP was 4.8% (95% CI=0.7; 8.9) and TP was 1.3% (95% CI=1.1; 4.3). Positivity was detected for serogroups Pomona, Canicola, Icterohaemorrhagiae and Ballum with titres of 1:100; the most frequent serovar was *L. interrogans* serovar Canicola (40.0%). The positive cats were domestic short hair breed (60.0%), males (80.0%), between 1 to 3 years old (60.0%), hunted rodents (80.0%) without clinical signs of leptospirosis (100.0%) and from rural areas (80.0%). Significant risk factors were contact with rodents and/or hares (OR=14.2; 95% CI=1.4; 142.4) and live inside their home (OR=17.4; 95% CI=1.5; 205.1). Is necessary to monitor the epidemiological situation of the infection in these areas and keep the owners informed about the preventive measures that may apply to pets and humans given the zoonotic potential of the disease.

What is a feral cat: management protocols in an undefined population

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There is no single accepted set of identifying characteristics for a feral cat. Within the United Kingdom, many charities work with feral cats, each with different guidelines and standards, causing problems when attempting to coordinate effective feral cat control. The aims of this study were to investigate the definition of a feral cat used amongst those working with them, and to establish what happens to cats once labelled as feral. An online database of cat charities was used to identify a sampling frame of 40 charities located in Nottinghamshire and Leicestershire. Of these, 13 were willing to participate and underwent face to face structured interviews. A follow-up focus group was run at the School of Veterinary Medicine and Science. The only characteristic that all study participants agreed on when defining a feral cat was that it would be 'unapproachable in its free roaming environment.' The most common term used to describe a feral cat by respondents was 'wild', with lack of socialisation towards humans also identified as a key feature. Of the respondents, 62% felt that a feral cat could be tamed, regardless of age. All charities neutered cats before release or re-homing. Although 92% identified neutered cats, only 54% did this through ear tipping, as recommended by WSPA, and 38% of shelters returned neutered cats without any form of permanent identification. In the UK, several different definitions of a feral cat are currently in use. Based on the opinions of those working with feral cats, this study proposes that a feral cat is both unapproachable and capable of thriving in its free-roaming environment. Taming of all ages of feral cat has been identified as common practice; this is a controversial process as confinement is extremely stressful for ferals. Provision of a common definition of feral cats is a necessary first step to more coordinated management and improved welfare of these animals.

Common conditions of pedigree dogs: vet and breeder opinions

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Pedigree dog health and welfare is a contentious issue. Little evidence exists on the health problems veterinary surgeons (VS) and pedigree dog breeders (PDB) most commonly encounter, or whether these are predominately inherited or acquired in nature. This study aimed to identify (1) the most common problematic body systems (BS) encountered in each of the 10 most registered breeds in the United Kingdom; and (2) the BS thought to have the biggest impact on the welfare of each breed based on VS and PDB opinion. PDB were recruited through the Champdogs website and VS, via both an existing contact list and the Royal College of Veterinary Surgeons' Register of Practices. Data were collected by electronic SurveyMonkey questionnaires. VS and PDB were asked to rate the 3 most commonly affected BS per breed. The datasets were totalled to give overall values for each BS. Data on welfare impacts were analysed as reported. Responses were received from 150 VS and 385 PDB. In Cocker Spaniels (CS) and Staffordshire Bull Terriers (SBT), VS rated the most common affected BS to be dermatological (CS: 29.5%, n=110; SBT: 30.4%, n=103) but PDB identified ocular problems (CS: 33.3%, n=36; SBT: 26.7%, n=16). In Labrador Retrievers (LR) and German Shepherd Dogs (GSD) both VS and PDB identified musculoskeletal conditions to be most common ([GSD] VS: 32.6%, n=123; PDB: 27.3%, n=39; [LR] VS: 35.8%, n=135; PDB: 32.2%, n=49). Fewer differences in opinion were seen on welfare issues. Both VS and PDB of Cavalier King Charles Spaniels (CKCS) and Boxers (B) rated cardiovascular issues as the biggest welfare issue ([CKCS] VS: 68.7%, n=79; PDB 50%, n=13; [B] VS: 45.8%, n=49; PDB: 47.6%, n=10). These data suggest that VS and PDB have differing views when identifying BS affecting pedigree dog health. PDB possibly focus on inherited conditions whereas VS focus on both acquired and inherited disease.

How often do pets get lost from home and return?

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Dogs and cats are kept as companions in many countries. Likewise, they can become lost from home or run away. No population-based data on the frequency of this occurrence or the success of finding a lost pet has been previously published. This study determined the frequency of pets getting lost and found as well as the ways they returned home. A cross-sectional random digit dial telephone interview was conducted between September and November 2010 in the USA. There were 2,587 households successfully contacted; 1,015 owned dogs or cats within the past five years. Pets did not have to be currently in the household. Eight hundred and sixteen households owned dogs and 503 owned cats (307 owned both in the past five years). The median number of dogs owned was 1 (range, 1 to 22) and the median number of cats was 2 (range, 2 to 27). In the past 5 years, 14% of dogs and 15% of cats were lost and 93% of dogs and 75% of cat were recovered. No pet or owner demographic variables were associated with pets getting lost. For dogs, searching the neighborhood and returning on their own were the most common methods of finding the dog; 13.9% were found through an identification tag. For cats, 59% returned on their own and 30% were found by the owner searching the neighborhood. Seven percent of dogs and 4% of cats were found through animal control/law enforcement. Dogs were more likely than cats to be lost more than once. Cats were less likely than dogs to have identification. Owners of dogs and cats rarely searched at shelters or contacted animal control/law enforcement. Knowledge of the most successful methods of finding dogs and cats provides invaluable advice for owners of lost pets, veterinarians, animal welfare professionals and law enforcement. More pets could potentially be reunited with their owners if collars and visible identification were used routinely.

Canine cancer registration: yesterday, today and tomorrow

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Cancer registration is an important tool to achieve cancer control and prevention, and is widely used within human oncology. The distinction between population-based and hospital-based cancer registries is important, particularly because the latter include no information regarding the catchment area or background population at risk which then precludes the estimation of incidence. Veterinary cancer registration has a long history, but is faced with specific challenges e.g. related to representativeness of the included sample and individual animal identification. The aim of the presentation is to give an overview of the history of veterinary cancer registration, as well as to present an outline of current efforts in this field and discuss future challenges. The inventory of active registries is based on a recent workshop on canine cancer registration hosted at the Norwegian School of Veterinary Science in Oslo, Norway. Since the first population-based veterinary cancer registry was established in California in the 1960ies several others have been founded, but have mostly been short-lived. Current efforts to record cancer occurrence among companion animals are predominantly hospital- (or diagnostic laboratory-) based. Proportional measures of disease frequency can be estimated based on such registries, and the case-series have also been successfully used as a basis for case-control studies. Other important sources of information on canine cancer are presented, including: animal insurance data, tumor banks, and necropsy data. In summary, there appears to be a trade-off between quality of the diagnostic information included and representativeness regarding the background population. Future challenges are discussed and include issues relating to harmonization of diagnostic coding, defining the population-at-risk, individual animal identification and data quality.

Meta-analysis of risk factors for *Leptospira* spp infection in dogs

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A meta-analysis was performed to assess the association between *Leptospira* spp infection in dogs and risk factors of animals characteristics described in different studies. A literature search was conducted using electronic databases, scientific journals and internet based search engines to find publications in english, spanish and portuguese with unrestricted publication year. After abstract and quality screening, 9 publications describing risk factors for positivity of *Leptospira* spp infection were used and 3 risk factors were selected to perform 3 meta-analysis because this were described in more than two publications. In each meta-analysis, to determinate the pooled OR it was evaluated the presence of heterogeneity based on the significance of heterogeneity statistics for using the fixed effects or random effects model. Publication bias was not detected only in the meta-analysis of male dogs. In the meta-analysis of 'male dogs' it was included 5 studies in which no heterogeneity was detected, so the fixed effects model was used and the pooled OR noted that to be a male dog was a risk factor to *Leptospira* spp infection (OR=1.7; 95% CI=1.4-2.1). In the meta-analysis of 'mixed-breed dogs', it was established the presence of heterogeneity in the 5 studies included and the random effects model was used. To be a mixed-breed dog was a risk factor to *Leptospira* spp infection, but not significant (OR=1.2; 95% CI=0.8-1.9). The meta-analysis of 'urban dogs' included 3 studies in which heterogeneity was detected and the random effect model was used. To be a urban dog was a risk factor to *Leptospira* spp infection, but the association was not significant (OR=1.7; 95% IC=0.8-3.7). *Leptospira* spp infection in dogs have risk factors that coincide in different studies, therefore the results of this study can be used for strengthening some control measures.

Attitudes to and opinions of neutering in dogs: a survey of veterinary surgeons and nurses

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Most of the literature pertains to the advantages, disadvantages and prevalence of surgical neutering in dogs with little research or emphasis on other options. A survey on canine reproduction was commissioned by Virbac Animal Health UK in December 2009 in order to obtain information from veterinary surgeons, veterinary nurses and the general public. The aim was to gather information on perceptions about canine neutering by questioning respondents about their attitudes to and opinions of neutering options and alternatives to surgery. An on-line survey was conducted over an 8-week period from March-May 2010 using SurveyMonkey. An invitation to participate was placed on AnimalOracle.com, and was sent via e-mail to all members of vetsurgeon.org and press releases were also sent out. Questionnaire items were attitude statements with a 5-point Likert scale of agreement: Strongly agree, Agree, Disagree, Strongly disagree and No opinion. Examples include: 'I believe that surgical castration reduces the likelihood of occurrence of certain medical conditions later in life' and 'Temporary medical castration is an option when an owner cannot decide whether to have their dog permanently castrated with surgery'. Cross-tabulations and Fishers exact tests were used for categorical variables including type of respondent (gender, dog owner or not). Non-parametric Wilcoxon rank sum tests for 2 independent samples or Kruskal-Wallis analysis of variance (AOV) for more than 2 independent samples was used to examine differences in the distribution of responses by type of respondent. There were 681 respondents, 60% (411) of which were veterinary surgeons (VS). The results of analysis of the 411 responses from VS will be presented. The results of this survey suggest that there is some awareness of the various alternatives to surgical neutering, although perhaps not as wide as desired. This survey has produced some interesting and useful results that can be used to educate veterinary professionals and the public.

The reliability of a survey for cat owners/caregivers regarding their cat's socialization to humans

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Animal shelters and rescue groups accept cats with unknown backgrounds and have to determine if the cat is unsocialized to humans or if the cat is socialized but too frightened to show normal behavior. Adoptability and euthanasia decisions often depend upon how well-socialized the cat appears to be. However, no validated methods of determining socialization status exist. A survey (CS) was designed for cat owners, fosterers and caregivers to report cats' behavior towards people in their normal environments. Respondents rated cats' behavioral propensities in various situations from 0 (never) to 10 (always). An overall socialization score (OSS) was calculated as the median of these ratings. Two sanctuaries with long term resident cats were studied. Two caregivers independently completed the CS for each cat (inter-rater reliability) and repeated it one month later for the same cat (test-retest reliability). At one sanctuary 2 staff caregivers rated 31 cats each. At the other sanctuary 36 staff and volunteer caregivers with 48 unique pairings rated 54 cats (inter-rater) and 48 cats (test-retest). Spearman correlation coefficients and 95% confidence intervals were calculated for each question and the OSS. Inter-rater and test-retest agreement was higher at the first sanctuary (0.71-0.98) than the other (0.21-0.85). Inter-rater correlations were <0.5 for questions about cat's reaction to a new place, reaction to caregiver approaching while cat eats, cat's activity level and cat staying near caregiver. Test-retest correlations were <0.5 for questions about reaction to caregiver approaching while cat eats and cat's response to an unfamiliar person arriving. The OSS had high inter-rater and test-retest correlations at both sanctuaries (0.81-0.99). The CS shows promise as a reliable instrument to assess cats' socialization to humans.

Relinquishment Factors Affecting Stray Dog Population in Urban Fragments

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The stray dog's population has been a problem in modern society and raises discussion on different issues like animal welfare, environmental responsibility and public health matters such as dogs bites, zoonosis and traffic accidents. Sao Paulo is a city with eleven million inhabitants and a population of owned dogs around 2.5 million animals. There are no surveys on the distribution of the population of stray dogs and this affects any plan of intervention. In this work, the problem was addressed from the standpoint of relinquishment's probability and environmental carrying capacity. A score was created with thirteen variables out of known risk factors for relinquishment. The data was grouped by district and classified in to three categories (terciles). A convenience sample of six areas was defined (two of each category), chosen to be small and isolated areas, liable to go through on foot. The number of animals was estimated by the pseudo capture method, using photos and notes to identify the animals. Simultaneously, a questionnaire was administered in a systematic random sample of households in each area. Of the six visited areas, only two had dogs roaming in the streets, and only one seemed to have a resident stray population. The score was not as good to predict the presence of stray dogs as the degree of human-dog proximity and environmental factors were. Intervention on these factors through encouraging responsible ownership and enhancing garbage collection could be a solution to gradually reduce the population of stray dogs.

Demography and management of British horses, 2009-2011

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The equine population of Great Britain (GB) is estimated at over one million, yet data regarding demographic characteristics are limited. This study aimed to describe the demographics and assess seasonal and geographical variations in management of the British horses. A cross-sectional study was conducted, using a postal questionnaire survey of randomly selected horse owners registered with 30 veterinary practices in GB. 797 questionnaire responses were received. Median age of animals was 13 years; 56% were male; 33% were ponies (≤ 147.3 cm) and the most common breeds were Thoroughbred (TB)/TB-cross (25%) and Welsh/Welsh-cross (17%). Most animals (87%) were kept at or within 10 km of their owners' home premises. Only 4% were stabled 24 hours/day, with a greater proportion stabled full time in winter compared to other seasons ($P < 0.001$). Duration of stabling differed between seasons ($P < 0.001$) but not geographically. Most (92%) had access to pasture (median 91 hours/week), with seasonal and geographical variation in pasture turnout (both $P < 0.001$). Most animals received forage (83%) and concentrate feeding (86%). Retired animals and ponies less frequently received any supplementary feed and feeding practices varied seasonally. The majority of animals were used for pleasure riding (61%) and 18% were used primarily for competition, with geographic variation in proportions participating in certain ridden disciplines. Animals were exercised for a median of 5 hours/week. In the 7 days, 22% had been transported by vehicle, for a median of 35 minutes, with seasonal variation in distance travelled and journey time ($P = 0.01$). Demographic characteristics of this study population are similar to previous descriptions of the GB equine population. Seasonal and geographical variations in feeding and management practices were identified, and primary use and management differed for horses and ponies, which will be relevant in the investigation and management of diseases.

Comparison of prevalence of feline leukemia and immunodeficiency viruses in feral cats on the San Francisco peninsula, 2001-2003 and 2005-2007

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Peninsula Humane Society's spay/neuter clinic provides discounted or free services for feral cats in San Mateo County, a mixed suburban and rural county of 700,000 people south of San Francisco. If cats receiving free services test positive for feline leukemia virus (FeLV) or feline immunodeficiency virus (FIV), they are euthanized. Some colony caretakers objected to this policy, prompting this study to determine the prevalence of FeLV and FIV among feral cats presented to the clinic. Between 2001 and 2003, 28 of 1772 (1.6%) and 85 (4.8%) cats tested positive for FeLV and FIV, respectively. FeLV-positive results among male cats ranged from 0.6% to 3.3%; females had similar results. FIV-positive results ranged from 7.8 to 8.2% for males and 1.7% to 2.6% for females ($P < 0.01$ for each year). These proportions did not decrease during this first 3-year period. Overall, the prevalence of FIV was higher, and for FeLV was lower, compared with other U.S. studies. From 2005 through 2007, 22 of 1846 (1.2%) and 107 (5.8%) cats tested positive for FeLV and FIV, respectively. FeLV-positive results among male cats ranged from 0.7% to 2.5%. For females, FeLV-positive results were significantly fewer in 2006 ($P = 0.01$). FIV-positive results ranged from 9.5 to 13.0% for males and 1.1% to 2.6% for females ($P < 0.01$ for each year). Male cats were more likely to be FIV-positive in the later 3-year period ($P = 0.3$). Feral cats from certain cities in San Mateo County were more likely to be positive for these diseases in both 3-year periods. Efforts at neutering of feral cats, and thus disease reduction, have been focused in communities where FeLV and FIV prevalences are highest. Curiously, FIV prevalence for males has increased in spite of increased spay/neuter opportunities in the area ($P = 0.03$ for trend). This trend has been reported elsewhere, and raises questions regarding the best way to control this disease in free-living, community cats.

Populational coverage of mass vaccination against rabies in São Paulo

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Rabies is an important zoonosis that affects almost all mammals and has wide geographical distribution, with a lethality of 100% in humans with clinical signs. Despite of its reservoir in Brazil being bats, the occurrence of human cases was more related to the contact with rabid dogs and cats. The authorities implemented in 1968 a prophylactic program and with capture of strays and public vaccination campaigns for companion animals, since 1983 the city of São Paulo did not register an autochthon case of animal rabies. In 2010 the mass vaccination was suspended due to technical difficulties and was not resumed since. In this work, we aimed to determine the vaccination coverage in the year of 2007, prior to the sudden interruption of campaigns. We used data of population size and distribution and proportion of that population that looked for vaccination in private clinics and compared with the vaccination points location given by the authorities. We assumed homogeneous distribution of the population in each study area (districts), after excluding water bodies and forest, and assumed the range of vaccination points to be similar to those of Guarulhos, observed in the 2000 campaign. With the median range of coverage, the mass vaccination campaign would reach 1,329,230 dogs and 329,166 cats, which added to the 698,947 dogs and 128,802 cats vaccinated in private clinics makes estimated vaccination coverage of 84% of dogs and 83% in cats. It is important to notice that 66% of vaccinated dogs and 72% of vaccinated cats would have received the vaccine in the public campaign. That data shows clearly the impact on vaccination coverage of the interruption of the campaign. Considering that immunity may last around 3 years and that we still have positive isolation in the city bat population, the lack of effective public vaccination since 2009 is the a possible cause of a new rabies case.

Associations between exercise and joint injury in Thoroughbred racehorses in training

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This study aimed to identify exercise-related risk factors for carpal and metacarpo-/tarsophalangeal (MCP/MTP) joint injury occurrence and progression in young Thoroughbreds in flat race training. In a 2-year prospective cohort study, daily exercise and joint injury data were collected from horses in 13 training yards in England. Four injury categories were defined: (1) localised to a carpal or MCP/MTP joint based on clinical examination and/or use of diagnostic analgesia, no diagnostic imaging performed (n=21); (2) localised to a carpal or MCP/MTP joint, no abnormalities detected on diagnostic images (n=21); (3) evidence of an abnormality of subchondral bone and/or articular margin(s) identified using diagnostic imaging (n=72); (4) evidence of discontinuity of the articular surface identified by diagnostic imaging (n=70). Survival analysis using Cox regression was used to identify risk factors for injury type, category and progression. 647 horses spent 7,785 months at risk of joint injury and 184 injuries were recorded (82 carpal, 102 MCP/MTP injuries). Increasing distances cantered in short periods were associated with a decreased risk of sustaining any joint injury, Category 1, 2 and 3, and MCP/MTP injuries. Greater canter distances in 30 days increased the risk of Category 4 injury. Risk of Category 1 injury increased with increasing distances of weekly high-speed exercise. MCP/MTP injury risk increased with accumulation of canter or high-speed exercise since entering training. Progression of joint injury was associated with increasing exercise distances in short time periods and medical treatment. In conclusion, modifications to exercise regimens could reduce joint injury occurrence and progression. The use of medication in horses with joint injury clearly requires further research.

A nested case-control study to identify risk factors for recurrent colic

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A nested case-control design was used with cases and unmatched, randomly selected controls selected from a previous longitudinal cohort study of 127 horses recruited via first opinion equine veterinary surgeons subsequent to an episode of medical colic. Telephone questionnaires at 4 monthly intervals collected data on risk factors and on recurrence of colic. All recurrent colic episodes were selected as cases and the data relating to 30 days prior to the colic were used to determine exposure status. Three controls per case were randomly selected from all horse time at risk. Multivariable logistic regression analyses were used to determine risk factors for recurrence of colic with a random effect term for 'horse'. In total 59 recurrent colic episodes and 177 controls were included. The final model showed that horses that displayed crib-biting/windsucking behaviour (CBWS), weaved, had reduced access to pasture and were fed probiotics had an increased risk of colic. Fruit/vegetables as part of the diet appeared to have a protective effect against recurrence. A significant interaction was found whereby the risk associated with CBWS was modified by feeding fruit and vegetables. The use of a nested case-control design within the cohort study enabled capture of time-varying exposures. In contrast to previously published case-control studies on colic the exposures were recorded prior to becoming a case. Recurrent colic is a risk for horses that have experienced a medical colic and the study findings provide evidence to support approaches to colic prevention. The behavioural risk factors identified may highlight individuals at higher risk for recurrent colic whose colic prevention strategies should be carefully managed.

Tail injuries in working dogs in Scotland

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The pre-emptive docking of dogs tails to reduce the risk of injury remains a controversial issue in the UK. In 2007, England, Wales and Scotland introduced a ban on non-therapeutic docking of dogs' tails. England and Wales introduced exceptions for certain working breeds and working breed types, such as dogs destined to be used for shooting, whereas Scotland opted for a complete ban on all non-therapeutic docking. The Scottish Government made a commitment to examine the evidence on the effect of this all inclusive ban some years after the original decision. As part of that review we have conducted research with the following broad aims: (1) estimate the prevalence of tail injury in working dogs and working dog breeds which have been docked to different lengths; (2) identify risk factors for tail injury in working dogs in Scotland. We conducted three studies to address these aims: an online survey; examined clinical veterinary records; and a prospective case-control study. This abstract briefly describes the results of the online survey. The incidence of owner reported tail injury varied significantly with respect to breed and tail length. Spaniels and Hunt Point Retrievers were significantly more likely to incur a tail injury, while working, than other working breeds ($P < 0.001$). Compared to undocked tails or tails that had just had the tip removed, docking by one-third, half or short was associated with a significant reduction in the likelihood of tail injury ($P \leq 0.001$). There was no significant difference in the likelihood of tail injury between dogs that had tails docked by one-third, half or short. These results indicate that docking by one-third may be sufficient to provide the maximal reduction in the likelihood of tail injury in working dogs and that docking to a shorter length may be of no significant extra benefit in terms of preventing future injury. The authors gratefully acknowledge the Scottish Government for providing the funding for this project.

An epidemiological investigation of the African horse sickness (AHS) outbreak in the AHS surveillance zone of the Republic of South Africa during 2011

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African horse sickness (AHS) is an insect-borne (*Culicoides* spp.), highly fatal disease of horses caused by African horse sickness virus (AHSV). Four AHS control zones occur within the Republic of South Africa (RSA) and the outbreak investigated occurred within the AHS surveillance zone (AHS SZ) within the Western Cape Province of RSA. Outbreaks of AHS have occurred within the surveillance zone in the past, the most recent occurring in 1999 and 2004. The outbreak of AHS serotype 1 described here occurred between February and May 2011, which is during the late summer and autumn months and corresponds with the period of highest appropriate vector activity. The outbreak began in the small informal settlement of Mamre in the AHS SZ. The community keeps horses in communal grazing areas outside of the town with some animals roaming free within the town's confines. The initial detection was based on clinical and *post mortem* signs associated with acute AHS. The outbreak most affected Mamre but there were cases in other small settlements within a 20 km radius. In total there were 72 confirmed cases during the outbreak and a location specific incidence of the disease within Mamre itself reached 0.17 (95% conf. 0.13-0.22) as 56 of the cases occurred in this area. Total outbreak case fatality rate was 0.89 (95% conf. 0.79-0.95). Control measures implemented during the outbreak included equine owner education, movement control in the district and a ring vaccination campaign with OBP polyvalent AHS bottle 1 vaccine containing AHS serotype 1. The vaccination campaign influenced the extent and impacts of the outbreak and an estimated 95% coverage of equines was attained. The source of the outbreak was never confirmed although it is thought to be as a result of an unreported movement into the surveillance zone.

The antimicrobial resistance learning site for veterinary students

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Recognizing the crucial role of veterinarians in mitigating antimicrobial resistance (AMR), the U.S. Centers for Disease Control and Prevention (CDC) funded the development of a suite of multimedia, open-access, web-based educational materials to promote responsible veterinary use of antimicrobials. The website was completed in early 2011, and is now publicly available at <http://www.amrls.msu.edu>. The modular organization allows for convenient integration into existing veterinary courses and for use as homework. Pre-clinical modules cover basic topics regarding antimicrobials, mechanisms of resistance, spread of AMR, and ways in which AMR impacts animal and public health. Largely through presentation of basic foundational information, case-studies, and examples, the AMRLS helps teach veterinary students to assess and balance competing stakeholder interests and arrive at treatment plans for selected clinical presentations where antibiotic conservation may be possible. Presentations utilize varied learning formats such as animations, audiovisual lectures, case-based presentations, graphic illustrations, interactive quizzes and videos. Modules are also downloadable as PDF files for those who prefer to study hard copies or need to review learning materials offline. Questionnaires, documentation, and analytics were used to determine user feedback, describe marketing and promotional activities, characterize the site traffic, and determine whether AMRLS improved veterinary student attitudes, normative behavior, perceived control, and intentions in practicing prudent antimicrobial usage in the future. This initial evaluation showed that the AMRLS can be an effective resource for teaching veterinary students about AMR.

Managing the risk of antimicrobial resistance by maximising the use of the available evidence

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Antimicrobial resistance is a public health issue of increasing global relevance. In Europe, risk management decisions related to the use of antimicrobials in food animals are shared between the European Commission (EC) and The European Medicine Agency (EMA). Risk assessments are conducted by EMA, the European Centre for Disease Control (ECDC) and the European Food Safety Authority (EFSA). Whilst, in Europe, the use of antimicrobials as growth promoters has been banned since 2006, the EC has recently published a risk management action plan. One element of the plan is the promotion of 'prudent use' principles. Another key suggestion is improvements in the monitoring of resistance development. Data are currently collected by EMA from EU Member States (MS) on the amount of antimicrobials sold for veterinary use. Also, annual reports on trends in resistance are being collated for zoonotic and indicator bacteria by ECDC and EFSA. However, appropriate surveillance must be part of a mitigation strategy in order to achieve economic benefits. Surveillance conducted as a stand-alone activity is not an effective risk management measure. Surveillance should rather provide feedback on the impact of mitigation activities. Examples exist that demonstrate that data on antimicrobial usage and resistance are mainly used descriptively. However, there is potential for these data to feed into a larger risk assessment framework, for example, as part of post-licensing pharmaco-vigilance. Currently, a formal feedback loop linking usage data with resistance is not established nor is the prevalence of resistance linked to possible interventions, such as limiting the use of a substance or its withdrawal. In only a few cases are monitoring data utilised as part of a risk mitigation decision. Here we present the current gaps in utilising antimicrobial usage and resistance data and present a roadmap for the development of an integrated framework that would permit more complete utilisation of the available data.

Molecular epidemiology of pig-associated ST398 MRSA in Scotland

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ST398 is a major pig-associated methicillin-resistant *Staphylococcus aureus* (MRSA) lineage in Europe. It is of great interest in terms of animal wellbeing, livelihood, economy, and also for the potential risk of transmission to humans and within human populations. This latter example of transmission known as zoonotic MRSA (also as livestock- or farm-associated MRSA (LA- or FA-MRSA)) is becoming increasingly prevalent in Europe as the incidence of MRSA in livestock increases. It most commonly affects those that work closely with livestock and domestic animals including farm workers and veterinary staff but it can also spread to their families and potentially the wider community. In the 2010 EFSA report on MRSA in breeding pig holdings in Europe, no MRSA was found in breeding pigs in the UK. Despite this, ST398 has been found in human public health data in Scotland. The question remains as to the origin of the strain in Scotland. Here, using tools in molecular epidemiology and evolutionary genetics, we investigate whether these isolates were likely zoonotic in origin and if they have likely been imported from abroad or have evolved locally from methicillin-sensitive *Staphylococcus aureus* (MSSA) strains.

The use of antibiotics in livestock: pilot study 'VetCab'

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Similar to other European countries in Germany the use of antibiotics in livestock husbandry shall be registered. In order to establish a monitoring system a feasibility study was carried out in 2007 and 2008 that tested a data collection and evaluation concept. This project is continued by a pilot study in 2011 and 2012 which aims at evaluating representative data in farms and veterinary practices. In this pilot study, every use of antibiotics in pigs, cattle and poultry is registered retrospectively (one year) via the veterinarians' official application records. Data are pseudonymised and stored in a central database. Agricultural structures of German districts are analysed in order to choose a representative sample of farms and practices. The analyses concentrate not only on the amount of drugs used, but also on the number of applications and the estimation of the average number of application per animal within a farm or within a region. Furthermore, the use of different substances, indications, treatment duration and change of substances are analysed. As the use of antibiotics is linked to the selection for resistant bacteria, possible hazards regarding the use of antibiotics will be addressed in the discussion. This includes the identification of important aspects of antibiotic use (treatment duration, formulation, substances concerning human health, etc.) as well as possible measures to reduce the need of antibiotic treatment. On the conference the progress of the study as well as first results will be presented.

The use of informatics to describe patterns of antimicrobial use by companion animal veterinarians
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Increasing antimicrobial resistance among the common enteric pathogens such as *Campylobacter*, *Salmonella*, *Bacteroides*, *Helicobacter*, *Clostridium*, and *Giardia* has diminished the clinical utility of some antimicrobials in human and veterinary medicine. There a growing number of case reports demonstrating that people can share multidrug resistant bacteria with their pets but there have been minimal investigations into the diagnostic and treatment regimes in companion animal medicine that can contribute to antimicrobial resistance. The antimicrobial use data that is necessary to estimate the strength of association between antimicrobial use and antimicrobial resistance have not been available. A data extraction program was developed and installed at 12 computerized sentinel companion animal practices in the city and the surrounding rural communities of Calgary, Canada. Data was collected from January 1, 2007 to Dec 31, 2009. The extracted data was integrated and stored in a data warehouse for analyses. A linguistics-based text mining program was used to automatically encode and extract cases of diarrhea. There were 13,063 cases with a complaint of diarrhea. It was determined that 37% of the cases were treated with antimicrobials and 97% of the prescribed antimicrobials are considered of very high importance for treating life-threatening infections in humans (Nitroimidazoles, Penicillin β -lactam inhibitors, 3rd and 4th generation Cephalosporins and Fluorquinolones). In the group that was treated with antimicrobials 34% had diagnostic testing performed and 15% had a positive etiological finding. The empirical treatment of cases of diarrhea in pets has resulted in the substantial use of antimicrobials also important in the treatment of human infections. Surveillance of the antimicrobial resistance profiles of commensal and pathogenic bacteria from pet fecal samples is advocated.

Belgian veterinary surveillance of antimicrobial consumption report 2010

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This second BelVetSAC report, covers the data on veterinary antimicrobial consumption in Belgium in the year 2010. Data consist of all veterinary antimicrobials sold to a veterinarian or pharmacist and of antimicrobial premixes incorporated in medicated feed for the year 2010. It includes thus consumption data for farm animals as well as companion animals. The denominator for animal production was the biomass (in kg) calculated as the sum of the amount of beef, pork and poultry meat produced, plus the number of dairy cattle present in Belgium. The overall evolution in total tons of active substance (antimicrobial pharmaceuticals + antimicrobial premixes) shows a slight decrease of 1.6% from 2009 to 2010. The use of antimicrobial pharmaceuticals has decreased with 5.2%, however the use of antimicrobial premixes has increased with 16.3%. These evolutions are a confirmation of the trend already seen between 2008 and 2009. When looking at the antimicrobial use in function of the biomass a comparable evolution is observed with a decrease of antimicrobial pharmaceuticals of 9.0% and an increase of antimicrobial premixes of 11.6%, resulting in a total decrease of antimicrobials used per kg biomass present of 5.6%. The opposite evolution in use between pharmaceuticals and antimicrobial premixes is likely to be the result of a shift in use from on farm applied pharmaceuticals to in feed administered premixes. The most applied antimicrobial classes are the sulphonamides and trimethoprim (89 tons, 29.7%) followed by the penicillines (80 tons, 26.7%) and the tetracyclines (74 tons, 24.7%). Although these data show a favorable evolution towards a decreased antimicrobial consumption they also show that the reduction is limited in comparison to several other European countries with comparable animal production systems. These results reemphasize the need for vigorous actions directed to all stakeholders, towards a reduced use of antimicrobials.

Quantification of antimicrobial usage in farm animals: ABcheck a free online web application

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Knowing the magnitude of antimicrobial usage in a herd is of great importance to implement changes and focus on prudent use. To quantify antimicrobial usage on pig, poultry and turkey farms an 'antibiotic check' scoring system has been developed. From June 2011 onwards the system is freely available online (www.ABcheck.ugent.be) in Dutch, English and French. A ruminant module is expected soon. ABcheck gives farmers, veterinarians and herd advisors the opportunity to calculate treatment incidences (TI), using herd specific data. Additional information is provided, for example if the antimicrobial is critically important according to the World Health Organization (WHO) or World Organisation for Animal Health (OIE). The system works totally anonymous. The only information that needs to be provided is the number of animals per production round, product, amount used and treatment duration. Herd specifics like production round duration and animal weight are prefilled, but can be adjusted. ABcheck can be used for prophylactic and curative treatments. Scores can be saved and reclaimed after registration. Benchmarking is visually done by showing a graph. The database behind the calculator consists of all antimicrobials registered in Belgium for specific animal categories. For each antimicrobial, the animal daily dose (ADD) was established by taking average dosage prescriptions from product leaflets. Factors for long acting antimicrobials were estimated from available scientific research papers. All used ADD's can be found on the website. At the moment data from 20 reproduction, 69 piglet and 36 finisher herds, 47 broiler and one turkey flock are in the database. The database is dynamic. Newly saved data are added directly to the graphs. The graphs show a wide variety in antimicrobial usage amongst pig and poultry herds in Belgium, with treatment incidences from zero till 275 for reproduction animals, nearly zero to almost 1,800 for piglets, zero till 650 for finishers and 50 till 500 for broilers.

Spatial description of *Escherichia coli*, *Salmonella* sp. and *Pseudomona aeruginosa* antibiotic resistance findings in livestock in southern Chile in 2010-2011

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Antimicrobial resistance (AR) is one of the most important issues in animal and human health worldwide. AR means the full or partial resistance to antibiotics acquired by some pathogens, especially bacteria. The overuse of antibiotics in domestic animals and crops is considered as one of the main causes of AR, together with overprescription by medical doctors and improper use by patients. The OIE provides methodologies and recommendations to appropriately address the emergence and spread of resistant bacteria, recognizing as a key element, the development of antimicrobial resistance surveillance and monitoring programmes. The aims of this study were to describe the AR of the most relevant pathogens in Southern Chile's livestock production and to spatially characterize these findings. In this study, 50 animal registers were found to have antibiograms in their files. All the relevant information associated with these animals was collected and analyzed. AR was found in 25 samples of *Escherichia coli* (50%), 14 (28%) of *Salmonella* sp. and in 11 (22%) of *Pseudomona aeruginosa*. From all the different antibiotics tested, the most resistance was found for amoxicillin-clavulamic acid (78%, 39 samples) and oxytetracycline (73%, 35 samples), whereas the most sensitive antibiotics were found to be cefoperazone (4%, 1 sample) and gentamicin (4%, 2 samples). Moreover, all these samples had shown patterns of multiresistance. All these cases were geographically referenced and the spatial distribution is provided. The AR status needs to be monitored and these findings should be used to help veterinary practitioners, veterinary authorities and public health authorities to improve the responsible and effective use of antibiotics.

Identification of the best antimicrobial usage indicator for resistance analysis: an application to time series in poultry production

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The best antimicrobial usage indicator for the analysis of the relationship between animals antimicrobial exposure and resistant bacteria carriage has not yet been defined. To check for any differences between indicators (such as percentage of flocks exposed or amount of live weight treated) a joint time-series analysis of monthly data related antimicrobial usage and bacteria resistance in turkey and chicken broiler productions was carried out. As part of French monitoring programs, pathogenic *Escherichia coli* resistance towards 11 antimicrobials was studied and linked to corresponding antimicrobials usage expressed as (1) a percentage of flocks treated at least once; (2) a number of treatments recorded (standardized according to the corresponding number of flocks produced); and (3) the amount of live weight treated (standardized according to the corresponding amount of live weight slaughtered). SARIMA Box and Jenkins models were fitted. Criteria such as AIC, BIC and R², were secondly analysed to compare transfer function models performances and check for the 'best' antimicrobial usage indicator considering the strength of the relationship and the proportion of best models fitted. Results displayed significant relationships between usage and resistance trends, consistent across indicators. No obvious and unique 'best usage indicator' could be formerly identified as conclusions differed depending on the species studied. Other studies have to be performed and other criterion related to cost and feasibility of data collection will also have to be taken into account defining a 'best indicator'.

Center of expertise on antimicrobial consumption and resistance in animals AMCRA in Belgium

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In view of the transmission risk of highly antibiotic-resistant strains between animals and humans, controlling resistance is essential to safeguard the future efficacy of antimicrobial agents in veterinary as well as human medicine. Therefore, a Center of expertise on Antimicrobial Consumption and Resistance in Animals (AMCRA) has been recently founded in Belgium by the Belgian Agricultural Organizations, pharma.be, the Order of Veterinarians, the Belgian Association of Compound Feed Manufacturers, the Faculties of Veterinary Medicine of Ghent and Liège, together with the Federal Agency for Medicines and Health Products and the Federal Agency for the Safety of the Food Chain. AMCRA has become operational from the 2nd of January 2012 and will propose guidelines to direct the whole animal industry towards a rational reduction of antimicrobial use. The mission of AMCRA is to collect and analyze all data related to antimicrobial use and resistance in animals in Belgium and to communicate the outcomes in a neutral and objective manner, in order to safeguard both public and animal health and welfare, and to achieve a durable policy of veterinary antimicrobial use in Belgium. The main objectives for the first working year of AMCRA are the establishment of national guidelines for antimicrobial use in food animals, the provision of autoregulatory measures in livestock production, the proposition of an antimicrobial consumption data collection system that allows accurate measurement and trend monitoring per animal species, and the development of information and awareness campaigns for veterinarians and farmers. To achieve these goals, working meetings will be organized ensuring maximal participation of all stakeholders involved. Only through concerted action, the challenging goals of this industry-wide and unique initiative can and will be met.

Identification of highlight areas for antibiotic soil accumulation and antimicrobial resistance in the EU
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Release of antibiotics into the environment through the agricultural reuse of animal manure is considered a cause of chronic environmental exposure that often leads to adverse ecotoxicological effects, as well as to the introduction of antibiotic-resistant bacteria into the environment. The vulnerability of soil to antibiotic contamination plays a major role in determining the extent of the contamination and the likelihood of the appearance of environmental effects. Understanding how soil vulnerability varies geographically, the resource allocation among surveillance programmes could greatly improve. This paper performs a risk analysis of the EU region for 12 antimicrobials by using a spatial assessment: (1) antibiotic release was estimated based on livestock density; (2) exposure was estimated based on antimicrobial soil contamination; (3) consequence was modelled based on soil uses; (4) risk was estimated by combining release, exposure and consequences using spatial multicriteria decision analysis (ArcGIS 9.3). The Getis-Ord Gi statistic was used to identify clusters of areas at high risk for antibiotic soil contamination. Enrofloxacin was the highest-risk antibiotic in the EU, followed by tetracyclines, tylosin and sulfodiazine. The highest risk was found in Belgium, Ireland, Netherlands, Switzerland, Denmark, Germany and the UK. The results suggest that this methodology can be used successfully for evaluating the contamination potential of antibiotics over large areas with limited input data. This work is a preliminary step in the prioritization of the use of veterinary medicinal products (VMPs). It represents a good way in guiding both, monitoring studies and antimicrobial surveillance programmes, and also to inform on the sustainable decision-making for interventions designed to mitigate the risk of VMPs. This work was financed by S2009/AGR-1489 and RTA2010-00066-C02-01.

Antibiotic residues and antimicrobial resistance in cow manure

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The usage of antibiotics in animal husbandry has dramatically increased the concentration of antibiotic residuals and has promoted the development and abundance of antibiotic resistance in manure and farm environments. The use of manure as fertilizer is a common agricultural practice. When the manure is spread onto agricultural land, both residues of antibiotics and bacteria carrying antibiotic resistance genes may be introduced into the environment. In this research, we isolated resistant gram negative bacteria from manure produced in two dairy and two feed cow farms, located in Madrid, Spain, to determine their resistance to seventeen representative antibiotics commonly used in veterinary therapy. Sampling was performed in winter and summer. The average bacterial densities were $6.85E+05$ colony formation units (cfu)/ml (feed cow) and $2.80E+05$ cfu/ml (dairy cow) in summer and $1.10E+06$ cfu/ml (feed cow) and $2.03E+06$ cfu/ml (dairy cow) in winter, respectively. The bacterial isolates were identified as: 22% *Escherichia coli*, 17% *Comamonas testoteroni*, 9% *Pseudomonas aeruginosa*, 8% *Proteus vulgaris* and 8% *Serratia marcescens*. They were found to be mainly resistant to tetracycline (68%), sulphamethoxazole (55%), ampicillin (52%), cephalothin (47%), chloramphenicol (44%), nalidixic acid (39%) and trimethoprim-sulphamethoxazole (32%). Additionally, we examined the presence of three tetracyclines in all manure samples with stable recoveries (76-82%) and high sensitivity (limit of quantification 0.015-0.03 µg/kg). The concentrations of tetracyclines detected (0.1-10 mg/kg) were consistent to the estimated tetracyclines levels in manure according to the excretion rate of these antibiotics and the livestock data and amount of tetracycline used in Spain. This work was financed by S2009/AGR-1489 and RTA2010-00066-C02-01.

Trends in antimicrobial susceptibility patterns of *Staphylococcus aureus* from bovine mastitis in Israel
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Staphylococcus aureus is a major bovine mastitis pathogen causing enormous economic losses in the dairy industry worldwide. Although in Israel major contagious pathogens like *S. aureus* are responsible for less than 3% of the isolates from individual bovine milk samples, considerable effort is made to control their prevalence and to monitor their antibiotic resistance. The laboratory for udder health and milk quality of the Israel Dairy Board performs antimicrobial susceptibility tests for udder pathogens by agar disc diffusion method (Kirby-Bauer) according to CLSI recommendations and with respect to an annual scheme. *S. aureus* isolates are tested against a panel of antibiotics, including penicillin, nafcillin, marbofloxacin, lincomycin and more. This data provides a good estimate of the antimicrobial susceptibility of udder pathogens on the national level and on the herd level. In the last decade the susceptibility results of *S. aureus* reveal interesting findings: there is a constant rise in the susceptibility to penicillin with only 51% susceptible isolates in 1999 to more than 80% susceptible isolates in 2011. Different factors can contribute to this phenomenon including antimicrobial usage on the farms. Data collected from 2000 to 2011 includes 4,174 penicillin-antibiogram results for *S. aureus*. In a logistic regression model the adjusted odds ratio (OR) for penicillin resistance was 1.4 for isolates from Moshav (family farms) compared to Kibbutz (cooperative farms) (95% CI 1.3-1.6) whereas the OR for sub-clinical isolates compare to clinical mastitis isolates was 1.3 (95% CI 1.1-1.5). Other significant factors were the parity of the cow (resistance of heifer's isolates was 1.5 times less compared to adult cows), the herd size (higher resistance in smaller herds) and the geographic region in the country. The results of this study indicate that antibiotic resistance is influenced by environmental and human associated factors.

Antimicrobial resistance of equine *Salmonella* isolates in the Northeastern United States (2001-2010)
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Our objectives were to describe the antimicrobial resistance status of equine *Salmonella* isolates from the northeastern U.S. and to identify trends in resistance over time. Data were collected retrospectively for all equine *Salmonella* isolates with antimicrobial minimal inhibitory concentrations (MICs) identified at the Cornell University Animal Health Diagnostic Center from January 1, 2001 to December 31, 2010. MICs of isolates were determined using the microbroth dilution method (TREK Sensititre). Data for 459 equine *Salmonella* isolates with MICs were retrieved (median of 45 isolates per year; range 20-83). The majority were from clinical submissions (feces) either from regional veterinarians or the Cornell University Hospital for Animals. Of 146 isolates that were serotyped, the most common serovars were Typhimurium (including the 5- variant; 32.2%), Oranienburg (23.3%), Holcomb (6.8%), Newport (6.8%), and Thompson (6.8%). Most isolates (98.4-100%) were susceptible to amikacin, enrofloxacin and imipenem. Cochran-Armitage tests showed a decreasing trend in resistance over time ($P \leq 0.005$) to amoxicillin/clavulanic acid (AUG), ampicillin (AMP), cefazolin, cefoxitin (FOX), ceftiofur (TIO), chloramphenicol (CHL) and tetracycline (TET). Increasing resistance was not found for any of the 16 drugs tested. There were 380 isolates tested for nine National Antimicrobial Resistance Monitoring System (NARMS) panel drugs. The most common resistance patterns were pan-susceptible (38.2%), AUG-AMP-FOX-TIO-CHL-TET (16.6%), AUG-AMP-FOX-TIO-CHL-TET-Trimethoprim/sulfamethoxazole (SXT) (12.4%), AUG-AMP-FOX-TIO-CHL-TET-SXT-Gentamicin (GEN) (11.3%), and AMP-TIO-CHL-TET-SXT-GEN (7.6%). Although antimicrobial resistance among equine clinical isolates did not increase for any drug and declined for several antimicrobial agents, multidrug resistance was common in the region with 60.5% of isolates showing resistance to two or more drugs on the NARMS panel.

In vitro screening for antibacterial activity of lactic acid bacteria against *Campylobacter jejuni* and applying a selected *Enterococcus faecalis* strain in a broiler seeder experiment

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Human campylobacteriosis is mainly caused by consumption of *Campylobacter jejuni* contaminated broiler meat. Lowering the *C. jejuni* excretion and external contamination of broilers prior to slaughter can lead to a reduction of campylobacteriosis cases. The objective of this project is to lower *C. jejuni* colonization and excretion during primary production using living lactic acid bacteria as probiotic additives. 1,149 *Lactobacillus*, *Lactococcus*, *Leuconostoc* and *Enterococcus* strains were tested for anti-*Campylobacter* activity using different plating methods. We excluded the influence of acid and hydrogen peroxide production and investigated bacteriocin production by performing proteinase, heat and catalase treatments on partly purified supernatant. Based on inhibitory properties, six strains (*Lb. salivarius*, *Lb. helveticus*, *Lb. reuteri*, *Lb. agilis*, *Enterococcus faecalis* and *Enterococcus faecium*) were selected. No bacteriocin production was identified. Next, controlled batch fermentation studies to simulate broiler cecal environment were performed with a selected lactic acid bacterium. We used three experimental designs: (1) inoculation of *C. jejuni* followed 6 hours later by inoculation of a lactic acid bacterium; (2) simultaneous inoculation of both strains; or (3) inoculation of a lactic acid bacterium, followed 24 hours later by *C. jejuni*. Obtained results suggest that at least 1 log reduction of *C. jejuni* is possible when the *E. faecalis* strain is co-inoculated. Finally, broiler chicks were inoculated daily with 10⁴ cfu/ml *E. faecalis* strain in an *in vivo* experiment. At the age of 15 days two seeder birds per group were inoculated with *C. jejuni*. The *E. faecalis* strain was unable to reduce cecal *C. jejuni* colonization.

Antimicrobial usage and antimicrobial resistance on veal calf farms in the Netherlands

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Antimicrobial drug use is considered to be the major risk factor for development of resistance in the intestinal flora of food producing animals. The aim of our study was to determine the prevalence of resistance to 5 common used antimicrobials within veal calf herds and to investigate the influence of administered antimicrobial drugs throughout the fattening period within these herds on the resistance levels. In total 50 veal calf fattening farms were visited approximately 2 weeks before slaughter. Per farm, faecal samples from twenty veal calves were collected manually per rectum and prepared into one pooled sample. From this pooled sample 90 *Escherichia coli* isolates were tested for their resistance to 25 mg/l amoxicillin, 25 mg/l tetracycline, 0.5 mg/l cefotaxime, 0.125 mg/l ciprofloxacin and 8/152 mg/l trimethoprim-sulfamethoxazole (tmp/s). Data on antimicrobial usage during the fattening period on the sampled farms were collected by the Agricultural Economics Institute of Wageningen UR (LEI), and provided as the animal daily dosage per production cycle (ADD/pc). Logistic regression analysis showed that administration of fluoroquinolones was associated with a significant higher odds of resistance to ciprofloxacin (OR 1.89, P<0.05), administration of penicillines was associated with a significant higher odds of resistance to ciprofloxacin (OR 3.73, P<0.05) and tetracycline (OR 2.35, P<0.05) the administration of tetracyclines was significantly associated with tetracycline resistance (OR 3.40, P<0.05) and the administration of tmp/s was significantly associated (P<0.05) with a higher odds on resistance to amoxicillin (OR 3.34), tetracycline (OR 3.09) and tmp/s (OR 3.35).

Antibiogram of bovine mastitis pathogens in Canada

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Monitoring of antimicrobial resistance (AMR) in bacteria has clinical and public health significance. The present study determined antibiogram of common mastitis pathogens, including the prevalence of methicillin-resistant *Staphylococcus aureus* (MRSA) (n=1,810), and extended-spectrum β -lactamase (ESBL) producing *Escherichia coli* (n=394) and *Klebsiella* species (n=139) isolated from milk samples of 89 dairy farms in 6 Canadian provinces. MIC were determined using Sensititre bovine mastitis plate and National Antimicrobial Resistance Monitoring System Gram-negative panel containing antimicrobials commonly used in a clinical setting. Denim blue chromogenic agar and real-time PCR was used to screen and confirm MRSA, respectively. Resistance proportion estimates ranged from 0% for cephalothin and oxacillin to 9% for penicillin in *S. aureus* isolates, while 15% of the resistant *S. aureus* isolates were multi-drug resistant (MDR). One MRSA isolate was confirmed (prevalence: 0.05%). Resistance proportion estimates ranged from 0% for ceftriaxone and ciprofloxacin to 15% for tetracycline in *E. coli*, and 0% for amikacin, ceftiofur, ciprofloxacin and nalidixic acid to 19% for tetracycline in *Klebsiella* species isolates. Further, 63 and 55% of the resistant *E. coli* and *Klebsiella* species isolates were MDR, respectively. Resistance to >5 and >2 antimicrobials was most common in *E. coli* and *Klebsiella* species isolates, respectively. No ESBL producers were found. In conclusion, resistance to antimicrobials of very high importance in human medicine such as third-generation cephalosporins, penicillin- β -lactamase inhibitor combinations and fluoroquinolones is uncommon to rare in bovine mastitis coliforms. MRSA was rarely found and ESBL *E. coli* and *Klebsiella* species isolates were absent in Canadian milk samples. The study results suggest a low risk of transmission of AMR bacteria from milk or milk products to human populations.

Fluoroquinolone resistant *Escherichia coli* carriage in Australian dogs, with particular emphasis on ST131

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Multidrug resistant *Escherichia coli* of sequence type ST131 is a pathogen of humans and animals that has disseminated globally since its recent emergence. The well documented ability of ST131 to spread quickly among humans as well as pets within a single household make it a strain of significant veterinary public health concern. An Australian study has shown that out of 125 fluoroquinolone resistant (FQ-R) canine clinical *E. coli* isolates, nine (7.2%) belonged to ST131. As to non-clinical isolates, a survey of a major small-animal referral hospital found that 23 out of 123 surveyed dogs carried FQ-R *E. coli*. Two dogs (1.6%) were shown to carry ST131. This study investigated if this prevalence was typical for eastern Australia by enrolling an additional nine hospitals across two states (NSW & QLD). Faecal samples were taken from dogs at admission and discharge and spread on media containing 0.25 and 2.0 $\mu\text{g/ml}$ ciprofloxacin (intermediate and resistant levels, respectively). Isolates were tested for *E. coli* phylotype, ST131 status, virulence gene (VG) profile and fingerprint (RAPD) by PCR. A total of 114 faecal samples (range 1-32, median 10 per hospital) were received from a total of 72 dogs. One of the hospitals yielded FQ-R *E. coli* isolates (>2.0 $\mu\text{g/ml}$) from two dogs out of 14 sampled (14.3%). All FQ-R isolates were phylogenetic group A and carried VGs qualifying them as extraintestinal pathogenic *E. coli* however they were not ST131. Although only one out the nine hospitals had FQ-R *E. coli*, the potential pathogenic nature of these isolates suggest that veterinary hospitals should include screening for FQ-R *E. coli* as part of their infection control.

Changes in the prevalence and antimicrobial resistance of multilocus sequence types of *Salmonella* on Michigan dairy farms in 2000 and 2009

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Dairy farms serve as reservoirs of *Salmonella* that cause foodborne illnesses. Prior cross-sectional studies of *Salmonella* on dairy farms in the United States suggest important changes within this microbial population. We used a retro-prospective study and molecular subtyping techniques to test the hypothesis that the prevalence of *Salmonella* multi-locus sequence types (STs) has changed between 2000 and 2009. Retrospective data collected in the year 2000 from 29 Michigan dairy farms were retrieved, and comparable prospective data were collected from 18 of the same farms in 2009. Where farms were positive in both years, isolates underwent further subtyping and antimicrobial resistance (AMR) testing. The ST was identified by determining the partial gene sequence of seven housekeeping genes. A generalized linear mixed model was used to analyze changes in the prevalence of *Salmonella* between 2000 and 2009. Fisher's exact tests were used to compare the distribution of ST's within farms. The proportion of samples positive for *Salmonella* was significantly higher in 2009 (11%) than in 2000 (5%). In 2009, *Salmonella* was more frequently recovered from cows, whereas in the year 2000, calves were more frequently positive. Six farms that were positive for *Salmonella* in both years, and 11 and 9 different STs were recovered in 2000 and 2009, respectively. Six STs were recovered in both years. The within-farm distribution of STs between cow and calf samples varied depending on the AMR profile. Multidrug resistant ST's recovered in 2000 were more likely to be recovered from calves. In 2009, susceptible strains of the same ST were more evenly distributed between cows and calves. These results suggest population changes in *Salmonella* that have resulted in less frequent antimicrobial resistance and more frequent colonization of adult dairy cattle.

Using milk from cows on antimicrobial therapy as feed for calves: a potential risk for selection of resistant bacteria?

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The aim of this ongoing study is to describe how and to what extent waste milk from cows on antimicrobial therapy is fed to calves on Swedish dairy farms and whether this approach can be linked to the high prevalence of antimicrobial resistance among fecal *Escherichia coli* from calves. In a web-based survey, a representative sample of 457 farmers responded to questions covering the use of colostrum and milk from cows subjected to antimicrobial therapy. On 300 of the farms, fecal swabs from three preweaned calves will be collected for antimicrobial susceptibility testing. For each sample, resistance to 14 antimicrobial substances and the within-sample prevalence of *E. coli* resistant to cefotaxime, streptomycin and quinolones will be determined. Additional data regarding use of antimicrobials will be collected from databases as well as through a second questionnaire to the farmers. Eighty-nine percent of the farmers feed newborn calves colostrum from cows treated at drying off. When a cow is treated with antimicrobials during the lactation, 80% of the farmers use milk produced during the treatment period and/or the withdrawal period, as feed for calves. Preliminary results from antimicrobial susceptibility testing of fecal *E. coli* show that antimicrobial resistance is more common on farms that give calves waste milk, and on farms where more than one type of antimicrobials is used for treatment of calves and more than three types of antimicrobials are used for treatment of cows. This study indicates that use of milk from cows treated with antimicrobials is widespread on Swedish dairy farms and that this approach in combination with use of several types of antimicrobial drugs might have an impact on the prevalence of resistant *E. coli* from calves.

Evaluation of the quality of data on antimicrobial use in Swiss dairy cattle herds

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Monitoring antimicrobial use is crucial for designing strategies to contain antimicrobial resistance. In most countries, detailed data on the application of antimicrobials can only be obtained from records kept by farmers or veterinarians. However, incomplete or absent treatment information can result in substantial bias of these data. The aim of this study was to compare the quality of on-farm treatment data recorded by veterinarians and farmers and to examine whether prior instruction leads to an improvement of data quality. Farmers from 97 dairy cattle farms were asked to record in detail all treatments given within 1 year. On 15 farms, farm records were compared to the record of the responsible veterinarian. At a later time point, we also evaluated records from 8 veterinary practices and 204 dairy cattle farms. These additional data originated from routine treatment documentation involving farmers and veterinarians with no prior instruction and no involvement in the first part of the study. Our results show that both, records from farmers as well as from veterinarians, contained substantial deficiencies. Of all treatments, 9% were only recorded by farmers, 23% only by veterinarians and just 68% of treatments were recorded by both. An agreement between treatment date, drug used, and applied dosage was only seen in 52% of both records. Due to lack of standardization, the analysis of routinely documented data proved to be very elaborate. As an example, 17% of records had no information on dosage and for 88% treatment indication was missing. Our results show that a reliable documentation of antimicrobial use is only possible through standardized methods and detailed instructions of those involved. An electronic record system is certainly advantageous since it allows a standardized record keeping and an automatic analysis of the data.

A qualitative study of factors associated with use of antimicrobials in first opinion small animal practice in the UK

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Responsible use of antimicrobials in veterinary practice is essential to mitigate the risk of antimicrobial resistance (AMR). However, there are scarce data on factors that influence veterinarians when selecting antimicrobial therapy in everyday practice. Qualitative methods (i.e. framework and grounded theories) were selected to investigate the decision-making process involved in the selection of antimicrobials. A convenience sample of 21 veterinarians from 7 first opinion veterinary practices in the UK were interviewed. Veterinarians combined both their clinical experience and acquired knowledge when selecting antimicrobials. Easiness of administration of antimicrobials was an important factor as it often conditioned the selection of a specific preparation and consequently the antimicrobial substance used. Extrinsic factors associated with pet owners were perceived compliance to prescribed therapy, socio-economical background, willingness and ability to treat their animals. At practice level, cost of therapy was found to be influential in the decision-making process. Cost issues were particularly observed in veterinary practices located in mixed and deprived demographic areas. In these cases, veterinarians stated that they would consider changing their selection of antimicrobials and consider cheaper antimicrobial therapies. Selection of less efficacious antimicrobials could lead to the selection of AMR, with compromise of the animal's health and welfare. Cost of diagnostic tests was a barrier to achieve a confirmed diagnosis and consequently, affected selection of antimicrobials. Overall, factors other than existing guidelines and scientific knowledge influenced veterinary surgeons when selecting antimicrobials in everyday practice.

Identification of *Salmonella* and *Escherichia coli* strains circulating in backyard poultry in the central zone of Chile

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The Chilean poultry sector had improved its production and quality standards by the early 1990s. These sector is highly integrated at both the geographical and industrial levels. However, other kinds of animal production can be identified. Backyard production systems (BPS) also breed poultry and are the most common form of animal production worldwide, being recognized as an important component of small farmers' livelihoods. BPS have been generalized as production units having severe biosecurity deficiencies, the animals and their by-products are usually consumed by their owners, sold locally and used as gifts. BPS can play a major role in the circulation of animal diseases and zoonotic pathogens, such as *Salmonella* and *Escherichia coli* strains. BPS management conditions facilitate the interaction between poultry and humans, which may result in an increased risk for the human and or animal health. Nevertheless, there is a lack of research which surveys for the presence of pathogens circulating in BPS, to determine if these animal production units represent a real risk for human and or animal health. This research will identify the presence of *Salmonella* and *E. coli* strains in BPS in central zone of Chile, test the susceptibility of the organisms to antibiotics and evaluate risk factors for the circulation of these pathogens. The initial activities for this research will be performed between March and May 2012, in the region of LGB O'Higgins, where there are approximately 9,000 farmers who breed backyard animals. Samples will be collected by cloacal swabs and analyzed in the laboratory of infectious diseases (Faculty of Veterinary Science). A survey will be conducted, to identify the risk factors for the circulation of antibiotic resistant *Salmonella* and *E. coli* strains in BPS, through logistic regression analysis.

ESBLs in pig farming in the Netherlands

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Antimicrobial resistant bacteria in livestock are considered an emerging public health concern, due to possible transmission to humans through food or contact with livestock. A recent example is the presence of extended-spectrum beta-lactamase producing bacteria (ESBLs) in poultry (meat). Infections in humans with ESBLs may lead to treatment failure. Little is known about prevalence and dynamics of ESBLs in other production animals (e.g. pigs). This study aims to determine the prevalence and determinants of ESBL carriage in people working or living on pig farms and in pigs. We enrolled 40 Dutch pig farms and analysed per farm 10 pools of 6 faecal swabs each. On 36 farms, 141 farmers, family members and/or employees also submitted a faecal sample for analysis. These samples were analysed for presence of ESBL microorganisms by selective plating and analysis of ESBL genes by means of microarray analysis and gene sequencing. Questionnaires were filled out on antimicrobial use, hygiene, contact with animals and/or meat, farm characteristics, possible confounders, etc. Preliminary results indicate that 13 participants (9%) were positive for ESBL genes. These participants, of whom 8 were farmers, originated from 7 farms where ESBL genes were found, and 3 farms where ESBL genes were not found. In total, on 22 farms (55%) ESBL genes were found in pigs. The ESBL types found included mainly CTX-M-1, commonly found in poultry. This is the first study to determine ESBL presence in people working and/or living on pig farms and in pigs. There are no detailed studies available on ESBL prevalence in the general Dutch population, so a comparison cannot be made. However, a recent study showed ESBL-producing *Escherichia coli* in 6 out of 18 broiler farmers. Preliminary analyses indicated that carriage was associated with intensity of animal contact.

Modelling costs of highly pathogenic avian influenza control in Australia

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Australian emergency plans for highly pathogenic avian influenza (HPAI) recognise that vaccination, pre-emptive culling and early slaughter of meat chickens, ducks and turkeys in abattoirs (process slaughter) may support stamping-out under some scenarios, but the effectiveness of these additional measures are uncertain. We used a spatial stochastic simulation model (AISPREAD) to investigate the effectiveness of six disease control strategies measured by the number of infected farms, epidemic duration and number of destroyed birds. AISPREAD models HPAI spread between individual chicken meat and layer, duck and turkey farms, includes farm production cycles, and simulates HPAI transmission between farms by 'local spread', poultry movements, and indirect spread via service provider networks. We simulated epidemics in two high poultry density areas of Australia. Control strategies included a baseline strategy involving the quarantine and culling of infected premises (IPs), zone-based movement restrictions in 3 km Restricted Areas (RAs) and 10 km Control Areas (CAs), tracing, and surveillance. This was modified to investigate effects of: increasing RA and CA zones to 10 and 20 km; pre-emptive culling in 3 km of IPs; process slaughter of meat farms in 3 km and 10 km of IPs; and combining process slaughter of meat farms and vaccination of other farms in 10 km of IPs. Costs of compensation, disease control centres, purchase and use of vaccine, lost export earnings, and post-vaccination surveillance were compared using partial budgeting. Process slaughtering meat farms within 10 km of IPs was the most effective strategy in terms of the model outputs. Additional vaccination of other farms in this zone had similar effects on epidemics, but cost \$A 6-7 million more. This suggests vaccination is not cost-effective for the control of HPAI epidemics in Australia.

Assessing the risks of Rift Valley fever virus introduction from international aircraft and ships: implications for emergence

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Rift Valley fever (RVF) is a vector-borne viral zoonosis that can cause abortion storms, high mortality rates in young ruminants, and flu-like symptoms in humans which may lead to permanent disability, in particular visual impairment, and even death. RVF was first described in 1910 in the Rift Valley, Kenya. Since then, its geographical distribution has been steadily expanding to beyond the geographical borders of the African continent. A qualitative risk assessment identified international aircraft and ship movements as high risk for RVF introduction into the Netherlands. This paper presents the results of the subsequent step: a quantitative risk assessment of introducing RVF by international aircraft or ship. The estimated mean annual number of RVF infected mosquitoes introduced was thirteen. With a 95% CI: 1-56. The probability per year that the import of RVF infected mosquitoes by aircraft leads to at least one infected Dutch ruminant was calculated to be 0.089, or once every 12 years, with a 95% confidence interval of 0.003 and 0.440 (between 2.3 and 330 years). Ruminants around Schiphol airport near Amsterdam, The Netherlands are most at risk, while ruminants around the harbour of Rotterdam have a very low risk of infection. The main reasons for this being the large area covered by the harbour, the heavy urbanization of the area, and the lack of ruminants in close vicinity to the actual harbour. This study has wider implications because the results add to the existing evidence that aircraft and ships are very efficient vehicles for the global dispersal of vectors and thus play an important role in the introduction of various exotic (zoonotic) diseases in hitherto disease free countries. Therefore, it is recommended to (1) adequate coherence to aircraft disinfection guidelines and policies, and (2) to implement targeted, risk-based surveillance of exotic mosquitoes at airports and harbours.

***Alaria alata*: new approaches for identification and differentiation of a re-emerging parasite**

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Alaria alata is a trematode, the adult of which is found in mammalian carnivores throughout Europe and Asia. The mesocercarial stages of the *Alaria* spp. may infect almost all vertebrate species, including humans, and especially omnivorous scavengers such as wild boars serve as paratenic hosts for the parasite. The pathological consequences of human alariosis, relevant symptoms, and therapeutic strategies have been described. However, the wide variety of possible symptoms makes this parasitic disease difficult in diagnosis and requires specific detection methods for exclusion of other diseases. Since 2002 an increasing number of findings of *A. alata* mesocercariae in meat of wild boars in Germany and other European countries during official meat inspection initiated an assessment of the potential foodborne human health risk posed by this parasite. In view of the insufficient data, a final risk assessment could not be performed, which led the German Federal Institute for Risk Assessment to a preliminary recommendation to declare carcasses of wild boars found to be infested by *A. alata* mesocercariae during official inspection for *Trichinella* spp. unfit for human consumption. Within the framework of two research projects (funded by the German Federal Ministry of Food, Agriculture and Consumer Protection through the Federal Office for Agriculture and Food) our own studies concentrate on (1) the development, optimization, and validation of methods for reliable *Alaria* spp. mesocercariae detection; (2) the distribution of the mesocercariae within their paratenic hosts, i. e. identification of predilection sites, particularly in wild boars; and (3) their prevalence in sylvatic populations of animals with respect to their introduction into the human food chain.

Serological survey in captive tayassuids (Mammalia:Artiodactyla) in Guatemala, searching for antibodies against viruses and bacteria

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In 2008, blood samples were collected from 13 white-lipped peccaries (*Tayassu pecari*) and 64 collared peccaries (*Pecari tajacu*) in several captive populations in Guatemala. In 2010, blood samples were collected from two *T. pecari* and 26 *P. tajacu* at Petencito Park (Petén) to firstly assess diseases status of these wildlife species in Guatemala. The prevalence of antibodies in the 2008 samples was 35% for Classical Swine Fever, and 0% for Brucellosis and Mycoplasmosis; all positives had a vaccination history. For tayassuids sampled in 2010, prevalence of antibodies was 29% leptospirosis (serovars Pomona, Pyrogenes, Autumnalis, Bataviae and Icterohaemorrhagiae) and 0% for Brucellosis and Classical Swine Fever. *Mycoplasma* was not evaluated in the 2010 samples. There was no influence of sex over the prevalence for leptospirosis (Fischer's exact test $P=0.4198$). The relevant results are the report of a *Leptospira* strain (Pyrogenes) not previously reported in peccaries in the cited references. The absence of other pathogens does not mean that the species cannot harbour them as proven in literature; nevertheless, the husbandry of these captive populations could have contributed to the health improvement. Incidental findings of haemoparasites such as *Trypanosoma* sp. and *Babesia* sp. are also reported. These results serve as a basis for further studies focusing on peccaries and other Guatemalan native species and contribute information about the health status and the potential pathogens within captive populations of tayassuidae in Guatemala.

Investigation of occurrence and geographical distribution of canine dirofilariasis in Bosnia and Herzegovina

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Recently many research efforts were done to map and estimate spread of dirofilariasis and its competent vectors in countries and regions previous thought to be free from this disease. However, countries of Central and Eastern Europe are still considered as zones where data on this disease are inconsistent, incomplete or completely lacking. We will present the findings of the first comprehensive study of canine dirofilariasis in Bosnia and Herzegovina (BiH) aiming to detect whether canine dirofilariasis is present in the country as either 'autochthonous' or imported infection and to estimate rough geographical distribution of this parasitosis. Blood samples were collected from 418 dogs coming from different locations across the country during period from May 2008 to November 2009. Data on sex, age and previous traveling were noted for all dogs. All samples were tested by Knott test in order to detect, enumerate and differentiate microfilaria belonging to agent species. In addition two serological tests; Snap canine test and ELISA test were also used to detect *D.immitis* infection (both produced by IDEXX laboratories). Animal was considered to be diseased with at least one positive result on any of the tests used. Two etiological agents were found; *D.immitis* and *D.repens* in 3,1% and 1,9% of samples, respectively. Canine dirofilariasis was proven to be 'autochthonous' diseases present in areas of the country with Mediterranean and Moderate Continental climate. Due to the effects of the global warming previously unseen species of dirofilariasis vectors are noted BiH, such as Asian tiger mosquito (*Ae.albopictus*). Since this is an anthropophilic mosquito species, there is a risk for dirofilarial infections of humans as well.

Efficacy of a control program for brucellosis in small-holder sheep and goats flocks in Tajikistan

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Cross-sectional serological surveys conducted in Tajikistan in 2003 and 2009 were used to evaluate the efficacy of a 5 year pilot control program which was based on initial whole flock conjunctival vaccination of sheep and goats with Rev1 and biannual vaccination of immature animals thereafter. Seroprevalence was reduced from an initial 8.9% (95% CI 7.8, 10) to 1.8% (1.3, 2.4) in eight districts where vaccination was generally well implemented and the prevalence of households with evidence of infection in their animals was reduced from 25.1 to 7.5%. Seroprevalence was modestly reduced to 60% (50, 80) of 2003 levels in 10 districts where vaccination was intermittent and coverage was low in some years. It was unchanged in 19 districts where there were no interventions. Constraints associated with subsistence type agriculture, a low budget, numerous private smallholdings, communal grazing and annual migrations to summer pastures influenced the design of the pilot program. Experience from the program identified needs for biannual vaccination, surveillance to measure efficacy and coverage, quality assurance of cold chain and vaccines and consideration of sheep and goats separately rather than together as small ruminants. Sheep and goats vaccinated one or more times were found to be 2.5 and 6.4 times more likely to be serotest positive than unvaccinated sheep and goats respectively, suggesting longer persistence of vaccinal titres in goats than in sheep. Future programs will incorporate partial cost recovery for services and will make some changes to the sampling strategy based on experience from the pilot program. Failed activities such as tattooing for identification will be discarded. A pleasing outcome from the pilot program has been the adoption of its methods in national control programs in two other Central Asia countries with similar husbandry systems.

Rift Valley fever in a temperate and mountainous area of Madagascar

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A serological study was performed in 2009 in Madagascar highlands to evaluate the point prevalence rate of RVF antibodies in ruminants and identify environmental and trade factors potentially linked to RVF persistence and transmission. Nine hundred ruminants were randomly selected among 51 villages and sampled. Sera were analysed using a commercial validated ELISA test. For each ruminant, the following variables were recorded: age, location of the night pen, minimum distance from the pen to the closest water point and the forest, water point type, and the way owners use to renew their herd: auto-renewal vs purchase. Serological data were analysed using a generalized linear mixed model, the individual serological status being the binomial response, and the above-mentioned variables the explicative factors, and the breeder as random effect. The overall IgG seroprevalence rate was 28% [IC95% 25-31]. The main effect on prevalence was due to age ($P=10^{-4}$) suggesting an endemic RVF circulation in this area. The distance to the closest water point was a protective factor ($P=5 \times 10^{-3}$) but the type of water point had no effect on the prevalence rate: a substantial part of the transmission is due to vectors and several mosquito species are probably involved. Ruminants belonging to owners renewing their herd by purchase were significantly more infected than others ($P=0.04$), suggesting that cattle trade may contribute to the circulation of the virus in this area. This is the first evidence of a recurrent transmission of RVFV in such an ecosystem which associates a wet, temperate climate, high altitude, paddy fields, and vicinity to a dense rain forest. Persistence mechanisms need to be further investigated.

Managing FMD hotspots in the Mekong region

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FMD is endemic in the Mekong region and recent studies in northern Lao PDR and southern Cambodia have confirmed that although outbreaks of mainly O serotype do occur widely, they have tended to recur in particular 'hotspots' where significant trading of mainly large ruminants from adjacent countries exist. As the epidemiology of FMD in these 'hotspots' is poorly understood, we conducted a longitudinal study in the 'hotspot' area of Paek district in Xiengkhoung province in northern Lao PDR, where a major FMD outbreak occurred in early 2009 that was largely prevented in 2 villages by prior vaccination, and again in early 2010 when vaccination was unavailable. On both occasions, collection of tissue samples from infected animals confirmed infection with FMD virus serotype O (Myanmar topotype) and surveys documented high morbidity in unvaccinated cattle and buffalo (>90%), with occasional mortality. We also identified the risk factors of increased trading in animals after the end of the rice harvest and failures of biosecurity at the village level as major contributors to the severity of disease expression. A pre and post vaccination serological study conducted of the large ruminant population in late 2010 and early 2011 (n=40 and 72 serum samples respectively) analysed by serotype-specific LPB-ELISA assay to detect antibodies to serotype O, A and Asia1 FMD virus structural proteins, confirmed both previous exposure to FMD virus, plus significantly rising post-vaccination titers indicating likely protection against future infection. It was concluded that to manage future FMD outbreaks in this 'hotspot', regular annual vaccination of the majority of the adult large ruminant population prior to the peak risk period in December-January, plus improved farmer knowledge of disease transmission risks to address failures in biosecurity are required.

HP-PRRS in Southeastern Cambodia: an epidemiological study

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The aim of our study was to investigate the presence of highly pathogenic PRRS in the Cambodian pig population. Six provinces in the southeastern part of the country were selected. Between July and September 2010 a cross-sectional study (Study 1) was carried out, to estimate the prevalence of the disease in semi-commercial farms (SCF), while a second, parallel study was designed to detect the disease in villages, sampling backyard farms (BF) only. Questionnaires on husbandry practices and spatial coordinates were collected from each farm. The target population for Study 1 were the entire SCF in Takeo province. A sampling frame with all active SCF was available and farms were randomly selected. Pigs were then selected through systematic sampling in each farm. For this particular study lot quality assurance survey (LQAS) method was chosen to calculate the number of farms to be sampled. The target population for Study 2 were all the villages in the six provinces. A sampling frame of villages by district was available. A qualitative assessment for a-priori risk of viral introduction at district level was designed to prioritize district to be sampled. Within prioritized district, villages were selected by simple random sampling. Within village the selection of individual BF was done through random walking method and the selection of the single pigs through systematic sampling. Our results showed that the virus was present in the semi-commercial pig population (herd prevalence $\geq 85\%$), but appeared very sporadically in the backyard pig population in that region. Presence of sow and gilts in the farm, farms density and water contamination were significantly associated ($P < 0.05$) to the introduction and the presence of PRRS in SCF. The identification of risk factors associated with the introduction and the presence of the virus in the farm, and the spatiotemporal visualisation of our results, gives valuable insight into potential viral transmission patterns.

Cattle trade network in Madagascar highlands and Rift Valley fever virus circulation

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In 2008-2009 a RVF outbreak occurred in the Anjozorobe area, a temperate and mountainous area of Madagascar highlands. A serological study conducted there in 2009 showed an IgG seroprevalence rate of 28%. Data analysis suggested a recurrent circulation of RVFV. The objectives of this study were to describe the cattle trade network in this area and analyze the link between network structure and RVFV circulation. Questionnaire survey among 386 breeders from 47 villages was carried out to collect trade data. Yearly village-level seroconversion rate was estimated in 2010 by testing 516 cattle negative in 2009. Association between the occurrence of seroconversion and network centrality parameters, distance to the nearest water point and 2009 seroprevalence level was tested. Due to the non-independence of the centrality parameters, a bootstrap procedure was used to assess the effects of the independent variables. Average village-level seroconversion was 7%, ranging from 0-20%. Two types of trading practice were observed: exchanges and buy/sale. The corresponding networks appeared both scale-free, and a significant but low correlation was observed between them. A negative association was observed between the occurrence of seroconversion in the village and the 2009 seroprevalence level, as well as the distance to the nearest water point. After RVFV introduction, vector-based transmission may support the within-village circulation. The node degree in the exchange network was positively linked with the occurrence of seroconversion. It was not the case for the buy/sale network. Both networks could thus have distinct roles in RVFV circulation. The exchanges network could be the support for RVFV introduction in villages, the buy/sale network being probably rather implicated in the introduction of RVFV in the area, from other parts of Madagascar.

Survey of selected zoonotic and animal pathogens in muskoxen (*Ovibos moschatus wardi*) of Victoria Island, Nunavut, Canada

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The purpose of this study was to determine baseline prevalence of zoonotic and animal pathogens in muskoxen on Victoria Island, Nunavut, Canada. Muskoxen are hunted for subsistence, commercial sale, and sport; however, there are concerns for food safety, human health, and animal health. This information will provide the basis of a long term surveillance plan for the management of food security and food safety in northern communities. Muskoxen from two geographically distinct regions (one commercial harvest and two community harvests) were sampled during the winter of 2010. Tissues, feces, and sera were collected and tested for 18 different pathogens. Test methods included serology, bacterial culture, polymerase chain reaction, immunofluorescence assay, fecal flotation, Baermann, and histology. A total of 216 muskoxen were sampled. Positive seroprevalence results included: *Neospora caninum* (3/49), *Toxoplasma gondii* (1/49), and pestivirus (1/44). Samples tested negative for the following pathogens: alphaherpesvirus (n=44), *Mycobacterium avium* paratuberculosis (n=67), *Chlamydochloa* sp. (n=49), *Yersinia* sp. (n=67), *Giardia* sp. (n=202), *Cryptosporidium* sp. (n=202), and *Besnoitia* sp. (n=199). The lungworm *Umingmakstrongylus pallikuukensis* was present in all animals examined from the community hunts (n=26), but absent from commercially harvested animals (n=62). Overall, a low prevalence of pathogens significant to humans and animals was detected by the tests utilized. Additional work is required in validating these diagnostic test methodologies in this species. These results have contributed to the development of surveillance methodology to be used for monitoring changes in prevalence and changes in geographical distribution of pathogens, especially those of concern for human health.

Live bird markets as potential avian influenza A (H5N1) virus reservoirs in Vietnam and Cambodia: field survey and mathematical models of transmission

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In many parts of the world, wet markets are a key component of formal and informal food chains, providing fresh meat for consumers. They may, however, promote the emergence, spread and maintenance of livestock pathogens, including zoonoses. A survey was conducted to assess the potential of Vietnamese and Cambodian live bird markets (LBMs) to sustain circulation of highly pathogenic avian influenza virus subtype H5N1 (HPAIV H5N1). In 30 Vietnamese and 8 Cambodian LBMs, structured interviews were conducted with the market managers and 561 Vietnamese and 84 Cambodian traders. Multivariate and cluster analyses were used to construct a typology of traders based on their poultry management practices. Stochastic meta-population models of HPAIV H5N1 transmission were developed to assess the potential of LBMs to become virus reservoirs. As a result of their practices and large poultry surplus (unsold poultry reoffered for sale the following day), some poultry traders were shown to promote conditions favourable for perpetuating HPAIV H5N1 in LBMs. More than 80% of these traders operated in LBMs located in the most densely populated areas, Hanoi and Phnom Penh. The profiles of sellers operating at a given LBM could be reliably predicted using basic information about the location and type of market. Consequently, the risk of a given LBM becoming a virus reservoir could be relatively easily assessed and control strategies appropriately targeted to those markets. These findings are of particular relevance to resource-scarce settings with extensively developed LBM systems, commonly found in South-East Asia.

Dog ecology in Bali, Indonesia and implications for rabies transmission

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Over 100 human rabies deaths occurred during an ongoing epidemic in Bali, Indonesia. The basic reproductive number from this epidemic (1.2) is similar to estimates from elsewhere in the world, despite the high densities of dogs in Bali (>100 /km²). This lack of density dependent transmission has important implications for rabies control, but is difficult to explain. We investigated ecological factors affecting rabies transmission and spread in Bali. Household surveys (n=6,152) confirmed the high dog densities and that most owned dogs are free-roaming, with only 7% and 19% restrained in rural and suburban areas respectively, and these mostly restrained during the day only. We randomly selected and observed continuously 69 free-roaming dogs for 48 hours to quantify behaviour and movement during a period similar to the infectious period of rabies. Home ranges were small (90% kernel, median=0.6 km², mean=3 km²), but some displacements exceeded 4 km and most movements were constrained to roads. The skewed distribution of movements was similar to observations of rabid dogs. Most activity and contact occurred between 6-10am and 4-8pm, when dogs were less likely to be restrained. Despite small home ranges, high dog densities and frequent opportunities for contact demonstrate potential for sustained transmission and suggest that sociality can help explain the lack of density dependent transmission. Close correlation between movement and road networks should be used to improve epidemiological models and suggests means for strategic measures to contain rabies spread.

Shuni virus, an orthobunyavirus causing neurological disease in horses and wildlife in South Africa

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The cause of severe neurological disease in both humans and animals in South Africa remains largely undiagnosed. Horses are highly sensitive to some of these viruses and have been used as sentinels for the identification of arboviruses associated with neurologic disease in South Africa. During the seasonal occurrence of common vector-borne diseases such as African horse sickness and equine encephalosis, many horses have febrile, neurologic, and fatal infections for which the etiology remains undetermined. Our aim was to identify and characterise unknown viruses in cases of undiagnosed neurological disease in South Africa. In 2009 we identified a brain isolate as Shuni virus (SHUV) a horse with suspected viral meningoencephalomyelitis, using virus discovery techniques. SHUV-specific primers were then designed and used to test specimens from an additional 111 horses and 53 wildlife cases. We have been able to positively identify Shuni virus in 7 equine and 4 wildlife cases, including a rhinoceros, a buffalo, a warthog and a crocodile, presenting with neurologic disease. Phylogenetic analysis was used to further characterise the virus. Both equine and wildlife cases grouped together but showed geographical clustering distinct to the prototype strain from Nigeria. This virus has in the past been isolated from apparently healthy cattle, sheep and goats. Our study has assigned a disease association to this virus and suggests it may play a noteworthy role in encephalitis in South Africa thus emphasising the need for increased surveillance and disease characterisation in South Africa.

Detection of antibodies to tuberculosis antigens in free-ranging lions (*Panthera leo*) infected with *Mycobacterium bovis* in Kruger National Park, South Africa

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Bovine tuberculosis (TB), caused by *Mycobacterium bovis*, has become established in Kruger National Park (South Africa) in the Cape buffalo (*Syncerus caffer*) population and other species. Tuberculosis in prey species has resulted in infection and morbidity in the resident lion (*Panthera leo*) prides. The only validated live animal test currently available for lions is the intradermal tuberculin test. Because this test requires capture twice, 72 hours apart, of free-ranging lions in order to read results, it is logistically difficult to administer in a large ecosystem. Therefore, development of a rapid animal-side screening assay would be ideal in providing information for wildlife managers, veterinarians, and researchers working with wild lion prides. This study reports preliminary descriptive results from an ongoing project evaluating two serological tests for *M. bovis* (ElephantTB Stat-Pak and DPP VetTB). Disease status was determined by *post-mortem* culture and presence of pathological lesions in 14 free-ranging lions. Serological test results were found to be associated with *M. bovis* infection. Extended field studies are underway to validate these rapid animal-side immunoassays for *ante-mortem* screening tests for TB in lions.

Rabies surveillance methods in Bali and Flores, Indonesia

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Rabies is spreading in Indonesia, entering Flores in 1997, Maluku in 2003, North Maluku in 2006, Bali in 2008 and Nias and Larat in 2010, and extending its range in West Java. Early detection of new incursions and levels of prevalence is extraordinarily difficult due to rabies' long incubation period and very short period of clinical signs. Experience in combating rabies in Bali and Flores will be drawn on to discuss the different surveillance methods and strategies which are needed for early detection of rabies incursions to new areas, effectiveness of control strategies and programs, and eventual proof of freedom. Human deaths from rabies are often the first sign of new infected areas and by this time the disease may have been present for at least six months and be widespread in the local dog population. Media reports and increased public awareness can increase the rate of reporting of dog bites which increases the perception of disease spread but may not really reflect true incidence. Surveillance of dog brains is a more effective means of detecting rabies but selection of dogs for sampling can be very controversial, may be perceived as blanket culling, and may cause people to move their dogs, increasing the risks of spread. Some means to overcome the practical, social and institutional impediments to effective rabies surveillance in Indonesia will be suggested.

Wildlife as reservoirs of disease for livestock in Australia: the case of the feral pig

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Besides causing ecological damage and threatening native species in Australia, feral pigs potentially form a reservoir of diseases important for livestock production. These include both transboundary (e.g. foot-and-mouth disease, classical swine fever) and endemic (e.g. leptospirosis, *Salmonella*) diseases. We used *Salmonella* as a model to understand if and how FMD might spread in feral pig populations and form a reservoir which would delay or prevent disease eradication, should an incursion occur. We sampled (via aerial culling) 543 feral pigs at geo-referenced locations in a 5,000 km² study area in the remote Kimberley region of Western Australia. Both mesenteric lymph nodes and fecal samples were collected for *Salmonella* culture. In addition, fecal samples from 496 cattle in 47 geo-referenced groups cohabitating the study area with the feral pig population were collected and cultured for *Salmonella*. *Salmonella* was cultured from 240 (41%) pigs, mostly from fecal samples. A total of 39 different serotypes were isolated. *Salmonella* serotypes were further characterised using pulsed field gel electrophoresis. Nearly 100 unique pulsotypes were identified. *Salmonella* was cultured from 2% of cattle. Nine serovars were identified, but no dominant serotype was noted. There were 6 serotypes in common with feral pig isolates. Cattle isolates were more commonly recovered from areas without feral pigs. Based on PFGE analysis, cattle and pig serotypes showed only 58% similarity (compared to 84% similarity within the cattle serotypes). Spatial and molecular analysis results suggest that in this environment, feral pigs are unlikely to be an important reservoir of disease for domestic livestock.

Temporal-spatial epidemiology of 2010/2011 foot-and-mouth disease outbreaks in the Republic of Korea

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During the winter of 2010 to 2011, the biggest epidemic of foot-and-mouth disease (FMD) was ever recorded in the Republic of Korea. FMD infected animals were confirmed in a total of 3,748 farms during 144 days from 28 November 2010 to 21 April 2011. This study described the pattern of FMD outbreaks and analyzed aggregations of cases by time and space with 2010/2011 FMD outbreak data. Aggregation of FMD outbreak farms were analyzed by space-time permutation scan test. The numbers of FMD outbreaks were cumulated 16.5% by the end of December 2010, 80% by January, and 98.5% by February. Swine farms suffered from the worst damage during the 2010/2011 FMD epidemic. The largest numbers of outbreaks per day was recorded on the mid January when 127 farms were confirmed on one day. Four significant clusters of FMD infection were identified by space-time permutation method. The most likely cluster of FMD infection included 154 outbreak pig farms within 18 km radius in Hongseong-Boryeong-Yeosan, Chungcheongnam-do. These farms were infected between late January and early March. The spatial-temporal clusters of FMD outbreak insisted the potential spread of FMD virus by unidentified way within proximity, which is called 'local area spread.' Biosecurity strategies to minimize contacts among neighboring herds would be critical to prevent spread of FMD in local area through unidentified way.

Fighting cocks: risk for the Caribbean regarding avian influenza and Newcastle disease

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Cockfighting is an important tradition in many Caribbean countries and territories, with the legal status of cockfights varying by country. Uncontrolled movement of poultry may represent an important route for pathogen introduction and spread. The Caribbean Animal Health Network (CaribVET) conducted a survey in order to assess the risk of circulation of Avian Influenza (AI) and Newcastle disease (ND) through movement of fighting cocks. Potential risk pathways were identified by the CaribVET Avian Influenza and Newcastle Disease Working Group. A questionnaire was designed and sent to the 32 Chief Veterinary Officers of the Caribbean while additional information was collected through interviews with bird owners, breeders and fighting pit owners in five countries. Data analysis aims to: (1) improve the knowledge on gamecocks and understand activities carried out in the Caribbean, especially: the legal status of cockfighting, disease surveillance and control within the fighting cock population, as well as biosecurity measures; (2) assess the likelihood of contact between fighting cocks and commercial poultry in the countries/territories; (3) assess countries/territories' risk profiles based on the above-mentioned results. The movement patterns of fighting cocks were studied in order to identify pivotal countries/territories where increased surveillance for AI and ND may be warranted. Preliminary results show that almost all Caribbean countries/territories, as well as the American continent and Europe, are connected, either directly or indirectly. These results are being used for the development of adapted awareness campaigns for basic bird health and management and avian disease prevention and surveillance, in participating Caribbean countries/territories.

Determinants of vaccination coverage and consequences for rabies control in Bali, Indonesia

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Maintaining high vaccination coverage is key to successful rabies control, but mass vaccination of dogs is difficult and population turnover erodes coverage. Incidence decline following successive island-wide vaccination campaigns in Bali suggest good prospects for rabies eradication. To find gaps in coverage we used household surveys of owned dogs (n=12,234) and 23 transects of free-roaming dogs (n=1,079). Coverage was 10% higher in confined than in unconfined owned dogs, with more confinement in urban (77.3%) than rural areas (7.4%). Coverage was higher in adults (90%) than juveniles (<1 yr, 51%) due to births and insufficient targeting of pups. Fecundity studies suggest owners do not report pups which may be an obstacle for vaccinators. Villages with recent culling (4/27) in response to rabies reports had marginally lower coverage and higher proportion of juveniles than villages with no culling, suggesting replacement of culled dogs with unvaccinated pups. Coverage estimates from transects were much lower (39.9%) than household surveys (83.4%), possibly due to loss of vaccination collars, but also because free-roaming dogs include unowned or difficult to vaccinate dogs. Future campaigns should put more effort in vaccinating free-roaming dogs particularly in rural areas, with advertising to ensure owners vaccinate pups. Culling appears counterproductive to coverage, but sterilization could stabilize it by reducing births. Long-lasting collars would help identify vaccinated animals and reassure communities that campaigns are successful.

Why did H5N1 HPAI disappear from Nigeria: incidence and transmission characteristics of H5N1 HPAI outbreaks 2005-2008 in Nigeria

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Outbreaks of highly pathogenic avian influenza (HPAI) H5N1 occurred in Nigeria between December 2005 and July 2008. We described temporal and spatial characteristics of these outbreaks at State and Local Government Area (LGA) levels and estimated the spatially smoothed incidence risk. We also quantified the between-village transmission coefficient (β) and the reproductive number (R_e) in order to assess the effectiveness of control measures implemented. Thereby we classified the outbreaks into 2 phases: Phase 1 (Dec 2005-Oct 2006) represents the period when the Government of Nigeria managed the HPAI response measures, while Phase 2 (Nov 2006-Jul 2008) represents the time when the Nigeria Avian Influenza Control and Human Pandemic Preparedness project had taken over the management. A total of 25 of 37 States (67.6%; 95%CI: 50.2-82.0) and 81 of 774 LGAs (10.5%; 8.4-2.8) reported HPAI outbreaks between 2005 and 2008. The incidence risk of HPAI outbreaks at State level was 5.6% (0.7-18.7) for 2005, 50.0% (30.7-69.4) for 2006, 54.5% (29.9-80.3) for 2007 and 0% for 2008. Only few LGAs experienced HPAI outbreaks within affected States. The mean period between farmers noticing outbreaks and reporting them to veterinary authorities and between reporting and depopulation of infected premises was for both 4.5 days. We identified a large corridor in the western part of Nigeria and a smaller corridor in south-eastern part, where the risk of HPAI occurrence was lower than in the rest of the country. The overall mean β was 0.072/day (0.055-0.091), with both phases of the epidemic having comparable estimates. The R_e was between 0.55-1.35. These findings suggested that intervention measures implemented in the second phase had a comparable effect as those implemented in the first phase. The low R_e indicated that the epidemic was unstable and that H5N1 HPAI was unlikely to become endemic in Nigeria. The effect of HPAI control policies and possible ecological reasons why H5N1 HPAI did not become established in Nigeria are discussed.

Malignant catarrhal fever: a field trial of a novel vaccine strategy

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Pastoralists are among the world's poorest people, and in E. Africa face a precarious existence struggling to retain a traditional lifestyle in the face of growing pressures on livestock production. Increasing reliance on crop-based agriculture, and the resulting conversion of rangelands, threatens the integrity of some of the world's most important ecosystems. Control of livestock diseases is critical for improving pastoral production systems and supporting livestock-wildlife co-existence. Malignant catarrhal fever (MCF) is a fatal disease of cattle, caused by alcelaphine herpesvirus-1 (AIHV-1) that is transmitted from asymptomatic wildebeest calves, and has plagued Maasai communities for generations. The threat of MCF forces Maasai, at a time when forage quality is critical, to move cattle to less productive grazing areas to avoid wildebeest calves. This strategy carries a high economic cost and exacerbates the problems of a precarious lifestyle. Recent vaccination trials, using a live-attenuated AIHV-1 virus, showed that cattle were protected against experimental challenge. This study presents results of a randomized controlled field trial in Tanzania, using the same vaccination strategy but under conditions of natural challenge. The 2-year trial, involved a herd of 100 cattle, with 50 receiving vaccine and 50 adjuvant only. The herd was challenged by being grazed in proximity to wildebeest calves. Clinical data, and blood and nasal samples were collected to assess vaccine safety, immune response, infection status and clinical outcomes. We present data on the outcome of the trial, including results of clinical, serological and molecular analyses, which raise questions about vaccine protection in natural settings, and our conventional understanding of AIHV-1 transmission and pathogenesis.

Assessing classical swine fever control measures under uncertain viral constraints

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Classical Swine Fever (CSF) is a viral disease in wild boars (*Sus scrofa*) and domestic pigs causing huge economic impact on individual farmers and national economies. The management of the disease became even more complicated in the last decades due to endemicity in wild boar populations in several European countries. Huge effort is paid on CSF control in wild boar by oral mass vaccination, but few is known about the efficacy of the applied measures to control or eradicate the disease. Furthermore, virulence as a crucial parameter for disease dynamics varies widely between CSF virus strains and is highly uncertain. We implemented a spatially-explicit, individual-based wild boar population model, coupled with a CSF virus model on the level of individual traits. The model accounts for social behaviour of boar groups as well as individual variations in disease outcomes. Over a range of case mortality and duration of the infectious period (the virulence), we tested alternative spatial baiting strategies. We compared these scenarios regarding the performance of the management measured by final size of the infected area and long-term persistence. Our analysis showed that artificial immunisation can facilitate disease persistence under certain conditions. High success in virus eradication as well as prevention of disease spread was only possible with preventive vaccination in terms of baiting in front of the epidemic wave. Buffered vaccination was completely sufficient to exploit the effect of vaccination of the entire area, which translates strategic needs into a practical management plan. A buffer radius corresponding disease spread of one year revealed suitable to fully exploit the potential of oral mass vaccination. Although preventive baiting strategies are not yet implemented in the field due to EU legislation but with marker vaccines in sight, we recommend buffered baiting of the area with infected animals.

Epidemiology of subclinical salmonellosis in wild birds from NE Spain

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The epidemiology of subclinical salmonellosis in wild birds in a region of high *Salmonella* prevalence in pigs was studied. Three hundred and seventy nine fecal samples from 921 birds captured in 31 locations near pig premises and 431 (581 birds) from birds from 10 natural settings far from pig farms were analyzed for the presence of *Salmonella* spp. Positive samples were serotyped and antimicrobial resistance (AR) test performed. Phage typing and PFGE on isolates of *S. Typhimurium* were carried out. The prevalence of *Salmonella* positive samples was 1.85% (95%CI=0.93-2.77). A multivariable logistic regression, with observations clustered by site of capture, was used to determine major factors associated to prevalence of salmonellosis. Prevalence was positively associated with samples collected from birds in the proximity of a pig operation (OR=16.5; 95%CI=5.17, 52.65), and from non-migratory (or short distance migration) birds (OR=7.6; 95%CI=1.20, 48.04); and negatively related to mostly-granivorous birds (OR=0.4; 95%CI=0.15, 1.13). *Typhimurium* was the most prevalent serotype and 4 different XbaI PFGE patterns were detected that matched with the 4 phage types identified (U310, U311, DT164, DT56). The prevalence of multi-drug resistance was low (20%). In 3 farms a high degree of homogeneity among isolates from different birds was observed. These findings suggested that pig farms would facilitate the transmission of this infection among wild birds. The degree of bird congregation may have much to do on the infection transmission as phenotypic and genotypic relatedness among isolates from different birds were observed only in farms where abundant birds were seen.

Preliminary investigation into the epidemiology of endemic foot-and-mouth disease in cattle in the Far North, Cameroon

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The Far North Region of Cameroon is at a crossroads for multiple livestock husbandry systems, international livestock trade routes, and foot-and-mouth disease (FMD) virus pools. Though herders and government veterinarians in the region identify FMD as a problem in their herds and a significant portion of herders' veterinary expenditures go towards treating the disease, no vaccines are available in the region. This combination of herder and government interest, presence of different husbandry systems, and lack of artificial immunity make the area ideal for studying the epidemiology of endemic FMD. Preliminary serology data from a three-year prospective cohort study show an 81% prevalence of non-structural antibodies to FMDV in adult cattle; the presence of serotypes A, O, SAT-1, SAT-2, and SAT-3; and a 4% carrier rate based on presence of viral RNA in probang samples. Here we will present our initial analysis of these serology and PCR data as they relate to the different geographic areas and husbandry types in the region.

Towards eradication of rabies in Bali: review of progress

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Bali had been historically rabies free until the diagnosis of rabies in a human and in a dog in November 2008. As the first suspected case of rabies in Bali was diagnosed in a person, it is likely that the disease had previously gone undetected for some time in the dog population. A dog incubating rabies may have been brought in early 2008 by fishermen through unofficial ports into Bukit peninsula, Badung district in south Bali. By June 2010 rabies had spread throughout the island. Disease control efforts to date have been divided into three phases, namely district-by-district central point dog vaccination (December 2008-September 2010) then a first (October 2010-March 2011) and second (May 2011-September 2011) island-wide door-to-door mass dog vaccination program. In October-December 2011, all parameters used to evaluate control program success (average number of rabid dogs per month, apparent monthly attack rate, rate of spread, detection/village, number of known infected villages, human deaths, and incidence rate of dog bites over dog population) showed reduction since the first phase. Rabies was not eradicated from Bali, but in this period was almost entirely found in the owned free-roaming dog population with an increased proportion of puppies infected.

Epidemiological studies of H5N1 influenza virus in Vietnam: a review from both animal and human health perspectives

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To critically review epidemiological studies of H5N1 influenza A virus (H5N1) infection in both humans and animals in Vietnam. Published literature and reports, outlining epidemiological studies of H5N1 in Vietnam, over the period 2003-2011 and performed by researchers with both veterinary public health perspective and human health perspective, were reviewed. Although Avian Influenza viruses such as H5N1 circulating in animals pose threats to human health and increasingly are present in multi-strain mixed gene pool presentations and circulating among multiple hosts including humans, epidemiological studies of H5N1 from veterinary public health perspective were much more numerous than those from a human health perspective. This was true with respect to the scale of study as well as the comprehensiveness of the study i.e. consideration of key epidemiological components (e.g. full outbreak investigation, tracing, use of vaccination, spatial temporal analysis, modelling, and impact of social and social networks). Most studies considered either the health of either humans or animals. A few studies referred to and/or made linkages between human health and animal health. However, no joint efforts were identified that fully explored and validated the epidemiology of the animal and human interface of H5N1. Given the significant threats and potential impacts of H5N1 in both humans and animals, epidemiological studies in both veterinary public health practice and human health practice should be extended to explore the animal and human interface of disease. An ecohealth approach would be useful to target not only humans but also poultry and other animals in epidemiological studies of H5N1 and other emerging and re-emerging infectious diseases.

Geographic epidemiology of *Echinococcus multilocularis* in muskrats and red foxes in Lower Saxony

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Alveolar echinococcosis is an emerging infectious disease of public health concern. The cause of the zoonosis is the small fox tapeworm, *Echinococcus multilocularis*, which thrives among the canine and rodent populations in endemic areas in the northern hemisphere. The purpose of this study was to investigate the spatial epidemiology of *E. multilocularis* in muskrats in Lower Saxony (Germany). The regional prevalence of *E. multilocularis* in muskrats from 43 districts in Lower Saxony (Germany) from 2007 to 2009 was spatially analyzed. The overall prevalence in 2,963 muskrats was 2.6%, 95% CI=(2.0%, 3.2%). Choropleth maps were used to visualize the regional variation that ranged from 0% to 22%. Disease clustering was investigated by means of Moran's I and found to be very low: I=0.06. However, a disease cluster was identified using the flexible shaped spatial scan test. The cluster covered 9 regions with a relative risk of 2.9 in the same area where a cluster in foxes was identified previously. Furthermore a geographic correlation study revealed that significant risk factors for the prevalence of *E. multilocularis* in muskrats were the past prevalence in muskrats (1995-1999), the past prevalence in foxes (2003-2005), as well as the regional landscape elevation. While previous prevalence levels in muskrats and foxes are consistent with the tapeworm's lifecycle, landscape elevation might be an indicator for yet unknown risk factors. In conclusion, the geographic correlation of the fox tapeworm prevalence in muskrats and foxes has implications for human risk monitoring, as muskrats and humans are intermediate hosts of the tapeworm and might share a common root of infection.

A spatio-temporal analysis and detection of risk factors for bluetongue virus

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Bluetongue is a viral disease of domestic and wild ruminants, affecting particularly certain breeds of sheep with severe clinical disease, including mortality. In 2006, BTV was diagnosed in the Netherlands, Luxembourg, Germany, Belgium and France for the first time but by the end of the year the cases had been controlled. In 2007, there was a re-emergence of the disease in the region and in other surrounding areas including Denmark, Switzerland, the Czech Republic, as well as the United Kingdom. The focus of this paper was to carry out a risk factor analysis on the spread of the bluetongue virus, whilst taking into account spatial and temporal differences. Geographical factors available for analysis included climate data, land use, population, as well as available outbreak data on the scale of municipality. An initial exploratory analysis showed that there seemed to be a trend in the spread of BTV over time. Spatial autocorrelation tests also showed a significant autocorrelation between municipalities, a clear indication that local outbreaks may influence a municipality's outbreaks. A zero-inflated negative binomial model was used to analyze the data and this model accounted for overdispersion, inflated number of zeros due to some municipalities having no farms as well as some farms generally having very low risk of infection. The model also allowed for spatio-temporal effects.

Human and livestock brucellosis in two Mongolian provinces

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In Mongolia, human brucellosis is a huge public health problem and human reported cases increased steeply after breakdown of socialism with control of brucellosis in livestock. Study objectives were to assess representative human brucellosis seroprevalences among herder families and their livestock and dogs and to identify risk factors in Zavkhan and Sukhbaatar provinces. Also we wanted to explore associations of human and livestock species / dog seropositivity. We conducted cross-sectional studies with multi-stage random selection of herder families. We interviewed participants with an individual questionnaire, an animal and a hot ail (2-3 families sharing pasture) questionnaire. A blood sample was taken from randomly selected participants. Simultaneously, each 20 sheep and goats, 5-7 cattle or yaks and camels were sampled from selected hotail. Human sera tested by standard and modified Rose Bengal Tests (RBT) and indirect ELISA IgG and IgM classes' antibodies against *Brucella* spp. Livestock serum was subjected to RBT and two competitive ruminant IgG ELISAs. Total 169 hot ails participated in the study. The overall human seroprevalence was 27%. Half cooked liver was significantly associated with seropositivity in people. Seropositivity was linked to a series of clinical symptoms. In Sukhbaatar 7.1% of sheep, 5.1% of goats, 7.8% of cattle, 3.3% of camels, 0.9% of horses and 41.3% of dogs were seropositive. In contrast, in Zavkhan 0.06% goats and 5.0% of cattle were positive, but all tested sheep, yaks, horses and dogs were seronegative. We found an association on hot ail level between human and cattle seropositivity in Zavkhan. Human seroprevalence among herder families in Sukhbaatar and Zavkhan were very high. The livestock was hardly vaccinated against brucellosis in the past.

***Mycobacterium avium* subsp. *paratuberculosis* (MAP) and *Neospora caninum*: risk of transmission between cattle and elk in Southwestern Alberta**

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In Southwest Alberta, cow-calf operations and wild elk share the same pastures. This wildlife-livestock interface may be an opportunity for inter-species transmission of pathogens. Our multi-disciplinary group investigated the occurrence of MAP and *N. caninum* in this multi-host system. Elk herds (n=10) and cow-calf operations (n=30) were assigned to two groups based on exposure to the other species. Samples were collected from elk (284 sera, 697 faeces) and cattle (856 sera/faeces). To capture information on pasture rotation, water, feed, and health management, we conducted interviews with ranchers. We controlled the confounding effects of these factors in a multi-level regression analysis. Telemetry data obtained from collared elk and cattle were combined with interviews to study the spatio-temporal patterns of host interactions. Serological results suggested the circulation in both elk and cattle of MAP (<1% and 10.7% respectively) and *N. caninum* (7.1% and 5.0% respectively). There was no association between host interaction and MAP occurrence. This may suggest an independent circulation in the two hosts but does not rule out inter-species transmission. For *N. caninum*, elk presence, domestic dogs on farm and proper carcass removal were significantly associated with lower serological titers (P=0.026, P=0.014 and P=0.017 respectively), which may suggest that *N. caninum* distribution is mainly driven by wild carnivores. We studied the occurrence of MAP and *N. caninum* in elk and cattle in Southwestern Alberta using regression analysis. However, regression methods have some limitations when dealing with complex systems. We will explore agent-based models as an alternative to capture the dynamic of this multi-host system. Combined with intense site-specific field-based data collection we anticipate increased insights in the disease transmission dynamics.

Prevalence of *Coxiella burnetii* infection (Q fever) in sheep flocks and goat herds in Ontario, Canada and their farm workers with associated risk factors

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Q Fever is a zoonotic disease caused by the *Coxiella burnetii* bacterium. It is associated with abortion, stillbirth, and weak offspring in sheep and goats, as well as severe disease in humans. An ongoing human outbreak in the Netherlands connected to small ruminants has recently re-drawn attention to the surveillance, control and impact of this zoonotic disease. This study was undertaken to determine the seroprevalence and risk factors of *C. burnetii*, among small ruminants and their farm workers. This cross-sectional serological survey used multi-stage random sampling to select 35 breeding female animals on each of 148 small ruminant farms in Ontario. All farm workers in contact with the animals were invited to provide a blood sample. Serological analysis was performed with an IDEXX ELISA (animals) and an IFA (humans). Preliminary results indicate a farm-level animal seroprevalence of 56.9% (82/144 farms), and a farm-level human seroprevalence of 83.8% (31/37 farms). In a logistic regression univariate analysis, the following animal covariates had a statistically significant association with the dichotomous farm-level small ruminant serology status (P<0.05): the purchase of animals from sales barns (P=0.03), the use of traps rodent control (P=0.02), replacement animals having access to birthing areas after weaning (P=0.03), disposing of placentas in a manure pile (P<0.01), and the presence of other small ruminant farms within 5 km (P=0.04). Multiple logistic regression models will be constructed separately for sheep, goats and farm workers to examine potential risk and protective factors for *C. burnetii* seroprevalence. The information gained from this study will fill the knowledge gap for prevalence estimates and specific risk and protective factors in Ontario, and will be used to develop protocols to mitigate future risk to both humans and animals.

Seroprevalence of Q fever in small ruminants at the center of Portugal

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Recently, the increased number of Q fever cases in Europe warned health authorities. In Portugal, little is known about the infection by *Coxiella burnetii* in animals. A cross-sectional study was designed to investigate the exposure among small ruminants (SR) in the region of Coimbra, estimating the herd and individual prevalence. Sample size calculation followed 2 approaches: (1) number of herds to estimate the herd prevalence; (2) number of animals to detect infection in each herd. In the 4th trimester 2011, 89 SR herds were randomly selected: 24 of sheep, 52 of goats and 13 mixed herds. Blood samples were taken from 460 animals. Antibodies anti-*C. burnetii* were detected by using the ELISA LSIVET Ruminant Milk/Serum Q Fever® (LSI, Lissieu-France). Laboratory results were expressed in S/P values. Results showed an herd prevalence of 32.6%. Positivity rate by species was 37.5% in sheep, 28.8% in goats and 38.5% in mixed herds. Geographic distribution of positive herds showed a frequency of 32.8%(19/58) in Coimbra, 42.8%(7/16) in Vila Nova de Poiares, 30%(3/10) in Miranda do Corvo, 0%(0/1) in Lousã and 0%(0/4) in Penacova. Individual prevalence was estimated in 9.6%(44/460). Positive S/P titers ranged from 41.5 to 185.9. S/P titers ≥ 100 were found in 15.9%(7/44) of sera from distinct herds. We conclude that exposure to *C. burnetii* is important in SR in this region. To our knowledge, it is the first epidemiological study in this region. Other species may be involved, and further work is necessary to a better understanding of *C. burnetii* epidemiology. This study is crucial to implement a control program for *C. burnetii* in Portugal, to reduce the economic impact in herds and the risk for public health.

Risk factors for foot-and-mouth disease in Tanzania, 2001-2006

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The objective of this study was to develop a model to quantify the effect of factors influencing the spatio-temporal distribution of FMD in Tanzania. A database comprised of reported outbreaks of FMD for 2001-2006 was obtained from the Tanzanian Ministry of Livestock and Fisheries Development. A digital map of Tanzania was divided into a regular grid of 20×20 km cells and the study outcome defined as the presence of at least one FMD-positive village within each cell in each of the six study years. A mixed-effects Bayesian logistic regression model was developed to quantify the association between FMD presence and human population density as well as distance to major roads, railway lines, wildlife parks and international borders. For every year from 2001 to 2006 10 km increases in the distance of a cell from a major road decreased the odds of FMD by a factor of 0.73 to 0.83. Ten km increases in distance from a national park decreased FMD risk from 2001 to 2003 (OR 0.84-1.00) but increased the risk from 2004 to 2006 (OR 1.04-1.08). Ten thousand unit increases in human population density increased the odds of FMD in all years except 2005 (OR 1.03-1.14). The spatial distribution of FMD risk in Tanzania was variable and corresponded to endemic (2001, 2002 and 2005) and epidemic (2003, 2004 and 2006) periods. These results support the hypothesis that FMD occurrence in Tanzania is related to animal movement and human activity via communication networks.

Complexity and controlling rabies in Bali, Indonesia

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The first case of rabies in any species in Bali, Indonesia was diagnosed in November, 2008, resulting in at least 100 human deaths and hundreds of canine deaths. We used business decision management tools to examine the management response to rabies in Bali and conclude that the response has gone through a cycle of problem recognition which influenced control features. In October 2011, 14 participants of the Building Ecohealth Capacity in Asia project implemented by VWB/VSF-Canada met in Chiang Mai to discuss complexity of ecohealth problems. The Cynefin Framework is an application that matches a situation with a response, helping to distinguish among simple, complicated, complex, and chaotic contexts. We asked: (1) how is the situation being framed (simple, complicated, complex, and chaotic); (2) what are the implications of this framing relative to situational response; and (3) what are appropriate ways of managing rabies control based on the basis of this framing. Problem identification and response started as a simple process (kill the dogs), moved to a more complicated phase when cultural factors were identified as being important, and occasionally shifted into stages when control seemed out of reach (chaos according to systems theory). Currently in the complex phase vaccination, understanding dog ecology, and education programmes are being used concurrently. The vaccine confers solid protection but the ecohealth picture of rabies in Bali makes it difficult to analyze and control. Our team advocates an ecohealth approach addressing the fourth and final component of complex systems theory, complexity itself. We suggest identification and understanding of the phases of complex problems such as rabies is important to developing sustainable solutions.

Circulation of bovine ephemeral fever in the Middle East: strong evidence for transmission by winds and animal transport

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Bovine ephemeral fever virus (BEFV) is an economically important arbovirus of cattle. The main routes of its transmission between countries and continents are not completely elucidated. This study aimed to explore BEFV transmission in the Middle-East. A phylogenetic analysis was performed on the gene encoding the G protein of BEFV isolates from Israel from 2000 and 2008 with isolates from Turkey (2008), Egypt (2005), Australia (1968-1998) and East Asia (1966-2004). Calf sera collected during the years 2006-2007 were tested by serum neutralization in order to explore for recent exposure to BEFV before 2008. These were followed by a meteorological analysis, aimed to reveal movement of air parcels into Israel in the week preceding the first case of BEF in Israel in 2008. The 2008 Israeli and Turkish isolates showed 99% identity and formed a new cluster with the 2000 Israeli isolate. The serological survey showed no new exposure to BEFV during 2006 and 2007. These results coincided with the meteorological analysis, which revealed that air parcels originating in Southern Turkey had reached the location of outbreak onset in Israel ten days before the discovery of the index case. The Egyptian isolate clustered phylogenetically with the Taiwanese isolates, coinciding with data on importation of cattle from China to the Middle East in the year preceding the isolation of the Egyptian isolates. These results suggest that both winds and animal transport may have an important role in trans-boundary transmission of BEFV.

Risk factors for infection with *Babesia* species in cheetah-breeding centres in South Africa

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Babesiosis, which occurs world-wide in tropical, subtropical and even temperate regions, is a protozoal infection transmitted through the bite of an ixodid tick. The vector of cheetah-associated *Babesia* species is unknown to date, however, it is assumed to be tick-transmitted. Prevalence of *Babesia* species infection, gender, age and tick burdens of cheetahs were investigated at two cheetah-breeding centres in South Africa. A total of 103 cheetahs were included in the study; blood in EDTA was collected from each animal. The hypervariable V4 region of the 18S rRNA gene of *Babesia* species was amplified by polymerase chain reaction (PCR). Combination of PCR and reverse line blot (RLB) hybridization assay produced 500 bp DNA fragments specific for felid *Babesia* species gene on electrophoresis and revealed that 58% of cheetah blood samples tested positive. A total of 1137 ticks, recovered from cheetahs at both localities, were identified as *Amblyomma hebraeum*, *Haemaphysalis elliptica* and *Rhipicephalus simus* based on morphological features. A multiple logistic regression model showed that cheetahs with high tick burdens were more likely to be infected with *Babesia* species than those with low tick burdens (Odds ratio=32; 95% CI: 6.3, 166; P<0.001) and than those with medium tick burdens (OR=12; 95% CI: 2.4, 61; P=0.002). Adjusting for tick burden and locality, the risk of infection with *Babesia* species was significantly higher as the cheetahs aged (P=0.039). There were no significant effects of gender or locality on the risk of harbouring *Babesia* species. This is the first study to show a strong positive correlation between infection with *Babesia* species in cheetahs and the presence of suspected vector ticks.

Bluetongue and epizootic hemorrhagic disease in La Réunion; a burden on ruminant farming

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Since 2002, the livestock of Réunion Island has been subject to reoccurring outbreaks of Bluetongue (BT) and Epizootic Hemorrhagic Disease (EHD). To find out a solution to this problem, that can have severe financial implications to ruminant farmers, a study was carried out between March and September of 2011. The aims of this study were: (1) to confirm the circulation of the viral agents in relation to both host reservoirs and insect vectors; (2) to assess the health status of Réunion Island's livestock; and (3) to identify major risk factors pertaining to ruminant farming due to these viruses. A total of 254 cows from 51 farms and 206 sheep and goats were chosen randomly for testing. Multiple blood samples were taken from all sampled animals. Farming procedures and environmental conditions were assessed for each farm via a questionnaire. Any animal exhibiting clinical symptoms of viral infection was also tested. Serology was done using commercially available LSIVET kits, viral detection was performed via RT-PCR and genotyping was performed externally. Logistic regression was used to assess potential risk factors after a first of univariate analysis (Chi²). Serology studies suggested that ~50% of ruminants were positive for Bluetongue and ~40% for EHD. EHDV-1 virus was detected in ~5% of animals and bluetongue variant 2 was detected in ~1%. Statistical analysis showed that the major risk factors for Bluetongue and EHD viral infection of ruminant livestock include; the category of the reared livestock, the presence of organic waste, the presence of a water source and the proximity of another farm. Those results are the first step to a better understanding of what could happen in the futur in Western Europe.

Transmissibility and other characteristics of HPAI in Indonesian village poultry

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This study was designed to measure the transmissibility of Type A H5N1 highly pathogenic avian influenza (HPAI) in mixed populations of backyard and small-scale commercial chickens in Java. An approach adapted from infection tree reconstruction was used to trace affected chickens and households in neighborhoods (RTs) in which HPAI had been diagnosed by Indonesia's surveillance system. Of the 41 outbreaks studied, 15 were in RTs participating in a mass vaccination program. The study found that backyard chickens were free range, visiting a mean 4.2 households. Commercial poultry were present within the village in nearly half of the outbreaks, although they were affected in only 7.3%. The distance from the index to the closest unaffected household was significantly greater than that from the index to the closest affected. Mean morbidity was 80.9±28.8%, mortality 77.6±27.7%, and case fatality 97.3±12.3%. There was significant risk for outbreaks to occur in households where Muscovy ducks, non-commercial chickens, broilers and geese were kept, but there was not a significant risk associated with keeping pigeons or ducks (Anatidae family not including Muscovy). Introduction of new birds to a household flock was most frequently documented to have led to the introduction of the disease to an RT, while contact between birds from different household flocks was most frequently documented to have contributed to spread. Transmission between birds within flocks was significantly higher than transmission between flocks, between birds within flocks in vaccinated areas was significantly lower than in unvaccinated areas, and between flocks in vaccinated areas was significantly lower than in unvaccinated areas. Our findings indicate that backyard poultry populations as they occur on Java provide the necessary environment for indefinite HPAI transmission.

Epidemiology, ecology & socio-economics of disease emergence in Nairobi

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We describe a research programme aiming to understand the mechanisms of pathogen emergence into urban populations. We focus on livestock as sources of emerging diseases. What is it, exactly, about urban environments that might predispose to an emergence event, & what is the contribution of livestock keeping to this? We are investigating two key aspects. Firstly, does urban livestock keeping pre-dispose people to acquiring new or more diverse microbial flora? Is the risk compounded by poverty? How is the microbial flora influenced by the keeping of livestock? Secondly, we examine exposure to livestock products traded for food or other purposes. Do supply chains for these products bring people into contact with microbial diversity over & above what is otherwise experience? Why do people source food from particular places, & what influences the microbial flora to which people are exposed through food? Why do supply chains exist in the way that they do, & how might they change as demand for products changes with urban change? We address these questions examining in detail the city of Nairobi, Kenya.

Co-infections: biological patterns in multiple-infected hosts

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We report on the results of work on zoonotic and non-zoonotic pathogen co-infections arising as part of a large project dealing with zoonotic diseases amongst livestock, livestock keepers and non livestock keepers in a study site in Western Kenya. Domestic livestock are an important source of zoonotic infections to humans, particularly in rural parts of Africa. Understanding the relative risks of livestock-keeping in such systems, as well as the role of co-infection in driving disease burden, matter in the formulation of evidence-based public health policy. We explore the spatial distribution of co-infections between multiple zoonotic and non-zoonotic infections, in both humans and cattle, and examine the impact of co-infection on health status, measured by diverse clinical indicators, also in cattle and human hosts. For humans, we test whether livestock keeping, and whether the infection status of the livestock kept, explains infection status in humans. These results have an important bearing on the design of interventions to control the impacts of zoonotic diseases in endemic areas.

Risk of introduction of alphaviruses responsible for American equine encephalitides in Belgium

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Arthropod-borne viruses are a threat for human and animal health in regards with their dissemination out of their endemic area. The arboviruses reviewed here belong to the family *Togaviridae* genus *Alphavirus* and are small enveloped positive sense RNA viruses. They are considered as exotic equid pathogens in Europe and can cause severe diseases in humans in the context of an epidemic. Arboviruses have complex epidemiologic features characterised by interactions between viruses, vectors, reservoir or susceptible host species, and environment. A bibliographic search was performed to identify the main factors that influenced past outbreaks in America and the presence of potential vectors/vertebrate hosts that could play a role in the transmission cycle in Belgium. Three equine arboviruses, currently considered as the main current threats of emergence/introduction in Western Europe, were chosen as model for this study: Eastern equine encephalitis virus (EEEV), Western equine encephalitis virus (WEEV) and Venezuelan equine encephalitis virus (VEEV). In conclusion, taking into consideration the globalisation (increase of international exchanges) and climate warming, the analysis of the different features of the arbovirus cycles are essential to a balanced risk expertise in the Belgian context. Research supported by the Belgium Federal Public Service, Health, Food Chain Safety and Environment.

Slaughterhouse workers as reservoirs of zoonotic disease

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Slaughterhouse workers are considered a high risk group for zoonotic disease due to increased contact with animals, animal products and excreta. Globally, slaughterhouse workers have been shown to have an increased seroprevalence to zoonotic pathogens, though no such studies exist in Kenya. Slaughterhouse workers may also act as reservoirs of these zoonotic organisms and asymptomatic carriage of pathogenic bacteria has been demonstrated. This study aimed to determine the carriage of enteropathogens in slaughterhouse workers in rural western Kenya and to determine if there was asymptomatic carriage of *Staphylococcus aureus* specifically Methicillin Resistant *S. aureus* (MRSA). This study was conducted in the Lake Victoria Crescent region of western Kenya. Five hundred slaughterhouse workers from this region were asked a comprehensive questionnaire regarding risk factors for zoonotic disease, faecal samples were collected for examination and culture and a nasal swab was cultured for *S. aureus*. This study reports on the seroprevalence of *Salmonella* spp, *Shigella* spp, pathogenic *Escherichia coli* and *Campylobacter* spp. in these individuals as well as reporting the nasal carriage of *S. aureus* and MRSA. This is the first community based study regarding *S. aureus* and MRSA in Kenya. The asymptomatic carriage of these organisms in slaughterhouse workers highlights a reservoir that may be important in the dissemination of these pathogens. The study further comments on the risk factors for infection with these pathogens and suggestions are made for simple hygiene interventions that can reduce disease in slaughterhouse workers and dissemination to the wider community.

Population dynamics in Kampong chicken and consequences for HPAI vaccination: results of a field trial in Java

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Until today HPAI in poultry is considered to be endemic in most of the Indonesian provinces since it was officially declared in 2004. Vaccination is used as one of the control strategies targeting layer and breeder farms but also Kampong (village) chicken. Limited information is available on the scope of off-take and replacement occurring in Kampong chicken populations under field condition and their effects on HPAI vaccination. To collate information on population dynamics in Kampong chicken, twelve communities with 300-500 chickens each have been enrolled in this trial. Chicken exit/entries as well as disease/mortality events were intensively monitored in weekly intervals. The trial was carried out between July 2008 and August 2009 in two Districts of Yogyakarta, Java. Results indicate that 39-44% of chickens were younger than two months of age over time and more than two-thirds of chickens were younger than four months, respectively. Adult chickens represented only 10% (male) and 20% (female) of the total population. Though overall population size within the selected communities was relatively stable, the number of chickens changed widely within age classes. In each observed quarter, there was a 43% or higher turnover of the population (43-72%). Observed changes were related to socio-cultural events such as holidays or begin of school. From our results we can conclude that approximately 40% of a natural backyard population will be un-vaccinated by 60 days after the onset of a vaccination campaign. Considering this high population turnover rate, even a quarterly vaccination regime including a booster round is required will have difficulty achieving effective flock immunity levels. This results in high costs, poses a significant logistical challenge and suggests mass vaccination is not a practical approach to sustained control of HPAI.

Risk factors for foot and mouth disease in beef cattle herds in Israel

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Epidemics of foot and mouth disease (FMD) occur frequently in Israel and are mostly caused by viruses of serotype O. Due to this reason vaccination of cattle, sheep and pigs in Israel are mandatory. During 2011, a large epidemic occurred in Israel, which involved 26 localities that included 30 beef herds, 11 feedlots, 4 dairy herds and 8 sheep flocks. We analyzed the risk factors for the appearance of clinical signs in adult cattle in beef herds by comparing 25 affected herds (at least 1 case in an adult cow) and 26 non-affected herds. In multivariate analysis two risk factors were discovered; abundance of calves under the age of 6 months in the herd (adjusted odds ratio (OR)=10.6 (CI95%=1.7-64.7) and the elapse of more than 6 months from last vaccination (OR=8 (1.2-53.2)). In order to analyze the pattern of virus spread we measured the distance between each affected herd and the most adjacent herd affected prior to it. This analysis revealed that whereas for beef herds this distance averaged 3.2 km (range 0.2-8.9 km), for feedlots it averaged 19.9 km (range 2-43.7 km) (P=0.01). We conclude that the dispersion of FMD virus between beef cattle herds differs significantly from the dispersion to feedlots. In beef herds the virus spreads by direct contact between grazing herds and amplified by the abundance of young non-vaccinated calves, while spread to feedlots is mainly associated with long distance transportation of animals (mostly calves). These findings have important implications for the control of FMD.

Ovine seroprevalence of *Coxiella burnetii* in the U.S. and its meaning for disease control

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Coxiella burnetii, the causative agent for Q fever, is endemic in the US and is considered to be an important cause of abortions in both sheep and goat populations. Heightened awareness of the potential for large scale outbreaks in both animal and human populations has increased concern for knowledge of the background prevalence of infection in endemic areas. In response to this uncertainty, a seroprevalence estimate of a representative sample of the U.S. sheep population was conducted as part of the National Animal Health Monitoring System (NAHMS) study in 2011. A representative sample of flocks were contacted in twenty-two States which accounted for 70% of U.S. sheep operations and 85% of U.S. sheep. Blood was collected from 13,129 adult ewes on 563 operations. Sera were tested for antibodies to *C. burnetii* using the Enzyme-Linked Immunosorbent Assay (ELISA). Of the 563 operations 16.9% had at least one positive sample. Of ewes tested, 301 (2.3%) were seropositive for *C. burnetii*. The apparent operation-level seroprevalence was 12% in small operations (20-99 ewes), 17.3% in medium operations (100-499 ewes) and 26.7% in large operations (>500 ewes). Regionally, fewer operations in the West were positive (7.3%) than in either the Central (24.4%) or East (18.4%) regions. Additionally, 81% of producers who participated in the NAHMS study indicated unfamiliarity with Q fever. The low animal-level seroprevalence combined with lack of familiarity with the disease provides opportunities for potentially large numbers of newly infected animals and disease transmission. Vaccine is currently unavailable in the U.S. thus control is limited to producer education and Q fever risk mitigation through management of manure, birthing material, lambing management, and other biosecurity measures.

GIS based spatial and temporal analysis of rabies in Bhutan

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In this study, we describe the spatio-temporal patterns of rabies in domestic animals in Bhutan. A Geographic Information System and spatial statistics were used to visualize the spatio-temporal distribution of rabies cases in dogs and cattle. Moran's I test and LISA statistic were performed to assess the global and local clusters of cases. A spatial interpolation analysis using inverse distance weighting method (IDW) was used to interpolate the reported rabies cases. The resulting interpolation was then displayed as a continuous, graduated colour surface of the centroid of each reported sub-district. Rabies outbreak cases were mapped and analysed using directional tests (mean center and standard deviational ellipse), weighted by the date of report of cases to understand the distribution and direction of spread. Rabies cases in animals (mostly in dogs and cattle) were mainly reported in southern parts of Bhutan, bordering India. The trend of reported cases was relatively stable until 2005, but increased during both 2006 and 2008 due to reemergence of rabies in eastern and south west Bhutan. Significant clusters ($P < 0.05$) of high numbers of cases were observed in eastern, south central and south west Bhutan. There was also a significant ($P < 0.05$) spatio-temporal correlation between reported cases in dogs and in cattle. The distribution of cases during major outbreak followed the road network and towns with high human and dog density, suggesting human population characteristics played an important role in the spread of disease. Our analysis confirmed a significant spatial distribution of rabies in Bhutan, with increased incidences in southern Bhutan. We recommend that rabies prevention program should be focussed in these 'hot spots' and highly endemic areas. Mass vaccination of dogs in this region would create an immune buffer (cordon sanitaria) and prevent rabies incursions into the interior Bhutan.

Sanitary and phytosanitary measures regulating sheep exports from Sudan

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Sudanese sheep is exported from Port Sudan quarantine in the Red Sea to many countries one of them is the kingdom of Saudi Arabia which sometimes rejects some ships using sanitary reasons arbitrarily. If Sudan joins the World Trade Organization (WTO), then, the Agreement on the Application of Sanitary and Phytosanitary Measures (SPS) will play an important role in regulating animal trade and Sudanese sheep exporting sector can benefit from this agreements in protecting its exports and create new markets for the Sudanese sheep. Data was collected from Port Sudan veterinary quarantine in the Red Sea from the annual and monthly reports during the period from 1999 to 2005. Results showed that about 4.4% to 14.5% from the monthly exports of sheep were rejected in the year 2005 and 5% of the annual exports of the year 2000 due to sanitary reasons, there is no rejection during the months of the Pilgrimage hence there is an increasing demand for sheep to ElHaddi (sheep slaughtering during Pilgrimage). The other important point that the rejected sheep is re-inspected and re-tested thoroughly and then re-exported and it is accepted by the same veterinary administration of Saudi Arabia which reject it due to disease reasons just before days or weeks. This could be an indicator for using sanitary measures as a disguised restriction for trade.

Risk-based prioritisation of surveillance for exotic animal diseases in northern Australia

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The Australian Department of Agriculture, Fisheries and Forestry conducts surveillance for the early detection of exotic animal diseases across northern Australia through its Northern Australia Quarantine Strategy program. A review of relative risks posed by significant diseases was conducted in order to prioritise risks for each of 28 geographic 'risk areas', thus enabling informed surveillance planning and resource allocation. In a three-day expert opinion elicitation workshop 14 diseases with potential for introduction via unregulated or natural pathways were allocated relative likelihood scores for each of introduction, establishment and spread in each risk area. The scores were then normalised and combined to produce a risk profile for each disease across the risk areas. Risk maps were produced for each individual disease and for combinations of diseases with similar epidemiological parameters to assist in communicating the outcomes of the risk review process to decision-makers and the public. The final 'risk rating' for each area combined likelihood scores for multiple diseases, using weightings based on their relative (among-disease) likelihoods of occurrence and scores for their likely national consequences. This ensured that resulting surveillance policy would reflect economic and social risk. This risk review process provided a practical approach for the prioritisation of targeted surveillance effort for exotic animal diseases across a broad geographic region of Australia.

Assessment of the financial consequences of ten years bovine spongiform encephalopathy in Germany

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The first autochthonous case of Bovine Spongiform Encephalopathy (BSE) in Germany was detected on 26 November 2000 in the course of voluntary testing. Since then, a total of 413 BSE cases have been confirmed, resulting in the culling and destruction of 17,313 heads of cattle. In Germany, the legislation prevailing in the European Union was supplemented with a number of national regulations leading to extra requirements relating to (1) BSE surveillance in cattle; (2) the number of carcasses that had to be condemned after detection of a BSE case in a slaughterhouse; and (3) the feed ban, which also included animal fats. We assessed the cost implications of control measures enacted in response to BSE for Germany. The highest costs were caused by BSE-induced regulations on animal by-products (removal of Specified Risk Material, extension of the feed ban to all livestock, compulsory incineration of category 1 material, etc.) with a total of about 1.5 billion Euros. BSE surveillance in cattle cost 594 million Euros, an intervention programme to stabilize the beef market implemented in 2001/2002 about 64.7 million Euros, and compensation payments for culled cattle in BSE affected farms including animal value, culling, rendering and safe disposal about 20 million Euros. Other cost factors accounted for in this study included research with more than 7 million Euros, destruction of carcasses following the detection of a BSE positive animal in a slaughterhouse with 3.4 million Euros and epidemiological investigations on the BSE affected farms with about 1.2 million Euros. The total economic impact of BSE in Germany between 2000 and 2010 is estimated to amount to more than 2 billion Euros.

Use of the npv, irr and bcr in the ex-post financial evaluation of a vaccination program against foot and mouth disease during the period 2000-2006 in Venezuela

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The economy is increasingly present in all facets of the fight against animal diseases and in all areas of society. The economic and financial analysis can improve the quality of decisions on the allocation of funds to animal health control programs. The objective of this research was to financially evaluate (ex-post), the eradication program of foot-and-mouth disease (FMD) in the municipality of Bolivar, the state of Yaracuy, Venezuela, during the period 2000 to 2006. The methodology used was the Cost-Benefit Analysis (CBA), which is often used to evaluate and compare these programs ex-ante. The results of this CBA include a set of criteria such as the Net Present Value (NPV), the Internal Rate of Return (IRR), and the Benefit-Cost Ratio (BCR), all of which are components of the evaluation of investments. To undertake this investigation, the program costs for the producers and the state, as well as the losses caused by the FMD were estimated. A total of 40 production units engaged in the operation of producing cattle, which were affected by the disease during the year 2003, were surveyed. The NPV, IRR and BCR indicators for the eradication program of FMD in the study area during the period in question, produced the following results: NPV: 147,856 (Bs.F), IRR: 74% and BCR: 1.27. The results of the present investigation indicate that the vaccination program used was profitable during the period studied.

An industry-level analysis of potential intangible and economic impacts affecting Australian pork producers during an emergency animal disease control program

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Emerging and transboundary diseases have been responsible for dramatic impacts on human health, the economy, trade, animal health and biodiversity in Australia and around the world. The Australian pig industry's health status provides it with a competitive advantage. Freedom from major transboundary diseases – such as foot-and-mouth disease and classical swine fever – secures access to international markets and enables producers to invest in their businesses free from the complication of major disease incursions, ensures the industry's future sustainability and allows it to meet community standards for food production. Planning for a disease response is driven by many factors. Among these factors, the cost of the response is often the single most important driving factor. However, cost involves more than the actual financial cost of the response. It involves a number of intangible elements and the views of a diverse range of stakeholders. For example, human health, environmental and sociological consequences need to be considered. Currently, a unifying framework for such decision-making is unavailable. Application of a newly developed framework to several diseases that concern the Australian pig industry will facilitate dialogue on what is the best response to minimize the impact of incursions of such diseases. This novel framework for economic analysis of animal health emergencies incorporates risk assessment, tangible and intangible elements and a value-added cost-benefit analysis. These case studies assess the comparability, applicability and accountability of different response actions through producer perspectives. An example of the application of this framework for a disease which threatens the Australian pig industry will be presented.

Resource needs predicted for an FMD outbreak in Minnesota, USA

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Foot-and-mouth disease (FMD) is a trans-boundary disease occurring regularly around the world generating major international concerns. Outbreaks of FMD that occur in FMD-free countries cause major disruptions not only in livestock production, but affect other industries as well. The impacts of outbreaks can be large and may affect international trade, national, state and local economies in a variety of ways. This paper builds on our work simulating and describing FMD spread and control in Minnesota (MN)(see companion papers). The objective of this study was to use estimates of the epidemiological consequences of FMD spread and control in MN to estimate resource needs during an outbreak. The North American Animal Disease Spread Model (NAADSM) was used to develop and compare scenarios. Epidemiological output included means of number of infected herds, duration of outbreak, duration of active disease spread, and herds and animals vaccinated or depopulated. Mean disease duration and mean number of animals infected were larger when disease began in a dairy as compared to a swine operation. When vaccination was not implemented, these mean values were 27 days and 8,000 animals when disease began on a swine operation and 54 days and 62,000 animals when disease began on a dairy. These results suggest that we may anticipate that an FMD outbreak beginning in a MN dairy is likely to result in longer and larger outbreaks than an outbreak beginning in swine. This has important implications for resource needs for outbreak response. In a dairy herd index scenario, with maximum capacity of 1,500 herds vaccinated per day, the mean number of animals infected and destroyed ranged from 14,000 to 17,000. We will describe important resource needs such as doses of vaccine used, numbers of herds vaccinated and the number of personnel used for different modeled scenarios.

Agricultural resource management survey and national animal health monitoring system data analysis: cow-calf case study

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The USDA-National Animal Health Monitoring System (NAHMS) collects farm-level animal health and production information through national studies. The USDA-Economic Research Service (ERS) collects farm-level financial and economic information through the Agricultural Resource Management Survey (ARMS). This research will evaluate if appropriate data and methodologies are available to add value to both data sets. The first phase of this research compares demographic estimates from ARMS and NAHMS to the 2007 Census of Agriculture values to determine if ARMS and NAHMS samples represent the national population. The second phase of this research compares estimates for similar topics from ARMS and NAHMS to determine response similarity. For Phases 1 and 2, statistical tests were conducted to determine if operations in five size categories and four regions from NAHMS and ARMS were different from each other. The third phase of this research seeks to complement estimates from NAHMS related to animal health with estimates from ARMS related to economics. This phase attempts to identify segments of the U.S. cow-calf industry that are more likely to use certain production practices that promote animal health and then evaluate economic measures of profitability for those segments. Initial results from Phase 1 show that most sample proportions and the national population proportions for segments of the cow-calf industry are the same. Even though some sample and national population proportions are statistically different from each other, the numerical difference is small. Initial results from Phase 2 demonstrate that responses to questions about specific topics asked on both surveys are similar, thus producers responded in a consistent manner. Phase 3 does not reveal statistical empirical evidence to determine causal relationships; it reveals trends, patterns, and associations between producer's production practice decisions and the associated economic benefits.

Development and assessment of animal-based welfare indicators at the slaughterhouse for monitoring cattle welfare

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A very recent scientific opinion of EFSA on the welfare assessment of dairy cows concluded that animal-based welfare indicators, identified on the basis of scientific evidence, can be effectively used in the evaluation of the welfare of dairy cattle on farm in relation to laws, codes of practice, quality assurance schemes and management. Some of these animal-oriented (instead of resource-oriented) measures are applicable for *ante-mortem* or *post-mortem* inspection and thus can be taken at the slaughterhouse. The identification, development and assessment of such objective indicators that are easily and reliably to record on a nationwide basis meets a political demand (e.g. EU strategy for the Protection & Welfare of animals 2012-15). Little work in this area has been dedicated to cattle so far, thus our study aims to develop and assess animal-based welfare indicators for calves, beef and dairy cows recordable at slaughter. In a first step, we carried out a questionnaire based survey among Swiss veterinarians working in slaughter animal inspection and meat control to integrate their opinion on prevalence and feasibility on a list of indicators derived from literature review and expert opinion. In a second step, we carried out a continuous data collection over one year in two of the largest Swiss cattle slaughterhouses and developed simple, rapid, repeatable scoring systems for the assessment of the potential indicators (ongoing). A third step will validate the significance of the indicators by tracing back from our slaughterhouse findings to the situations on the farms of origin. Such indicators, collected nationwide, stored in a central system and analyzed on farm level could be used for categorization of farms with respect to welfare quality and be implemented in the frame of planning risk-based official welfare controls on farms. The ongoing work, current results, and a preliminary repertory of indicators will be presented.

Shorter-term risk of *Mycobacterium bovis* in Irish cattle inconclusive reactor to the single intradermal comparative tuberculin test

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In Ireland, bovine tuberculosis (bTB) is detected using abattoir surveillance and an annual single intradermal comparative tuberculin test (SICTT) on all cattle. Animals are standard inconclusive reactor (SIR) if the bovine response is >2 mm and 1-4 mm > the avian response at the SICTT. The owner has three choices for SIR management: 1 have the SIR retested after a minimum of 42-days (inconclusive reactor retest, IRR); 2 slaughter the SIR and, provided it has no visible lesions, have a full herd test 42-days after the SIR left the herd; 3 slaughter the SIR and have lymph nodes bTB examined by histology and/or culture. We examine the bTB risk for SIRs at slaughter prior to the IRR, at the IRR, and the future bTB risk of TIR animals ('transient SIRs'; SIRs negative to SICTT at IRR) that left the herd within 6 months of the IRR. We also investigate factors associated with the future bTB status of SIRs at slaughter prior to the IRR and at the IRR. The study population included all SIRs identified between 2005 and 2009 inclusive in a herd otherwise Officially TB free (OTF). Between 11.8% and 21.4% of SIRs slaughtered prior to the IRR were confirmed bTB positive at *post mortem* (using histology or culture if histology was not definitive), compared to 0.13-0.22% of SICTT -ve cohort animals. TIRs that moved out of the disclosing herd within 6 months of the IRR were 12 times more likely to be bTB positive at the next test/slaughter compared to all animals in the national herd. The same increased risk did not apply to the SICTT -ve cohort animals that moved out of the same herds at the same time. Based on a range of measures, SIRs and TIRs are each at increased bTB risk into the future. Consequently, differential treatment of TIR animals would be justified.

Longer-term risk of *Mycobacterium bovis* in Irish cattle inconclusive reactor to the single intradermal comparative tuberculin test

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In Ireland, new bovine tuberculosis (bTB) cases are detected by field and abattoir surveillance. During field surveillance, an animal is a 'standard inconclusive reactor' (SIR) to the single intradermal comparative tuberculin test (SICTT) if the bovine response is >2 mm, and 1-4 mm > the avian response. Little is known about the future infection risk posed by transient SIR (TIR) animals (SIR animals that pass a subsequent test). We critically evaluate the future bTB status of TIR animals, by examining the future risk of bTB diagnosis over the 4 years following initial SIR diagnosis and clearance at the subsequent retest. The study included all TIRs initially identified as SIRs in 2005 in otherwise free herds at tests with no other reactors. The analysis is restricted to cows that did not leave the herd, other than direct to slaughter, to the end of 2009. Five control cows were randomly selected from each study herd. A parametric survival model with shared frailties, to account for clustering within herds, was developed to model time from passing a retest to future bTB diagnosis. The final parametric survival model contained the variables: TIR status in 2005, inconclusive status during the follow-up period, location, herd restricted during the study, time since last restriction within the herd and age. The time ratio for the TIR status variable was significant (P<0.001) indicating that on average the time to diagnosis with bTB for TIRs was 78% shorter compared to the non-TIRs. The frailty term was significant (P<0.001) indicating that animals within some herds were more likely to become reactors compared to other herds. These results have important implications for national policy and future management of TIR animals.

Export market recovery in the face of disease outbreaks: a summary of findings for various diseases and species

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In some countries, the livestock sector is heavily dependent on income generated from exports. During or after disease outbreaks, trade bans may be imposed by trading partners and some countries may self-impose export bans. This loss of customers may extend the time for a country's export market to recover from a disease outbreak. Other factors such as disease type, product type and value, world supply, disease management timelines, outbreak size and duration, and country credibility may all influence the length of market recovery. In addition, political changes, price changes, weather, consumer response, and many other factors can have an impact on the length of export market recovery. Over the last decade and a half, countries throughout the world have experienced disease outbreaks that affect cattle, poultry, and swine. The World Organization for Animal Health (OIE) has guidelines for regaining free status for diseases of paramount concern. Many of these guidelines state a three to six month timeline after utilizing a stamping-out policy. Countries in Asia, Europe, North America, and South America all experienced outbreaks of disease over the stated time period. The species affected included cattle, poultry, and swine. An evaluation of the impacts of 8 different diseases affecting these species in 16 countries is presented in the analysis. An analysis of time elapsed from the announcement of a livestock disease outbreak until a country regains its international market can inform other countries of the potential impacts following an outbreak. Analysis shows that export markets can take longer than three to six months for export revenues to return to pre-outbreak levels. In some cases export markets may not recover. This work focuses on the drivers of differences in recovery times. The analysis shows that recovery time is dependent on the disease, the species impacted, and the trading partners of the affected countries.

Improving research utilization and evidence-informed policy-making in agri-food public health through knowledge translation and transfer

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Knowledge translation and transfer (KTT) aims to ensure that the best available research knowledge is used to inform policy and practice decision-making. Many frameworks, methods and terms have been used to describe KTT, primarily in the health sector, and there is a need to summarize these principles and how they could be applied on agri-food public health issues. A mixed-method review was conducted to identify and synthesize comprehensive reviews, reports and commentaries describing KTT in various sectors. A pre-tested search strategy was implemented in five online databases (Medline, Scopus, CAB Direct, Current Contents Connect and CINAHL) on July 25, 2011. Two independent reviewers screened the identified abstracts for relevance, characterized the relevant articles, and conducted a qualitative thematic analysis on a prioritized selection of these articles. A total of 160 relevant articles were characterized and 33 were prioritized for thematic analysis. Most articles were narrative reviews (81.9%) and were published in the health sector (80.0%). Twenty-two KTT methods were identified, including five synthesis (e.g. systematic review), nine dissemination (e.g. policy briefs) and eight exchange (e.g. knowledge brokering) methods. Five thematic areas were identified as key characteristics for successful KTT: relevant and credible research knowledge; ongoing communication and collaboration between researchers and end-users; organizational support and culture; monitoring and evaluation; and understanding the policy-making process and context. This review has identified key methods and principles for successful KTT that should be used by researchers and end-users to help bridge the gap between science and policy in the agri-food public health sector.

Using the analytic hierarchic process to priority mussels diseases in Chile

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Both an unfavourable relationship between needs and resources, and opportunity costs of resources are the reasons to prioritize in animal health. Setting priorities in animal health is the selection of health problems or animal health programmes (or activities) that must be addressed first so that an improved performance of the animal health system at any of its levels is achieved. Prioritization is always difficult, because it is normally done in a context of limited information and in a restricted space of time. This reality forces regional or national health services to assign budgets according to historical patterns, missing the opportunity to allocate resources in areas with greater returns. An additional difficulty for prioritization is the need to consider simultaneously different dimensions. The purpose of this study was to prioritize diseases of mitilids, according to their potential damage for Chilean industry, so that resources are allocated efficiently. To do so, a model using the Analytic Hierarchic Process was build and solved using Expert Choice. The model considered 10 diseases, only one of which has been found in Chile (heme Neoplasia of the mussels). The remaining diseases are unknown in Chile. Three decision criteria were used: (1) diffusion and infectivity probabilities; (2) economic consequences with impact on trade and productivity, biological consequences considering patogenicity and virulence; and (3) control or eradication. The models results showed that *Marteilia refringens*, mitilid viral disease and *Haplosporidium tumefacientis* are the diseases with highest priority, i.e. those on which Chile should take special attention. Although the use of AHP does not guarantee an optimal decision, it must be acknowledged that the use of AHP allows taking decisions based on a detailed analysis of the problem and a synthesis of relevant information based on knowledge, experience, and preferences of stakeholders taking part of the decision making process

Economic impact of an alternative cost and responsibility sharing scheme for epidemic livestock diseases in the EU

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To evaluate different options for enhancing the current EU scheme for co-financing of emergency measures by the Veterinary Fund (VF) the economic impact of alternative Cost and Responsibility Sharing Schemes (CRSS) were evaluated. The CRSS consist of the following parts: risk sharing based on a Bonus-Malus system (BM) instead of a fixed reimbursement rate by the VF to MS's, reduction of reimbursement rate in case of large outbreaks for MS's, and a Public Private Partnership (PPP) within a MS to facilitate responsibility and cost sharing between government and stakeholders. The impact of alternative CRSS compared to the present system were analysed by means of a stochastic dynamic simulation model. Diseases included were FMD, CSF and AI, and the analyses focussed on the Netherlands. Given a vaccination strategy for FMD and CSF and a culling strategy for AI, expected future total costs for the VF amounted 13.34 Million € per 10 year for a hypothetical BM scheme (90% CI 8.33-46.63) and 15.15 Million € (CI 90% 8.59-55.36) for the present scheme. If culling strategies are applied for FMD, CSF and AI, compensated losses by the VF comprised 15.49 Million € (90% CI 5.25-78.69) versus 17.75 Million € (90% CI 5.13-93.89). The impact of a reimbursement reduction in case of a large on-going outbreak in combination with a malus for future outbreaks will reduce the budgetary impact for the VF considerably. Implementing a bonus to MS's for implementing a PPP increases the costs for the VF. However, a 22% damage reduction per outbreak or a reduction in probability of outbreaks of around 30%, or a combined reduction of damage and frequency of 14% would offset the extra cost of a 5% point reimbursement bonus. The level of these reductions are likely to be feasible according to experts and stakeholders. More extreme values in the CRSS scheme will decrease the co-finance part by the VF, and vice versa. In general, the CRSS will achieve a more prevention-driven and incentive oriented approach than the current scheme.

Efficacy of primary processing interventions on contamination of beef carcasses with *Escherichia coli*: a systematic review-meta-analysis

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Interventions have been investigated to recommend effective strategies to reduce *Escherichia coli* on beef carcasses during primary processing. However, results are inconsistent or contradictory. A formal evaluation, synthesis and translation of the research knowledge is necessary to avoid recommending ineffective practices and to determine key knowledge gaps. Identify, critically evaluate and synthesize published intervention research reporting the efficacy of treatments at the abattoir level post-transport to chilling, on *E. coli* contamination of beef carcasses using replicable systematic review (SR)-meta-analysis (MA) methodology. A search of four electronic bibliographic databases identified studies for SR-MA. Separate random-effects MAs were conducted for each unique intervention outcome dataset and pooled effect estimates were presented with heterogeneity. Thirty-six citations reporting 202 trials were included in the SR-MA. MA of final carcass washing (OR 0.56, CI: 0.41-0.77), pasteurization (OR 0.09, CI: 0.06-0.14) and 24 hour dry chilling (OR 0.17, CI: 0.11-0.24) data showed a reduced odds of *E. coli* carcass contamination. The combined effects of potable water wash, steam or hot water pasteurization and a 24 hour dry chill, assuming no additional contamination and all other variables constant, resulted in the reduced generic *E. coli* prevalence of 1.22% (CI 0.17, 3.57). The existing research indicates that final wash, hot water or steam pasteurization, and dry chilling are beneficial for reducing the generic *E. coli* contamination of beef carcasses. Access to proprietary intervention research and in-plant processing unpublished data could increase understanding and confidence in current processing intervention knowledge.

Review of *Brucella abortus* surveillance in Great Britain

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Bovine brucellosis is a zoonotic disease traditionally caused by an infection with the bacterium *Brucella abortus*. *B. abortus* is now exotic to Great Britain and is notifiable; suspicion of disease must be reported to the Competent Authority so that infection can be controlled and eradicated. GB has been Officially Brucellosis Free (OBF) since 1985. Making the assumption that GB's OBF status that underpins cattle trade within the European Union is to be retained, a review of the surveillance and control activities in GB was conducted to assess whether they were still effective, legislatively compliant, proportionate and value for money. Existing surveillance was targeted at imports from non-OBF countries and GB-resident breeding cattle. A Qualitative Risk Assessment evaluated the risk of re-introducing disease to GB and the potential for disease to spread. The risk of importation has dropped significantly since a review in 2006 as a result of a reducing disease prevalence in countries that export cattle to GB. A total of 12 recommendations were agreed and implemented. These: (1) maintain and raise the awareness of the need to report clinical suspicion; (2) target imported and post-imported cattle on the basis of risk; (3) make no changes to artificial insemination bull monitoring; (4) reduce active surveillance in the national herd by reducing the frequency of bulk milk testing; and (5) define communication routes and consistency of approach in response to abortion notifications and disease suspicion. Implementation of the recommendations was undertaken collaboratively by the governments of England, Scotland and Wales and the veterinary and industry communities in GB. This paper uses a science-based logic to implement a fit-for-purpose, risk-based approach to surveillance for *B. abortus* in GB in order to maintain OBF status.

Developing a disease prevention strategy in the Caribbean: the importance of assessing animal health related risks at the regional level

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In 2009, the Caribbean Animal Health Network (CaribVET) conducted a survey among Caribbean national Veterinary Services to assess perceptions towards the use of risk assessment (RA) by animal health services in the region and to identify the main exotic diseases of concern in the region and their means of introduction. The results showed that the introduction of live animals was considered the most likely route of introduction of exotic animal pathogens into the region, followed by the informal introduction of animal products by boat passengers. The use of RA was considered important (in descending order): (1) to avoid or reduce contamination of the human food chain (food safety); (2) to identify vulnerability factors for potential impact of emerging (exotic) and re-emerging diseases in order to improve emergency plans; (3) to prevent the introduction of exotic diseases through live animals for trade; and (4) to identify high-risk areas for introduction of exotic diseases. The diseases considered by the countries/territories with a highest introduction risk were Highly pathogenic avian influenza (16), Foot and mouth disease (10), Rabies (9), Newcastle disease (7) and Classical swine fever (6). The results were used to define a regional strategy for assessing animal health risks that highlights the importance of intra-regional exchanges.

Cost benefit analysis of adoption of bovine brucellosis control measure in Brazil: preliminary results

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The aim of the present work is to estimate the costs and benefits of the adoption of bovine brucellosis control in 13 Brazilian States and to compare the strategies between the States and evaluate their economic viability. The base case is the scenario where no actions are taken, allowing the comparison with the implemented actions of control. The benefits of the base case are: meat and milk production; revenues with outward live animals. The costs of the base case are: reposition of females; inward live animals. The benefits of brucellosis control measures are: reduction of milk and meat production; abortion; infertility of aborted females; perinatal mortality; increase of interval between parturition; mortality of aborted cow; increase in replacement requirement. The costs of the control strategy are: vaccination of the eligible heifers and veterinary costs. So far, preliminary results for two States were achieved: In Mato Grosso and São Paulo, the prevalence of seropositive animals was 10,25% (2003) and 3,81% (2001), respectively. From this information, the evaluation period until a prevalence of 2% is reached and the benefit-cost ratio were calculated. Considering 70%, 80% and 90% of the vaccination of heifers, the evaluation period were 27, 24, 22 years and the ratio between benefit cost ratio of control strategy and the base-case was between 1,005-1,095 (optimist and pessimist scenario, respectively) in Mato Grosso State and 14, 13, 11 years and the ratio between benefit cost ratio was between 1,003-1,011 in São Paulo State.

Key factors for sustainability of regional animal health networks: CaribVET example

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CaribVET is a collaborative network of veterinary services, research institutes and regional/international organizations whose objective is to improve animal and veterinary public health in the Caribbean. Set up on a bottom-up process about 15 years ago, CaribVET progressively achieved recognition and was officially endorsed in 2006 by the CARICOM as the Caribbean Animal Health Network. In 2010, it expanded to 32 countries and territories and 10 regional/international organizations. Its operation relies on a Steering Committee, a Coordination Unit and 6 working groups. Efficient and coordinated set of initiatives, projects and funding from different partners, mutual trust and responsibilities handover are essential for its sustainability. Quality Assurance principles are being implemented including formalized organization, clear rules (trilingual charter), and traceability (members, data) to improve network efficiency and operation. Interaction between professionals working in research, surveillance or control allows the definition of (1) relevant research questions according to needs evidenced in the field; (2) scientifically-based recommendations/tools to improve prediction of emergence (pathogen evolution, population dynamics); disease surveillance (design risk-based surveillance) and control strategies (appropriate treatment, vaccine, vector controls). Such interactions ensure implementation by decisions makers of research outputs, guarantee of sustainable improvement of animal health. These approaches contribute to network long-term operation to be complemented by cost-benefit studies and performance indicators development to gain advocacy of policy makers at the highest level of country members, about the essential role of CaribVET to support national networks and improve their prediction, prevention and control capacities.

Horse managers' perceived vulnerability to a future equine influenza outbreak: application of behavioural theory

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A growing body of work shows the benefits of applying behavioural theory to investigate biosecurity practices. According to the protection motivation theory, used to predict protective health behaviours, perceived level of vulnerability contributes to threat appraisal, which influences behavioural change, such as adoption of a biosecurity practice, in complex interplay with other factors. This study, conducted following the first-ever outbreak of equine influenza in Australia in 2007, investigated factors associated with horse managers' perceived vulnerability to a future equine influenza outbreak. Face-to-face interviews were conducted with 200 horse managers and factors associated with ordinal ratings of perceived vulnerability were identified using logistic regression. When asked about their feelings of vulnerability to a future outbreak of equine influenza, 32% of respondents felt very vulnerable, 37% felt vulnerable and 31% did not feel vulnerable at all. Receiving infection control information from a sporting or breeding association or society (OR=3.02; 95% CI: 1.65-5.64) or a non-veterinarian horse professional (OR=1.92; 95% CI: 1.01-3.68) during the 2007 outbreak were associated with increased 'very vulnerable' ratings, adjusted for age and gender. In addition, managers who felt unprepared for a future outbreak were associated with increased 'very vulnerable' ratings (P=0.023). In contrast, being involved in horse racing (OR=0.21 95% CI: 0.07-0.61) and being located in rural areas further from the city of Sydney were associated with reduced levels of perceived vulnerability (P=0.024). To promote biosecurity compliance, we suggest that future biosecurity communication strategies take into account these findings and are targeted at the racing and rural sectors.

Effect of emergency vaccination against outbreaks of foot-and-mouth disease in the Republic of Korea

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An emergency vaccination against foot-and-mouth disease (FMD) was implemented during the biggest epidemic in the winter of 2010/2011 in Korea. Then it was extended throughout Korea and settled as a large-scale preventive scheme with a vaccination-to-live policy. A vaccination reduces the risk of transmitting FMD among animals and farms, however the levels of protection may vary by animal species and farm types. In this study, the effect of vaccination against FMD was measured to understand why pigs were more seriously affected even with emergency vaccination. Cases of Hongseong, Chungcheongnam-do, where the FMD was confirmed on 127 pig farms but not on beef and dairy cattle farms, were examined. A deterministic model on between-farm transmission of FMD was constructed under Susceptible-Infected-Removed structure. The model was fit in account of numbers of susceptible and new report of FMD positive farms in each day. Scenarios on control measures including vaccine coverage and efficacy, culling, and pre-emptive slaughter were simulated. The goodness of fit of the model was better when the study population constituted only swine farms than including whole cloven-hoofed animal farms in the area. Assuming that almost 80% of swine farms were already vaccinated when the first case of the area was confirmed, very little efficacy of preventing transmission among pig farms was measured from the vaccination. An increase of vaccine coverage did not influence to the number of infected farms in the simulation models, while increases of the vaccine efficacy proportionally decreased the number of infected farms predicted by simulations. It must be associated with the strategy of vaccination that the injection was not simultaneously carried out on all age classes in the swine farms, while all animals in each cattle farm were vaccinated at once.

Effect of parity on culling and fertility in dairy cattle in Japan: the Hamanaka study

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A present study was conducted in order to assess the actual status of effect of parity on culling and fertility in dairy cattle of grassland farming in northern Japan using event-time analysis. Dairy herd improvement data, clinical records and farm management data were collected from 2002 to 2010 in 170 herds in a region. The overall median of cow number, calving interval and days open were 61, 432 days and 159 days, respectively. Ratios of tie-stall feeding system and grazing system were 79 and 76%, respectively. Multivariable analysis was selected to moderate conditions depending on area, farm, herd, and/or cattle. The proportional hazards model with some confounder and moderator variables was used to analyze the effect of parity. Start time was calving, time events were set culling or insemination with the pregnancy (IWP) and follow-up time was 200 days after calving for clarifying involuntary events. Total 17 confounder or moderator variables were prepared for the analysis, which were the number of cows, production level, the state of farm management, year and season of calving and so on. The data of total 60,782 cows were extracted. Parity were divided into 5 groups, parity 1, 2, 3, 4 and more than 4 (>4). The adjusted hazard ratios (AHR) for culling of parity 2, 3, 4 and >4 compared with parity 1 were 1.17 (95% CI: 1.06-1.28), 1.82 (1.66-1.99), 2.46 (2.25-2.69) and 3.96 (3.66-4.28), respectively. The AHR for IWP of parity 2, 3, 4 and >4 compared with parity 1 were 0.91 (0.89-0.94), 0.85 (0.83-0.88), 0.79 (0.76-0.82) and 0.77 (0.75-0.80), respectively. These results show the increase in parity of dairy cattle in this region becomes high the risk of involuntary culling and loss of fertility. We propose that veterinarians should advise dairy farmers about herd health and production management with consideration for the parity status of the herd.

Economic consequences of immediate or delayed insemination of a cow in oestrus

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In several previous studies the optimal calving interval of a dairy cow was determined. Knowing the optimal calving interval is however not very useful because insemination decisions have to be made at the moment the cow is in oestrus. In the current study, a user friendly decision support tool that can be used by dairy farmers to determine the economic consequences of immediate or delayed insemination for a cow in oestrus is developed. The tool is a deterministic model and built in Microsoft Excel. The whole lactation of an individual cow was simulated and daily milk yields were estimated using modelled lactation curves. The probability of oestrus detection and conception are made cow-specific and are dependent on the daily milk production. The user of the tool has to enter average herd and cow characteristics, such as 305-day milk production, day in lactation and parity. The user of the tool also has to enter economic parameters such as the revenues for a calf and the costs per insemination. The tool calculates the expected number of calves, the number of inseminations, the probability of culling, the calving interval and the milk production of a cow for both insemination alternatives. These numbers were used in a partial budget approach to compare the costs and revenues of both insemination alternatives. The utility of the tool was illustrated using data on 90 cows in oestrus (provided by ten Dutch dairy farmers). For the majority of cows the best decision was to immediately inseminate the cow in oestrus, but for most heifers with a flatter lactation curve the best decision was to delay the insemination. The economic effect of delaying the insemination was however small, on average -€18 per cow per year. This tool can be used by farmers to help making the best economic decision for a cow in oestrus.

Assessment of the economic losses caused by trichinellosis in Croatia

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Trichinellosis is a zoonotic disease which can have a high health, social and economic impact. The goal of this study was to assess the direct or indirect costs associated with human and animal trichinellosis in Croatia. Since it is difficult to measure all the costs, especially indirect ones, the aim was to measure as many costs as possible, arising as an economic consequence of the disease in Croatia. These costs fall into two groups: (1) costs related to human trichinellosis (losses due to illness and sick leave: costs of treatment, diagnostics and hospitalisation of patients; employer costs for sick leave; costs during sick period met by the Croatian Institute for Health Insurance (HZZO), costs related to employees' income losses due to sick leave); and (2) costs caused by animal trichinellosis (the reimbursement of costs to the owners of infected animals; costs of safe disposal of animals; costs of diagnostic procedures and preventive treatments). The study was conducted for the period 1998-2006. In this period 1,527 diseased persons were registered. Out of 6.3 million examined meat samples from households and 7.1 million examined meat samples from slaughterhouses, positive were 0.22% and 0.032%, respectively. The total cost for this nine-year period amounts to 45.8 million EUR. The costs related to human trichinellosis amount to 4.2 million EUR. Economic losses caused by animal trichinellosis are estimated at 41.6 million EUR. Enormous losses caused by trichinellosis have a great impact on national budget and this zoonotic disease constitutes a great public health problem as well. Therefore, continuing implementation of control and preventive measures that could decrease losses is of great importance.

Production losses in small ruminants due to *Brucella melitensis*: a systematic review

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Robust epidemiologic and livestock production data is essential in order to conduct sound economic analyses of livestock disease impact and disease control. Brucellosis has long been thought to have a considerable effect on livestock production and most studies highlight the fact that the control of brucellosis is of economic importance. It has been reported that abortion due to brucellosis is about 3-5% and estimates on the drop in milk production fall between 10-25%. However, these estimates are based on studies conducted for *Brucella abortus* in cattle and there is an apparent paucity of readily accessible data estimating the impact of *B. melitensis* in small ruminants. Therefore the aim of the study was: (1) to identify, evaluate, critically appraise and synthesise research reporting the effect of *B. melitensis* on production in small ruminants (sheep and goats); and (2) highlight knowledge gaps or where evidence is weak, thus indicating areas where further research is needed. A systematic review was conducted according to a predefined protocol based on Cochrane guidelines. Published peer-reviewed studies were eligible for inclusion in the review, as was grey literature such as dissertations, conference proceedings, government papers and reports. Grey literature was subject to the same quality assessment as peer-reviewed studies. All studies concerning the association between *B. melitensis* and production parameters in small ruminants were included. Studies were then assessed independently for risk of bias and quality of evidence as classified according to the SIGN (Scottish Intercollegiate Guidelines Network) system, which was modified to include cross-sectional studies. The results will be presented and the implications for economic analyses discussed.

Estimating the total costs of rearing a dairy young stock using a simulation model that accounts for calf diseases

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Rearing a dairy young stock provides the future dairy cows. Most dairy farmers are not aware of the rearing costs, consequently the rearing of dairy young stock does not often get the attention it requires. Calculating the distribution of the rearing costs is difficult as the costs interrelate with biological processes. In this study, a calf level simulation model was built (using @Risk adds-on in Excel) to estimate the distribution of the rearing costs in the Netherlands from two weeks of age until first calving. The uncertainties related to calf diseases (calf scours and bovine respiratory disease) such as temporal effects on the growth were included. In addition, growth was modelled stochastically and in a detailed manner by using a two phase growth function. All input for the model was based on scientific literature and expert knowledge (veterinarians and nutritionists). Costs were estimated using 20,000 simulations. The output of the model consisted of non-economic output such as birth weight, first calving age and weight. In addition, the economic output consisted of healthcare costs (prevention costs and treatment costs), feed costs, barn costs, breeding costs and labor costs. The total costs of rearing a dairy young stock were estimated as €1,567 per successful reared heifer and varied between €1,423 and €1,715. Reducing the age of first calving with one month, reduced the total costs ranged between 2.6% and 5.7%. Although the average expenditures for diseases were not high, the rearing costs of a heifer that experienced disease (20% of the simulated heifers) were on average €95 higher than of a healthy heifer. In conclusion, the total costs of rearing a dairy young stock are high. The average costs for healthcare and mortality costs are relatively low. However, the costs for disease cases are considerable, making prevention of diseases during young stock rearing important.

Animal health and environmental pollution

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Animal production, like all land-based industries needs to satisfy societal demands for pollution control. We have examined the areas of greatest concern of environmental pollution arising from either lack of animal health or measures to improve animal health in sheep, cattle, pigs and poultry. In particular we have focussed on: veterinary pharmaceutical products such as acaricides; pathogens – (antibiotic resistance, VTEC, Johnes, listeria, toxoplasmosis and *Salmonella*); eutrophication (especially nitrogen enrichment from slurry); and greenhouse gases. We present an overview of the pollution problems associated with animal production in Scotland, compare animal production as a source of pollution with other sources of pollution in Scotland to provide context, and consider possible mitigation measures. In the process of reviewing this topic we have interviewed practicing vets to establish what they perceive the most important pollution from production animals and we present a summary of their responses.

Prevalence of ketosis in high producing dairy cows of Kagugu dairy farm, Shema farm and Tnk farm
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Malnutrition is a major affliction of the human population in Rwanda. A primary effort to combat this affliction is to increase the genetic potential of dairy cattle. Increased genetic potential requires increased management. National and international projects such as One Cow Per Poor Family are designed to distribute animals to impoverished families for combating human malnutrition but do not provide improved animal husbandry training. The inability of producers to meet the increased nutritional demand of lactating dairy cows can lead to metabolic disease such as ketosis. The objectives of this research were to determine the prevalence of clinical and subclinical ketosis through blood BHBA concentrations in 92 dairy cows from three prominent dairy farms near Kigali and to demonstrate the need to provide education recommendations for prevention. There was a prevalence rate of 6.5 for subclinical ketosis and 1.1 for ketosis. These prevalence rates are not high in comparison to developed countries but the level of milk production does not rival those from developed countries. Ketosis increased from primiparous to multiparous cows, increasing along with genetic potential for milk production. Cows under 60 days in lactation were more vulnerable to ketosis. Husbandry practices will need to improve in order to facilitate increased genetic potential for milk production in Rwanda.

Alternative strategies for risk financing of high consequence animal disease outbreaks in the United States

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High consequence animal diseases (HCADs) are diseases such as foot-and-mouth disease (FMD) and classical swine fever (CSF) that could have devastating economic and social impacts within the United States (US). For example, FMD losses for a US outbreak could be on the order of tens of billions US\$. Because HCADs would be so costly, it is essential to explore alternative risk financing strategies. An additional impetus for exploring alternative risk financing strategies is the apparent intensifying risk of these diseases worldwide (e.g. FMD in Asia, Africa, and the Middle East; CSF in South America and the Caribbean) together with increased intercontinental trade and travel. Currently, the US government offers financial compensation to animal owners for loss incurred as a result of the taking and destruction of their animals, animal products, equipment, and other property on the order of the government (e.g. due to the occurrence of certain animal diseases, including HCADs). This form of compensation by the government is referred to as indemnity in the US. We explore risk strategies that go beyond indemnity and a purely public sector approach. Alternative strategies (some theoretical, some in use internationally) are evaluated for their potential as an alternative risk financing instrument in the US. Major approaches examined include public-private partnerships (e.g. loans, levies, and tax relief), industry arrangements (e.g. farming contracts, cooperatives, and partnerships), and insurance models (e.g. government subsidized and private). Complexities of alternative strategies are discussed.

Small scale dairy farms and direction of feed management in tropical country, Sri Lanka

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Recently the demand for milk and milk product has been increasing, rapidly in Sri Lanka. But the domestic supply is not enough to meet the domestic demand. In 2009, self-sufficiency rate for milk and milk products was only 33% and large part of that comes from small scale dairy farmers in Sri Lanka. The dairy farmers in coconut producing countries use by-products of coconut milling as animal feed. It is commonly known as 'Coconut poonac', which is widely used as cattle feed supplement in Sri Lanka. A previous study suggests that there may be a positive relationship between coconut poonac feeding and milk yield; however it is known that coconuts has high fat contents and too much feeding might have bad effects on animal health. Therefore, this study identifies the coconut poonac feeding dairy farmers and analyzes the effects of coconut poonac on small scale dairy farm management. Finally, the study will draw policy implications for dairy development in Sri Lanka. The data for analysis were collected from 150 small scale dairy farmers from November 2009 to February 2010 in Kurunegala districts, North western province, Sri Lanka. The farmers were interviewed on dairy activities using structured questionnaire. Kurunegala district is famous for coconut production. We cleared two points. First, dairy farmers who have agricultural income and small land per cow tend to use coconut poonac. Second, if dairy farmers use coconut poonac with participation in dairy farm training, their milk yield and dairy income increases significantly. Strengthening dairy training programs and encouraging the participation are important for future dairy development in Sri Lanka.

Resource-use efficiency and dairy farm development in Sri Lanka

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The present study examines the resource-use efficiency in dairy production system in Nuwara-eliya districts, Up-country and Kurunegala districts, Coconut triangle, Sri Lanka. One year regular bi-weekly panel data were collected from sixteen (16) small scale dairy farms between 1st to December 31st in 2009 and 2010 from Up-country (10 farms) and Coconut triangle (6 farms) respectively. The dairy farmers were selected randomly representing different management systems. Firstly, the stochastic production frontier model was used to estimate the technical efficiency and secondly, the Tobit model was regressed to identify determinant factors of efficiency. Efficiency of feed resource use was estimated by determining the ratio of Marginal value product (MVP) to Marginal factor cost (MFC). The return to scale of 1,368 was obtained indicating that the resource allocation and production were inefficient at the present level. In addition, house hold size, feed cost per cow and training were found to contribute positively to technical efficiency while age and cattle disease occurrences reduce technical efficiency. Therefore, the government should concentrate on encouraging old dairy farmers to produce more efficiently by giving them trainings and extension services on new feed management technologies. Furthermore, the results of MVP to MFC ratio revealed that feed resources are under-utilized in Coconut triangle, while over-utilized in Up-country. Hence government should encourage the private sector to do more research on developing low cost feed rations for different agro-climatic zones using available feed resources.

Outbreak of HP-PRRS and economic evaluation of the disease control in T.T.Hue province, Vietnam
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The objectives of this study were to investigate the dynamics of Highly Pathogenic Porcine Reproductive and Respiratory Syndrome (HP-PRRS) outbreaks in Hue, Vietnam, and apply SIR model and Cost-Benefit Analysis to analyze the economic benefit of disease control program conducted in this high pig density area. Veterinary data was collected from veterinary department of Hue to clarify the dynamics of HP-PRRS outbreaks. The disease diffused quickly from one introduction to the whole observational area only used 11 days, but it was under controlled by culling program conducted by Hue government. Unlike other area in Vietnam, the outbreak never happened in Hue after 2008, so the culling program was effective. According to the result of estimation by SIR model, the benefit from HP-PRRS control program was 3.8 times or more than the cost. This control program should be a good example for other pig farming area in Vietnam.

Analyzing antibiotic use in Dutch livestock sectors using panel data

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Antibiotic use in livestock production has come under increasing public scrutiny due to its potential contribution to antimicrobial resistance both in livestock as in human health. For policy makers, it remains unclear whether antibiotic use can be drastically reduced and what economic consequences this will entail. In this paper we explored antibiotic use data in combination with microeconomic data on Dutch livestock production farms. The objective of our study was to provide quantitative insight into the extent and pattern of antibiotic use and its relationship with farm-specific indicators. We analyzed the use of antibiotics in four types of livestock sectors (broilers, dairy cows, fattening pig and sow farms) using panel data over the period 2004-2010. In the data analysis both cross-sectional and temporal variations were examined. Antibiotic use was expressed as the number of daily doses (ADD) in which an animal with year-round presence would be treated with antibiotics according to standard dosages. ADD in the period 2004-2010 averaged about 31.7, 6.2, 16.1 and 26.8 in the broiler, dairy, fattening pig, and sow farms respectively. The antibiotic use data showed substantial cross-sectional variations in each livestock sector for all years analyzed. The coefficients of variation (CV), calculated as the ratio of the standard deviation to the mean, were above 40% for all years analyzed. At the same time, the relative level of antibiotic use on the same farm showed a considerable level of stability across the years. On average, the probability that farms have approximately the same level of antibiotic use as in the previous year was estimated to be higher than 70%, which suggested the persistent role of farm-specific factors. While there seemed to be no clear relationships between antibiotic use and farm performance indicators, farm structure indicators such as herd size and up-to-datedness of the farm, affected antibiotic use significantly in each livestock sector.

Incidence and impact of classical swine fever on small holder pig production systems in Northeast India

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We conducted a cross sectional study in three states in Northeast India to estimate the incidence and impact of Classical Swine Fever (CSF) among small holder pig producers. Data were collected using participatory epidemiological methods and key informant interviews from a total of 60 villages distributed equally between 15 districts in Assam, Nagaland and Mizoram states. The impact on livelihoods was estimated from data on mortality, replacement and treatment costs. The study findings show that although a majority (over 80%) of the households in the area keep pigs and consider pig farming as an important source of income, level of production is low. Reasons given for this include: lack of feed, poor management practices, lack of capital, high prevalence of infectious diseases and poor veterinary infrastructure. The incidence, morbidity and case fatality rates of CSF were estimated to be 5.4% (95%CI: 3.5-8.0), 28.1% (95% CI: 20.4-36.6%) and 51.1-94.5% per year, respectively. The study also reveals that CSF outbreak lasts for about 36 days on average (95% CI: 19.0-53.8) suggesting that CSF outbreaks run their full epidemic course before burning out. Behavioural practices such as selling of infected or potentially infected animals during an outbreak as one way of avoiding mortality losses could be responsible for sustaining the transmission of the disease. Of the livelihood impacts estimated, the cost of mortality represents the single most important direct impacts (at 8.4% of the total expected annual income of US\$581 per household in Assam, 0.9% in Mizoram and 2.8% at Nagaland). Economic losses from other impacts are not substantial as the annual treatment and replacement losses range between 0.05-0.11% and 0.05-0.48% of the annual household income, respectively. This information is being used to design appropriate interventions for CSF in the region.

Cost of Post-weaning multi-systemic wasting syndrome and PCV2 subclinical infection

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The present study aimed to assess the economic impact of Post-weaning multi-systemic wasting syndrome (PMWS) and porcine circovirus type 2 (PCV2) subclinical infections (PCV2SI) at farm and industry level. A disease model simulated the varying proportions of pigs in a batch that will get infected with PCV2 and develop either PMWS or subclinical infection, depending on the farm PMWS severity level. The model, fitted with empirical data, generated six outcomes: infected pigs with clinical PMWS that die (PMWS-D); infected pigs with clinical PMWS that recover (PMWS-R); PCV2SI that die (PCV2-D); PCV2SI that reach slaughter age (PCV2-S); healthy pigs (H-S); and healthy pigs, infected or non-infected by PCV2, that die due to non-PCV2 related causes (H-D). Enterprise and partial budget analyses were used to assess the deficit/profits and the extra costs/extra benefits of a change in disease status of a pig, respectively. Results from the individual animal economic analysis were combined with the disease model's estimates of the proportion of different pigs produced at different severity scores to assess the cost of PMWS/PCV2SI and the overall profit at farm level. Stochastic simulations were carried out to account for variability and uncertainty. The economic impact of a PMWS-D pig was estimated to be £82.7 (80.0 to 84.4), £27.2 (16.2 to 23.4) for a PMWS-R pig, £84.85 (80.0 to 89.7) for a PCV2-D pig and £13.9 (3.72 to 25.8) for a PCV2-S pigs. At farm level, the greatest proportion of negative economic impact was due to subclinical pigs. The economic impact of PMWS for the English pig industry, prior to the introduction of PCV2 vaccines, was estimated to be £61.4 million per year (38.2 to 88.2). This is the first study to model the cost of PMWS and PCV2SI at different farm severity levels. The model showed the high cost of PMWS for the English pig industry in 2008 and highlights the importance of subclinical infection. Results from this model provide the basis to assess the cost-efficiency of different control measures.

Economic efficiency of different control strategies for post-weaning multi-systemic wasting syndrome and PCV2 subclinical infection

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The aim of this study was to assess the economic efficiency of different control strategies for Post-weaning multi-systemic syndrome (PMWS) and porcine circovirus type 2 (PCV2) subclinical infections (PCV2SI). The strategies consisted in the combination of up to 5 different control measures: (1) PCV2 vaccination; (2) ensuring age adjusted diet for growers (diets); (3) reduction of stocking density (stock); (4) improvement of biosecurity measures (bios); and (5) total depopulation and repopulation. A model simulating the production of batches over 5 years of a farm with 100 sows was developed. A PMWS/PCV2SI economic model, based on PMWS severity scores, was applied to the production model to assess disease losses. Eleven different farm scenarios, differing on the number of risk factors present, were investigated. For each strategy an investment appraisal was performed to assess the extra costs and benefits of reducing the PMWS severity score of a farm to an average slightly affected score and to input other intervention costs. The net present value obtained for each strategy was multiplied by its probability of success. The resulting expected values were then compared within each scenario. A stochastic simulation was performed using @RISK. The model identified PCV2 vaccination in combination with biosecurity measures as the most cost-efficient strategy for most farm scenarios. PCV2 vaccination alone, 'bios+stock' and 'bios+diets' were frequently identified as the second or third best strategy. The mean expected values of the best strategy for an average moderately and an average highly affected farm were £14,052 and £65,145, respectively. This is the first study comparing economic efficiency of different control strategies against PMWS and PCV2SI. The outcomes describe the economic benefits of PCV2 vaccination, but highlight the need of biosecurity measures to achieve optimal profitability. The model developed provides a useful decision support tool for farmers.

The use of probabilistic graphical models (PGMs) to develop a cost-effective vaccination strategy against *Campylobacter* in poultry

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Human campylobacteriosis represents an important economic and public health problem. *Campylobacter* originating from feces of infected chickens will contaminate chicken meat posing a risk to the consumer. Vaccination against *Campylobacter* in broilers is one probable measure to reduce consumers' exposure to *Campylobacter*. In this presentation we focus on the development of a computerized decision support system to aid management decisions on *Campylobacter* vaccination of commercial broilers. Broilers should be vaccinated against *Campylobacter* in the first 2 weeks of age. Therefore, the decision about vaccination needs to be made usually before *Campylobacter* is introduced in the flock. In fact, there is uncertainty regarding the introduction of *Campylobacter* into the flock that needs to be taken into account in the decision making process. Probabilistic Graphical Models (PGMs) integrate knowledge from diverse sources and can be used as decision support systems under conditions of uncertainty. The relationships between different entities in the model can be designed and conditional probability distributions are used to define the strength of these relationships. Important microbiological, epidemiological and economic factors (cost-reward functions) have been included in the models. The final outcome of the models is presented in probabilities of expected level of *Campylobacter* and financial terms influenced by the decision on vaccination. For example, if the best decision seems to be to vaccinate, the outcome will be expressed as the most probable number of *Campylobacter* in broilers and a cost-profit balance. There are other factors that could be considered increasing the complexity of the models, but we need to balance model efficiency with simplicity and usefulness for poultry managers to run the model as a tool for decision making on vaccination.

A framework for the economic analysis of rabies control

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To inform decisions on resource allocation and add to evidence on rabies control, the World Society for the Protection of Animals needed a comprehensive economic assessment tool. Control of rabies, that causes spillovers from its animal host into human populations, requires not only technical means of control, but also understanding of economic gains and the role of human behaviour in disease transmission. A conceptual framework was developed including economic, dog welfare, epidemiologic, and social acceptability assessments as basis for making an ethical judgement on the control process. It was applied to a rabies control programme in Colombo City, Sri Lanka. The rabies control programme included vaccination and sterilisation of owned and unowned dogs; education to prevent dog bites; dog managed zones; and training of dog handlers. The impact of rabies and control efforts on dog welfare was assessed using a qualitative scoring system that combined field records, literature data and expert opinion. Surveys and focus groups were conducted to assess changes in acceptance of dogs in society and control options. Monetary outcomes of the programme were calculated considering medical costs related to post-exposure treatment (PET) and control expenditures. Non-monetary benefits were the change in disability-adjusted life years (DALYs) caused by psychological distress due to dog bites. Burden of human death was near zero as PET was provided by hospitals at no cost to the individual. From July 2007 to June 2011, 133 DALYs were avoided, acceptance of dogs increased, and the impact on dog welfare was reduced at a net cost to society of US\$ 1.05 m (compared to the counterfactual). The lower number of dog rabies cases and estimated dog bites, and improvement in reporting and treatment of people indicated that the intervention was effective and the risk of people to contract rabies decreasing.

Estimating the financial consequences of a milk dioxin contamination in the Dutch dairy chain

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The aim of this study was to quantify the financial consequences of a milk-dioxin crisis on the stages of the dairy chain involved. The milk dioxin contamination impact model was designed for this purpose and also was used to estimate the net costs of control measures limiting the impact. Results obtained based on the assumption of the worst-case scenario in which the entire daily production of each business unit from feed supplier to milk processor is contaminated suggested that the financial impact of one dioxin incident would be J141.2 million. Another assumption was that the dioxin contamination started at one feed processing plant and was detected 2 weeks after initial contamination (the high-risk period), which would result in the involvement of 714 dairy farms, 26 milk processors, and 2,664 retailers. The stages of the chain that contributed most to the total net costs were the milk processor (76.9%) and the dairy farm (20.5%). If the high-risk period were shorter, i.e. 3 days, the estimated total financial impact decreases to J10.9 million. Thus, early detection of the contamination is crucial for decreasing the number of food businesses involved and lowering the total financial impact. The most influential inputs of the model were the sale price of milk at the processing stage, the daily amount of milk processed per processing plant, the farm-blocking period, and the daily amount of milk produced per farm. However, the effect of these inputs on the total financial impact was less than 10.0%. These results can be used to establish priorities in the application of control measures to limit the financial and public health impacts of a possible food safety incident.

Identifying critical management decision points in the heifer rearing process using individual animal-based bioeconomic modelling

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Replacement dairy heifers should have minimal mortality, with an age at first calving (AFC) of 24 months currently recommended. Recent focus in UK dairy herds has been on the economic impact of youngstock losses and delayed AFC. A reduction in reproductive efficiency, increasing calving intervals and high replacement mortality rates have all contributed to a decreasing availability of dairy heifers and a tightening in heifer replacement prices. Producers are therefore reluctant to remove replacements that show poor growth, repeated incidences of disease or suboptimal fertility. Most current models of dairy farm production systems are single component models primarily focusing on the milking herd. Multi-component models that include the replacement herd, or those specifically constructed to model an aspect of the replacement herd fail to incorporate the fundamental economic elements of the rearing period. Neither do they account for the effect of management decisions and genetic selection on the underlying biology of the heifer and the effect this has on herd dynamics and profitability. Our replacement herd model was developed in Microsoft Visual Basic with Microsoft Access as the database management system and user interface. It models individual heifers through stages of growth and development over a decision horizon of birth to first calving. This allows factors such as bodyweight, age and genetic merit (which impact on subsequent production, longevity and reproductive success) to be evaluated under UK conditions and practises. The model identifies critical decision points based on biology, health and genetics allowing the producer (1) to determine the likelihood of that replacement heifer reaching her AFC target; and (2) to estimate her longevity and milk production potential. This provides the producer with an evidence base for decision making on youngstock rearing production and health management and the monitoring and evaluation of the system.

Baseline study of infringement level of welfare regulations in Danish pig herds

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In order to secure the animal welfare in production animals, the Danish Food and Veterinary Administration (DVFA) decided to establish the proportion of pig herds in which welfare regulations were violated in 2011. This species has been subject to campaigns to improve compliance with welfare regulations in recent years (e.g. culling at farms). The objective of this study was to establish the proportion of Danish pig herds not complying with animal welfare regulations. To assess this, a random sample of 300 pig herds with at least 10 pigs was visited by veterinary officers from DVFA from August through December 2011. Veterinary officers were used for visits because herd owners cannot deny them access. A list of 380 regulation points was evaluated and for each point the herd could receive four marks: (1) no marks; (2) warning; (3) enforcement notice; or (4) police reporting. In total 150 herds received one of the four marks. Of the 300 herds, 127 (42%) herds receiving a warning, 42 (14%) an enforcement notice and 16 (5%) a police reporting. The most commonly noticed infringement of regulation was access to rooting material; pigs did not have access to rooting material in 72 (24%) herds. Providing soft bedding in sick pens for injured and diseased animals and isolation and treatment of injured and diseased animals received marks in 58 (19%) and 56 (19%) herds, respectively. Results from this study can be compared with future studies to evaluate if infringements of welfare regulations changes over time. It needs to be kept in mind that a control of compliance with welfare legislation cannot replace a full welfare assessment, but it is still an important indicator of the minimum standards.

Gross margin losses due to *Salmonella Dublin* infection in Danish dairy cattle herds estimated by simulation in the Dublin-Simherd model

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The objective of this study was to estimate losses in gross margin (GM) following introduction and spread of *Salmonella Dublin* in dairy herds. GM losses were estimated using an age-structured stochastic, mechanistic and dynamic simulation model (Dublin-Simherd). The model incorporated six age groups (neonatal, pre-weaned calves, weaned calves, growing heifers, breeding heifers and cows) and five infection stages (susceptible, acutely infected, carrier, super shedder and resistant). Twelve scenarios were included in the model, these were the combinations of three herd sizes (85, 200 and 400 cows) and 4 management levels of infection spread (very good, good, poor and very poor). Input parameters for *S. Dublin* effects on production and animal health were based on literature and calibrated to mimic real life observations. The effects of introducing one *S. Dublin* infectious heifer four weeks before calving were estimated through 1000 simulation iterations for each of the 12 scenarios. Mean annual GM per cow stall was compared between herds that experienced spread of *S. Dublin* and non-infected reference herds for over a 10 year period. Estimated GM losses were highest in the first year after infection, and increased with poorer management and herd size. E.g. for a 200 cow stall herd, mean GM losses were estimated to 57 Euros per stall in the first year after herd infection in a herd with good management and to 315 Euros per stall in a herd with poor management. Sensitivity analyses estimated that assumptions about milk yield losses for cows in the resistant or carrier stage had the highest influence on estimated GM losses, and that this effect was more influential the poorer the management was. Results from this study can be used to encourage farmers to prevent introduction and to control spread of *S. Dublin* within the herd.

Challenges towards natural calving in double-muscle cattle in the Netherlands

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The current high rate of caesarean sections (>90%) in double-muscle (DM) cattle has led to increased public concerns in the Netherlands. In general, DM cattle have a smaller pelvic area in comparison to other beef breeds, which in combination with a higher calf birth weight, results in problems at birth. Only a decrease in the proportion of caesarean sections in DM cows would make these breeds less controversial, which is only achievable by directed breeding efforts. Until now, no evaluation has been made to estimate the economic impact of an increased rate of natural calving in DM cattle in the Netherlands. The objective of this study is, therefore, to gain insight into these economic effects on individual animal level. Due to lack of quantitative information in the literature, interviews and questionnaires were used to collect quantitative farm data to parameterise a stochastic partial budgeting model. This model simulates the economic consequences of the current situation with 100% caesarean sections and of an aimed situation of having 50% natural calving in DM cattle. The model reflects the period after the second parturition of a DM cow till slaughtering after the fourth parturition, assuming that the animal has delivered her first two calves by caesarean sections. No striking differences in the average gross margins were found between the current and the aimed situation in DM cattle (€ 2,171 vs. € 2,160, resp.). In spite of a reduction in the gross margin in the aimed situation due to lower maintenance costs and veterinarian costs, these reductions were compensated by the expected reduced revenues (€ 4,196 current vs. € 3,938 aimed). The 90% confidence interval of gross margins ranged from € 901 to € 3,952 in the current situation and from € 885 to € 4,116 in the aimed situation, indicating some higher level of uncertainty in the latter. Given the expected economic impacts, economic motives will not prevail as incentive for DM cattle farmers to breed towards more natural calving in DM cattle in the future.

Economic consequences of Bluetongue disease, serotype 8, in Germany

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In August 2006, Bluetongue virus serotype 8 (BTV-8) was introduced into Central Europe and in 2006/2007 spread rapidly over Germany. In May 2008, Germany implemented a vaccination program with monovalent, inactivated vaccines against BTV-8. In 2008 and 2009, vaccination was mandatory for cattle, sheep and goats; since 2010, vaccination is optional. An economic model of the BTV-8 epidemic was developed based on data provided by the German Federal States, the animal health services, the animal disease compensation funds (Tierseuchenkassen), the German animal disease notification system and the Federal Statistical Office. Bluetongue disease had a high economic impact on the cattle and sheep industry in Germany. In 2007, the costs for a total of 43,000 animals (33,233 sheep, 10,240 cattle and 102 goats) were claimed from the animal disease compensation funds. On the basis of the animal market values, this corresponded to more than 20 Million Euros, including the safe disposal of the animal carcasses. Direct costs resulted from reduced milk and meat production, palliative veterinary care costs, and fertility problems. Indirect costs resulted from vaccination, movement restrictions, and adapted export certificates. The costs of BTV-8 were estimated at 10 million Euros in 2006, 79 million Euros in 2007, 72 million Euros in 2008, 38 million Euros in 2009, 16 million in 2010 and 7 million in 2011. While the direct costs (e.g. production losses, costs for fallen stock) caused the highest losses in 2006 and 2007, from 2008 to 2011 the vaccination costs played the main role. Options to improve control strategies will be discussed.

Bacterial zoonoses in East Africa: a major cause of human illness and economic burden?

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In sub-Saharan Africa, inpatient febrile illness and death is most commonly attributed to malaria, but malaria is over-diagnosed and there is growing evidence that many zoonoses are important causes of undifferentiated febrile illness. As well as direct impacts on human health, many zoonoses have economic impacts, reducing livestock productivity. We review data on three bacterial zoonoses, brucellosis, Q-fever and leptospirosis, generated through (1) human febrile disease surveillance; and (2) cross-sectional studies in linked human and animal populations, conducted in Tanzania and Kenya over the past 10yrs. Results from a febrile illness study in northern Tanzania indicated that, collectively, these zoonoses were the cause of 11 times as many cases as malaria, with leptospirosis diagnosed in 9%, Q-fever in 5% and brucellosis in 3% of febrile admissions. In a syndromic surveillance study in western Kenya, acute Q-fever was diagnosed in 3% of patients with acute respiratory disease and fever. In northern Tanzania, the seroprevalence of *Brucella* in humans (7-10%) was similar in pastoral and agropastoral settings, but differed in livestock (8-10% in pastoral, <4% in agropastoral areas). Very low livestock seroprevalences were seen in smallholder communities in Tanzania and Kenya. Bacterial zoonoses are likely to contribute significantly to the burden of human and animal disease in East Africa, particularly in pastoral and agropastoral communities. Efforts need to be made across medical and veterinary sectors to improve their diagnosis, treatment and prevention.

Distribution and economic impact of coccidiosis on small scale commercial poultry farms in Africa
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Coccidiosis, a species-specific intestinal disease caused by *Eimeria* spp. parasites, causes substantial production losses in the poultry industry worldwide. The objective of the study was to examine the distribution and economic impact of *Eimeria* spp. within small-scale commercial poultry farms in Africa. Faecal samples and data on production parameters and farm management were collected from small-scale (less than 2,000 birds per batch) commercial broiler and layer farms within Ghana, Tanzania and Zambia. The gross margin and enterprise budget per bird per year were calculated to assess individual farm profitability. The parasite presence and load was quantified through faecal oocyst counts and confirmed through *Eimeria* specific 5S rDNA PCR. The field samples were screened for the presence or absence of each of the seven *Eimeria* species that cause coccidiosis in the chicken using a diagnostic molecular PCR assay. Pathogenicity of species present was compared with farm profitability. *Eimeria* spp. parasites were found to be widespread within Africa and were present on 75% (60/80) farms sampled. Species complexity was comparable to that of Europe with all seven *Eimeria* species detected and 35% (28/80) farms concurrently infected by multiple *Eimeria* species. Farmers reported awareness of clinical coccidiosis and mortality rates of up to 80%. The profitability of farms varied substantially by country and production type, with gross margins ranging from -21.88 to 52.30 USD per bird per year in layer systems and from -4.01 to 8.01 USD per bird per year in broiler systems. Further studies are required to characterise the *Eimeria* population within Africa and the economic impact on poultry farms and to identify cost effective potential control strategies and interventions.

Association between first calving age and milk production at first lactation in 100 Dutch dairy farms
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The total costs of rearing a heifer will be reduced by lowering the first calving age (FCA). A lower FCA could, however, coincide with a lower development of the reared heifer, influencing milk production at first lactation. To establish the possible economic impact of lowering the FCA, the association between FCA and milk production in first lactation needs to be investigated. The objective of this study is to determine this association at cow level. Data on FCA and milk production at first lactation of 8,454 heifers in 100 intensive Dutch dairy herds from 2003 to 2010 were gathered. The average FCA was 26 months and the average 305 d milk production at first lactation was 7,493 kg. The median FCA of the herds ranged between 24 and 32 months of age. The difference between the FCA of the individual heifer and the median FCA of the herd was defined as the relative FCA. The association between relative FCA with 305 d milk production at first lactation was analyzed using a linear mixed effect model and included herd, year and calving season. Relative FCA was categorized monthly, and relative FCA not deviating from the median FCA of the herd was the reference category. Heifers having a FCA one or two months lower than the median FCA of the herd have a 90 kg and 179 kg lower 305 d milk production at first lactation, respectively. Heifers having a FCA one month higher than the median FCA of the herd have a 87 kg higher 305 d milk production at first lactation. Relative FCA gives a deviation of a heifer's FCA from a similar management. The results indicate that a lower FCA on a farm by earlier insemination but not adjusting the management to ensure sufficient development will reduce rearing costs but with a lower milk production at first lactation. A higher FCA results in a higher milk production but with a higher rearing costs. For dairy farmers, there is an economic optimum between rearing costs and FCA with regard to heifer rearing.

Economic evaluation of air filtration in large sow herds in North America

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Air filtration systems implemented in large sow herds have been demonstrated to decrease the probability of having a PRRSV outbreak. However, a large economic study comparing real production data from both filtered and non-filtered farms has been never been completed in order to assess the profitability of this investment. In 2010, the 14 filtered and 6 control participant herds were enrolled from a contemporaneous PRRSV epidemiological study. Repeated measures of quarterly production data, weather, PRRSV outbreak in the period together with air filtration status and number of different pig sites within 3 miles, were the variables analyzed in the longitudinal mixed model. Data management and statistical analysis was performed with a Statistical Analysis System (SAS) version 9.1. The retrospective and prospective timeline study was Oct 2004 to June 2011. For the cost analysis, three scenarios were compared in a spreadsheet model of weaned pig cost on a representative 3,000-sow non-filtered farm with feed cost of \$278/sow/year: (1) control; (2) filtered conventional attic; and (3) filtered tunnel ventilation. Scenario 1 was based on the data from control and pre-filtration periods of the future filtered farms. Scenarios 2 and 3 were identical except that the initial filtering equipment cost \$150/sow for the conventional versus \$200/sow for the tunnel. Filtration was assumed to change pigs weaned/sow/year, farrowing rate, female replacement rate, female death rate, veterinary expenses, and the annualized cost of replacing pre-filters every six months and replacing filters every three years. Filtered farm produced 6,028 more piglets than non-filter farm and the payback period for the investment was estimated in the model as 5.5 years for scenario 2 and 6.4 years for scenario 3. However, this could be considered a conservative estimation because no value penalty in selling PRRSV positive piglets was accounted for.

Poster topic 06**Poster 49****Modelling climate change impacts on livestock aid**

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Poor livestock keepers are faced with a future of uncertainty. Across the literature, there is broad consensus that current constraints to livestock production are likely to be exaggerated under climate change and the associated Extreme Weather Events (EWEs). This will have important implications for those poor households who rely on livestock for income generation, food security, and as source of investment. Traditionally, restocking programs have been instigated after EWEs to support poor households in the short-term and help break the poverty cycle over the longer-term through the provision of livestock. Other forms of aid such as supplementary feeding, destocking and more recently, cash transfers have also been tried as tools to support the rehabilitation of livestock-dependent populations post-emergency. However, while climate change is likely to change the duration and frequency of EWEs, little is known regarding the robustness of particular forms of livestock aid in meeting these new challenges. Therefore, in the following article, the authors create a simple deterministic model to explore the potential impacts of different forms of livestock aid on a range of livestock keepers across both subsistence and pastoralist production systems. The impact of critical global climate parameters such as the predicted 2 °C temperature rise are explored within the expected production shifts across the systems under review. The model demonstrates the importance of understanding the factors underpinning livestock aid at the household and production system levels and the potential limitations and benefits of a wide range of livestock-related interventions.

Venezuelan equine encephalitis (VEE) outbreak in Mexico and the Panamerican games

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In 2011 Mexico hosted the Panamerican Games (PG). Export certifications were agreed ahead of time with countries but conditions changed due to two outbreaks of VEE in southeast Mexico. Outbreaks were notified to OIE and several countries implemented restrictions for the movement of horses. Epidemiological reports and follow up of both cases were submitted to OIE, our main commercial partners and to WTO. Both cases were auto-limited I-E enzootic variant. Equine infections with this variant cause low level virulence and antibody response, but most cases show no clinical disease due to low pathogenicity. The epidemiological investigation concluded that mortality recorded was not the consequence of the identified I-E virus. OIE's recommendations for EEV do not differentiate among enzootic and exotic variants of VEE, nor does the format for declaring disease allow for this differentiation. These issues outlined the need to modernize conditions and logistics for international horse movements, especially regarding sporting events. The open communication with countries allowed the establishment of conditions for movement of horses participating in the PG, 137 horses from 47 different countries participated in the event. The thorough epidemiological investigations supported other schemes for risk mitigation for VEE. The experience gained through this event shaped a new approach for a faster establishment of sanitary requirements. Traditionally import and export requirements are based on country by country negotiation of bilateral certification as well as generic health certification based on presence of disease. In order to facilitate the movement of horses, an overall review of import and export requirements, an evaluation of disease risk and OIE's recommendations, helped establish a universal certification scheme that gives different options that minimize disease risks but do not unnecessarily restrain movement of horses, among them a regionalized approach to VEE.

New approaches to CSF surveillance schemes

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Mexico implemented for over two decades an eradication strategy against Classical Swine Fever (CSF) concluding by 2009. The original strategy was based on surveillance, vaccination, diagnosis, quarantine and movement controls. CSF was eradicated State by State a regionalization approach. As the country is currently free of the disease surveillance strategies have been modified. To provide assurances on CSF freedom status, Mexico has modified its epidemiological surveillance. In close collaboration with the United States Department of Agriculture, a clear case definition has been standardized, disease surveillance has been adapted to conform to high risk targeted surveillance, diagnostic tests have been harmonized and validated with reference laboratories protocols, and investigation protocols for very low pathogenicity strains have been implemented. As a result of these activities suspect cases of CSF were detected. The epidemiological field investigation and laboratory diagnosis concluded the absence of virus including any low pathogenicity strains. This surveillance scheme will be kept for subsequent years, and will focus to high risk areas. The Mexico-US collaboration has been based on inspection visits, joint training workshops, laboratory personnel exchange visits, criteria definition on surveillance and diagnostics case definitions, epidemiological investigations and laboratory protocols and thorough discussion of technical reports. These have allowed a greater understanding of how surveillance is done and has given greater confidence on CSF-free disease status, building strong bilateral science based collaboration among veterinary services of our two countries. Additionally the Mexican experience with this disease has been shared with Central American countries, passing on lessons learned, and strengthening surveillance systems and notification schemes regionally.

Using mixed methods to delineate the policy network and evaluate policy decision-making in response to the 2007 Australian equine influenza outbreak

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Decision-making is critical during disease outbreak response. We conducted this study to evaluate technical policy decision-making during the 2007 outbreak of equine influenza in Australia to describe the stakeholder network involved and the factors driving policy decision-making during an outbreak of emergency animal disease. Systematic review of the outbreak literature and the pre-existing national policy document revealed 6 policy issues involving policy modifications or differing interpretations by different state agencies. Data on factors influencing the decision-making process regarding these six issues and on stakeholder interaction were collected using a pre-tested, semi-structured questionnaire and snowball sampling. Face-to-face interviews were conducted with 24 individuals representing 12 industry and government organisations. Quantitative data were analysed using social network analysis and thematic analysis of qualitative data was used to develop explanatory models. Results revealed that technical policy decisions were framed by socio-political, financial, strategic and operational considerations. Industry stakeholders had influence through formal pre-existing channels and through alliances formed during the outbreak but outside the established system. Overall, the crisis management system and response was seen as positive, yet some criticism was expressed: some respondents stated that timely implementation of state policy was hindered by lengthy national committee discussions concerned with operational rather than strategic issues. Unbalanced stakeholder group representation by individual leaders was also voiced as an issue. The results of this research inform effective approaches to stakeholder participation in emergency disease management so as to improve preparedness for future emergency animal disease incursions.

Attitudes of sheep producers to use of the sheep health statement in Australia

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The Sheep Health Statement (SHS) is a nationally agreed document used by vendors in Australia to declare the health status of sheep, developed with the aim to support and protect producers from disease risks during the sales process. We conducted a cross-sectional survey in 2011 to explore current attitudes and practices of sheep producers towards its use. A questionnaire was developed to obtain information about producers' patterns of buying/selling in the last two years, use of the SHS and perceived drivers and barriers to its use. A sampling frame was developed in consultation with industry experts to capture data from a nationally representative sample of sheep producers with 100+ sheep. A total of 870 interviews were conducted with producers using a computer-assisted telephone interviewing methodology in which the interviewer follows a script using a software application that is able to customise the interview based on the answers provided. Multivariable logistic regression analyses were conducted to investigate factors associated with uptake of the SHS. Around a quarter of producers had never heard of the SHS and 17% had heard of it but were not aware of any of its content. The SHS was regarded favourably, with 70% of producers who were familiar with it reporting that it was an effective tool for disease management. Livestock agents were regarded as influential in uptake of the SHS, with most producers reporting they were willing to supply or request a SHS if their agent told them to. Stronger enforcement and education/awareness programs were identified most frequently as ways to encourage uptake of the SHS. The main factors associated with uptake of the SHS were related to operating climate and attitudinal factors; specifically whether use of the SHS was mandatory or not, whether agents requested the SHS, and whether producers had confidence in accurate completion of the SHS.

Constraints to cattle production in a semi-arid pastoral district, Kenya

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The objective of this study was to prioritize cattle production constraints and to assess diseases that have greatest impact on cattle production in Narok district. Data were collected through focus group interviews organized in different locations and disaggregated by gender. The participatory methods employed included listing of production constraints and diseases, pairwise ranking, proportional piling, disease incidence scoring, disease impact matrix scoring and probing techniques. The proportional scores for constraints and for diseases were used for descriptive statistical analysis. A long list of production constraints were obtained and those that were highly ranked were lack of water (0.19), lack of extension services (0.15), cattle diseases (0.12) and lack of markets and poor prices for cattle products (0.10). There was a significant statistical difference between the mean scores for production constraints with $P=0.001$. The cattle diseases with high estimated incidences included FMD (67.9%), trypanosomiasis (27.6%), ECF (6.7%), heartwater (3.9%) and CBPP (0.31%). The other diseases mentioned were malignant catarrhal fever, anaplasmosis, brucellosis, blackquarter, abortions, bovine ephemeral fever, eye diseases, heartwater, mastitis, anthrax, lumpy skin disease and plant poisoning. Diseases with the greatest impact on production according to their proportional mean scores were ECF (0.22), FMD (0.21), CBPP (0.08) and trypanosomiasis (0.07). There was a significant statistical difference between the mean scores for cattle diseases on production with $P=0.001$. There were however no significant differences between the mean scores by gender and locations. In conclusion, the prioritized production constraints and cattle diseases can guide policy makers on improvement of cattle production in pastoral areas.

Estimating the costs of mastitis in goats using stochastic simulation modeling

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Few studies have investigated the economic aspects of mastitis in goats. The aims of the current study were (1) to estimate the total costs associated with clinical and subclinical mastitis in a dairy goat herd; and (2) to estimate the costs of a subclinical infection with *Staphylococcus aureus*, with and without interventions. Two stochastic simulation models were constructed. Model 1 simulated a herd of 1,000 goats and the prevalence and incidence of subclinical and clinical mastitis were drawn from distributions. The corresponding subclinical and clinical cases were modeled and the monetary effect of mastitis in the herd was calculated. Model 2 simulated one subclinical *S. aureus* infection, including effects of transmission. The case could either stay subclinical ($P=0.8$) and infect other goats, or have a clinical flare-up ($P=0.2$). A clinical flare-up could result in death or survival. In case of survival, it became subclinically infected again and could again infect other goats. Three scenarios were calculated for goats that became clinically ill but did not die: treatment, no treatment, or culling. The total costs of mastitis in a herd of 1000 goats were estimated at around €3,200 per year, but could vary between €800 and €7,000 per year. The incidence of clinical mastitis was an important factor driving these costs, mainly because of lost milk revenues of goats that died. The costs of one case of subclinical mastitis (including transmission) were around €80. Differences between treatment, no treatment and culling were small. The transmission parameter and the probability of clinical flare-up had large effects on the total costs associated with a subclinical mastitis. This study shows that mastitis in goats causes economic losses, which are mainly driven by the number of clinical mastitis cases. Infection dynamics of *S. aureus* in goats are influential on the estimated costs.

Comparison of farm performance between participants and non-participants in veterinary herd health management in the Netherlands

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To determine whether farmers enrolled in a veterinary herd health management (VHHM) program obtain better farm performance than farmers not enrolled. In September 2011, 5,000 randomly selected dairy farmers participating in a dairy herd information program received a questionnaire per email, asking whether they participated in VHHM. If so, the farmer was asked to indicate which topics were discussed during farm visits in what frequency. From all farmers information on milk production parameters (e.g. milk yield), fertility parameters (e.g. calving interval, number of inseminations per cow), and udder health (e.g. somatic cell count (SCC), % new high SCC) was available. Relations between VHHM and production characteristics of farms were analyzed using general linear models. Response rate of the questionnaire was 20% (1,013/5,000). There were 695 participants and 318 non-participants in VHHM. Most important VHHM topics were fertility (regular topic at 85.5% of the farms), milk production (55%) and udder health (56.7%). Participants had significantly more cows (83 versus 81) and significantly better milk yield (kg/cow/year) (8.591 versus 8.230), bulk milk SCC (cells/ml) (218,000 versus 226,000), and calving interval (days) (416 versus 419). They had however significantly more inseminations per cow (1.9 versus 1.8). Farmers participating in VHHM overall have better farm performance parameters. Whether the economic benefits weigh out the costs of VHHM is an important future research question.

The formulation and analysis of a model framework for forecasting livestock demographics in Scotland

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The requirement to be able to accurately forecast the numbers, species and distribution of livestock on Scottish farms is vital for the management of rural economies, food security and predicting and managing the effects of disease introduction into a changed livestock demography. Furthermore, such a framework can be used for evaluating the effects of shocks such as CAP reform on the system. This paper describes the development of a stochastic simulation model framework for predicting the distribution of farms and numbers of cattle and sheep on the farms. The framework is based upon sampling from parameter and spatial distributions of changes to the sector. The model is parameterised through analysis of data from the Scottish agricultural census between 2006 and 2011 (inclusive). Between 2006 and 2011 there was a real fall of between 6 and 13% in the numbers of cattle, sheep and farms with either species. Using the model developed here a baseline scenario with 2006 as the starting point predicts the number of cattle, sheep and holdings in 2011 with either species to within 2% of the actual numbers. Furthermore, farm composition and distribution is accurately reflected in these predictions. The model was used to generate forecasts to evaluate the impact of shocks to the system, in particular the 2013 rounds of CAP reforms. The need to be able to forecast changes to the demographics of livestock are vital for agricultural management and to plan epidemic responses and these results will be used to populate epidemic models. Furthermore, the changes modelled here will be used to forecast changes in the pattern of movements within Scotland and between Scotland and its trading partners. This is a framework that could be readily applied to different countries and scenarios.

Reducing assessment time of the Welfare Quality® protocol for dairy cattle

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The Welfare Quality® (WQ) protocols are becoming a standard for assessing welfare of farm animals in the European Union. A disadvantage of these protocols is that they are time consuming (about one day per farm) and, thus, costly. Aim of this study was to predict some of the welfare indicators in the protocol instead of measuring them all, in order to reduce assessment time of the WQ protocol for dairy cattle. Seven trained observers quantified indicators of the WQ protocol in 181 loose housed and 13 tied Dutch dairy herds (herds size: 10 to 211 cows), using six assessments methods: (1) avoidance distance (AD); (2) qualitative behaviour assessment (QBA); (3) behavioural observations (BO); (4) clinical observations (CO); (5) interview (I); and (6) resources checklist (RC). Herds were selected based on stratified sampling, using a combined health score of mortality, udder health, and milk production. Based on the data collected on-farm, herds were attributed an overall welfare classification using the WQ multicriteria evaluation model. Indicators of each assessment method were predicted using the indicators of the other five assessment methods as independent variables in linear and logistic regression models. For each assessment method, predicted and observed values were compared, and the effect of using predicted values on classification of herds was evaluated. The correlation between predicted and observed values was low for each assessment method (R^2 between 0.01 and 0.33). When using predicted values for indicators of AD, QBA, BO, CO, I, and RC, still 94, 90, 79, 88, 86, and 86% of the herds were correctly classified, leading to an estimated reduction in assessment time of 37, 25, 150, 111, 15, and 15 min for a herd of 83 cows. It was concluded that dependence between welfare indicators of the different assessment methods in the WQ protocol for dairy cattle was low. However, replacing them with predictions did not lead to many incorrectly classified herds.

The contribution of agricultural research to managing zoonoses and foodborne diseases

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In 2012 the Consultative Group on International Agricultural Research (CGIAR) launched a major initiative on leveraging agriculture to improve human nutrition and health. Foodborne disease, zoonoses, and emerging diseases were identified as human health problems for which agricultural research can make a difference. Endemic zoonoses are of major importance to the health of the poorest and minor to the rich. In contrast, emerging infectious disease and food-borne zoonoses impose moderate health, and high economic, impacts on rich countries. This difference appears to be reflected in funding. Many negative impacts of zoonoses and emerging diseases are from inappropriate responses by authorities, farmers and general public rather than disease itself, and the CGIAR has a role in generating better evidence on disease priorities. Livestock populations are increasing and intensifying; we identify aspects that increase health risk and others that reduce it: overall intensification in poor countries is a significant health risk. Livestock also impair health through greenhouse gas production and environmental degradation. On the other hand, livestock offer a pathway out of poverty and a source of high biological value nutrition. Research can help ensure livestock intensification works for poor farmers and consumers and that present populations are nourished without putting future generations at risk. For many diseases with animal reservoirs, control in agro-ecosystems is more cost-effective, but it may not always be feasible or acceptable. Zoonoses and food-borne diseases are rarely the most important (or limiting disease) for livestock, much disease control is a by-product of development, and integrated development-based approaches may be more appropriate and sustainable than silver bullets. CGIAR research has a key role in understanding how agricultural and veterinary involvement can improve the management of health risks that have their origin on farms and food chains.

Expert opinion on feasible and cost-effective welfare indicators

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Monitoring and assessing farm animal welfare have been the cornerstones of the past European Community's Action Plan on Animal Welfare stating the clear objective of introducing welfare indicators. As a result, the Welfare Quality® protocol offers validated measures for several species of production animals. Like in any other on-farm assessment time-consumption and costs are high. The vast quantity of information from routinely collected data in modern dairy production together with additional system information hold a great potential as indicators, but only few studies report expert opinion on the use of register data for welfare assessment purposes. Hence the objective of this project became to investigate expert opinion on feasible and cost effective indicators of animal welfare. These indicators were divided into two groups: the easy feasible register based indicators from the Danish Cattle Database and into the slightly more expensive resource-based indicators, ultimately seeking out the most predictive combinations of indicators for animal welfare. A panel consisting of 15 experts on dairy cattle production and welfare were invited to an on-line survey on rating 28 presumed welfare related indicators from register data and 20 additional resource-based measures. The experts were asked to rank the importance of the measures in relations to a welfare assessment. Further, experts were asked to assign contributing weights to single measures within a combination of several measures in order to describe one of ten criteria derived from the Welfare Quality® protocol. Results showed good agreement between experts amongst the evaluation of the given measures. Although a number of the experts' uttered concern about performing welfare assessments and evaluation restricted to the use of this type of indicators, we believe they hold a great potential for a risk based identification of potential problem herds.

Surf and turf: surveillance and control of notifiable disease in UK aquaculture and agriculture

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Notifiable disease outbreaks limit production and trade in UK agriculture and aquaculture and the approach to cost sharing and veterinary involvement is often debated. To highlight the different strategies employed in livestock and fish production, surveillance and control measures are described for foot-and-mouth disease (FMD) and infectious salmon anaemia (ISA), both notifiable, exotic, non-zoonotic diseases which have occurred recently in the UK. Active, government-funded, sampling surveillance for ISA is carried out at regular intervals on UK fish farms. Livestock farms rely on observation by vets and farmers to detect FMD. The salmon industry must bear financial losses resulting from control measures as no compensation is given for ISA-infected fish stocks in line with other European salmon-producing countries. Farmers are compensated at full market value for FMD-affected livestock. Surveillance and disease control in aquaculture operates with minimal public veterinary input: non-veterinarian fish health inspectors collect samples and investigate and manage suspected cases of ISA. Vets carry out passive surveillance for FMD on farms and at abattoirs and government veterinary officers are responsible for outbreak investigation and control. In all recent UK outbreaks of ISA and FMD, the index cases were detected by veterinary surgeons. Veterinarians are more involved in livestock disease surveillance and control than in farmed fish; the origins of this are probably historical and linked to UK legislation which allows fish disease to be diagnosed without veterinary input. Current contingency plans and recent responses to ISA and FMD outbreaks are reviewed to explore how policy decisions affect financial support for producers and supply and demand for veterinary services related to control of notifiable disease.

Effects of control strategies against *Salmonella Dublin* infections in dairy herds estimated by the Dublin-Simherd model

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Control strategies against *Salmonella Dublin* infections in dairy herds were evaluated in the ‘Dublin-Simherd’ model – a dynamic, stochastic and mechanistic Monte-Carlo simulation model of *S. Dublin*. The model simulated infection dynamics and production losses in a dairy herd with additional young stock over a period of 10 years in weekly time steps. Control strategies were applied one year after the infection was introduced to the herd by one infectious heifer purchased into the herd four weeks before calving. The effect of 19 control strategies on incidence rate was evaluated in three herd sizes (85, 200 and 400 cows). The control strategies involved test-&cull, vaccination of preweaned calves and improved hygiene and management in one or more of 6 different age-groups (3×calves, 2×heifers and cows). The only control strategies that reduced incidence rate effectively involved improved hygiene and management in all six age groups. Second best strategy was improved hygiene and management in cow and breeding heifer barns, while improving hygiene and management only for the calves had a very small effect. Culling strategies based on detection of infectious animals using ELISA tests and bacterial culture in different combinations with a frequency of 1 or 3 times per year had almost no effect on the incidence rate. Culling had a minor additional reducing effect on the incidence rate when combined with improved hygiene and management only among cows and heifers. In some scenarios culling strategies increased the incidence rates because old resistant animals testing false-positive were replaced by younger and more susceptible animals. Vaccination of preweaned calves had a negligible effect on the incidence rate. With decreasing herd size most control strategies became more incidence-reducing.

Economics of an intensified monitoring and treatment strategy against clinical mastitis

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Mastitis is of great economic importance due to its effect on milk production, culling risk and treatments costs. The frequency of mastitis treatments is often used as a measure for udder health in a herd. Farmers typically have different criteria for treating cows which makes it difficult to compare the health status between herds and evaluate the efficacy of different treatment strategies. The aim of this study was to simulate the consequences of an intensified treatment strategy against mastitis. SimHerd, a dynamic and mechanistic Monte Carlo simulation model of a dairy herd including young stock, was used to study two different treatment strategies. In the low threshold strategy (intensive treatment strategy) all clinical symptoms of mastitis were treated. In the high threshold strategy mild cases were not treated unless they developed into severely inflamed quarters. The clinical mastitis cases were classified according to severity. The distribution among mild, moderate, severe and chronic cases was 0.0, 0.50, 0.25 and 0.25 in the high threshold strategy and 0.75, 0.25, 0.0 and 0.0 in the low threshold strategy. Compared to low threshold, only 25% of all mastitis cases were treated in the high threshold strategy. By simulating, among other effects, that mild and severe cases of mastitis reduce milk yield by 50% and 250% compared to a moderate case and by assuming that chronic cases of mastitis reduce milk yield capacity for life, by 15% the technical and economic effects of the two strategies were evaluated for an average Danish dairy herd. For the low threshold strategy, compared to high threshold, the simulation model found a higher milk yield of 391 kg ECM per cow-year, a 20% reduction in cow mortality, a 30,000 lower bulk tank somatic cell count but also €4,700 higher treatment costs in a 200 cow herd. Despite the higher treatment costs the contribution margin per cow-year was in total €85 higher for the low compared to the high threshold strategy.

Chilean ethnic groups and livestock: is there any association?

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Chile is composed of a large variety of aboriginal ethnic groups that have lived in its territory for thousands of years. Although initially only the groups in the north domesticated animals (llamas & guanacos), nowadays all of them practice animal husbandry at some level. In 2007 a full scale agricultural census took place in Chile, generating valuable information regarding both key elements: ethnic group of the owners and number of animals of each species simultaneously. Additional other information of agricultural interest was also integrated into the census data. This study therefore focuses on this association and describes the relationship of different Chilean ethnic groups and their animals especially with their non-aboriginal counterparts for the first time. The analyses are conducted in a multi-step stratified approach using administrative regions as well as geographical measures (altitude, agricultural zone etc) as classes to adjust for possible confounding and to study interactions in the different livestock systems. The results of this study can be of great interest to develop a new series of studies exploring the animal husbandry traditions of Chilean aboriginal ethnic groups, and by doing so, helping the government to develop their agricultural policies according to each specific group.

The impact of Q fever: a quantitative value chain analysis of the Dutch dairy goat sector

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The economic impact of an animal disease and its associated control measures are generally most evident on farm level. In contrast, the impact on sector level often remains unclear and is not fully understood. Many actors are involved in a livestock sector and they are all related to each other, in various ways. To measure the impact of a disease on all these different actors, a value chain analysis can be conducted. In this study, a value chain analysis was used to investigate the economic impact of the Q fever outbreak in the Dutch dairy goat sector and the associated control measures taken at the end of December 2009. In total, 34 actors of the goat sector were interviewed and provided information about their total revenues, gross margins and view on the sector. With this information a value chain was built and used to estimate the economic differences (in terms of gross margin) in the Dutch goat sector between 2009 and 2010. The results from this analysis demonstrate a major negative impact of the Q fever outbreak on the gross margins of the farmers (-28%) and most of the actors directly related to them, for example the milk collectors and (fodder)suppliers. Large differences among the actors in these groups were visible, especially between affected and non-affected farmers (resp. -67% and -16%). Even though not all of the actors were negatively affected by the outbreak, the gross margin of the total chain showed a decrease of 14% in 2010. The gross margins of the farmers revealed the most sensitivity to differences in goat milk price in alternative scenarios. Value chain analyses often remain qualitative and descriptive. In this study, however, the value chain analysis was extended with a quantification of the impact of an animal disease. This provided quantitative information of the considerable negative impact of Q fever on the Dutch dairy goat sector.

Social network analysis on innovative governance arrangements for the control of bovine brucellosis and tuberculosis in Brazil

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The aim of this paper is to analyze the governance arrangements (GA) developed in 2009 in the state of Rio Grande do Sul, which supported a unique performance of the National Program for the Control of Bovine Brucellosis and Tuberculosis (PNCEBT) by targeting the eradication of those diseases in six selected municipalities on the claim of veterinary public health. Documents related to the GA established in the county of Arroio do Meio were studied, as well as data on diagnostic tests performed in the county. Each participant institution and their responsibilities were arranged into a Social Network Analysis (SNA) scheme, which considered their sectors (public/private), administrative levels (local/state/national) and power branch (executive/legislative/judicial). The SNA showed the public sector having more activities to perform, while private sector players were especially important on raising awareness and bridging the distinct levels of command. Beyond that, all the deeds were performed in a complementary way by the actors, being the GA able to tackle all the strategies predicted by the PNCEBT. The tests performed on the county showed evolution of 1.748% (n=85,617) on the number of tested animal and of 1.912% (n=5,546) on the tested holdings, when comparing a two-year period before and after the launching of the GA. Results demonstrate that the proposed structure of analysis is valuable when planning animal health programs, in order to build commitment of stakeholders and prevent omissions or overlapping of duties. Besides that, it can promote collaborative approaches to address the limits inherent to the jurisdiction of each player in order to bring synergy and efficiency to the project, stimulating adhesion and curbing evaders.

The spatial ecology of free-ranging domestic pigs in the Lake Victoria Crescent: a prelude to understanding disease transmission within low-input production systems

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In this poster we will describe a spatial ecology study of free-ranging domestic pigs within the Lake Victoria Crescent region. The poster will describe collection and analysis of global positioning system (gps) data in order to determine the homerange of a domestic pig and how this data can be utilized in the understanding of disease transmission within this production system. A growing global demand for animal protein is being met in part by the expansion of pork production, which in many low-income countries is characterized by free-range systems. Free-range pigs are, however, at a higher risk of acquiring many diseases than their counterparts kept under intensive systems. These diseases may have serious public health or international trade implications such as *T. solium* cysticercosis and African swine fever, or have an economic impact due to poor production and carcass condemnation. Ten pigs in the Western Kenya region were identified through a multi-stage random sampling method and a harness with a gps unit was fitted to each for a period of 7 consecutive days. Position of the pig was recorded by the gps unit every three minutes and transmitted to a remote server via a mobile phone signal. The homerange was determined to be the area covered by 90% of the isopleths generated by a local convex hull technique. The average home-range of a domestic free-range pig was found to be 7,700 m² and the average distance moved a day was 6,720 m. We believe that the home-range data presented in this poster is the first time that such an estimate has been attempted and that it has great utility within further studies of disease transmission, particularly in the mathematical modeling of disease.

Cost effectiveness of fattening of Improvac® vaccinated versus surgical castrated boars under German field conditions

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Vaccination of boars with Improvac® is a proven and animal friendly alternative to surgical castration to prevent boar taint. An improvement of both growth performance (daily weight gain) and carcass quality is well known, but calculations of profitability in large fattening farms are still needed. Objective of the study was to determine the economic impact of fattening Improvac® vaccinated boars compared to surgical castrated boars under German field conditions. In the study a total of 660 Improvac® vaccinated boars and 755 surgical castrated boars were assigned to three fattening groups. Daily weight gain, number of days to market, carcass weight, lean meat percentage and price per kg carcass weight and per carcass were recorded and evaluated. Daily weight gain in Improvac® vaccinated boars was significantly higher than in surgical castrated boars (1,013 g versus 978 g). Improvac® vaccinated boars reached a significantly higher carcass weight (98.6 kg) in 99 fattening days and had leaner meat percentage (55.6%) than surgical castrated boars (97.6 kg, 101 days and 53.5%). At slaughtering general price per kg carcass weight (56% lean meat) was between 1.50 € and 1.56 €. Results presented in this study showed that Improvac® vaccinated boars realised a significantly higher average price per kg carcass weight and per carcass (1.52 €, 150.55 €) compared to surgical castrated boars (1.47 €, 143.99 €). In consistence to previous studies better growth performance and better carcass quality were reconfirmed at our study under field conditions too. An equal payment at slaughterhouse provided, the economical impact of vaccination with Improvac® compared to surgical castration is relevant (6.56 € per carcass at our study) and will compensate and mostly exceed the costs for the vaccination.

Economic evaluation of two PRRSv-elimination strategies for an endemic infected multiplier pig farm using Monte Carlo simulation

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Porcine Respiratory and Reproductive Syndrome virus (PRRSv) causes decreased production efficiencies and increased health costs in pig farms. Elimination of PRRSv on farms can be reached by depop-repop or herd closure with offsite rearing of weaning piglets. Pre-elimination cost-benefit analysis is often based on partial budget methods, while stochastic modeling could include variation between farms with regards to production parameters and therefore variation in outcome. A Monte Carlo simulation model calculating the gross margin of a multiplier pig farm was created. Data and distributions for farm parameters were derived from 900 Dutch pig farms and agricultural databases. Both PRRSv elimination strategies were evaluated and for herd closure elimination reached at 4 and 8 months was evaluated. Conservative estimates for the change of technical parameters after elimination were derived from literature and used in a uniform distribution. The time until breakeven of the accumulated gross margins for the old versus the PRRSv free situation, including the elimination period, was calculated. Next to this, the minimum increase in piglet price was calculated when a farmer wants to break even in 1 or 3 years. When pig prices would not increase after elimination, the breakeven in gross margins was reached in 11.7 years (8.4-18.4) for full depop-repop and within a year for both of the herd closure scenarios. The piglet price needed to increase with 5 euro to reach the breakeven of gross margins within 3 years and with 13 euro to break even in 1 year, for the full depop-repop method. Sensitivity analysis showed that piglet price was the most influential parameter on gross margin and years till breakeven. Herd closure is more profitable for farmers as elimination strategy, when only elimination of PRRSv is considered.

Cost assessment of rabies eradication in north-eastern Italy

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After more than 10 years, fox rabies was diagnosed during October 2008, in the Friuli-Venezia Giulia region of north-eastern Italy. In 2009, the infection spread to the neighbouring Veneto region, reaching part of the provinces of Trento and Bolzano in early 2010. An aerial emergency oral fox vaccination (OFV) programme was implemented for the first time in the winter of 2009-2010. Three other emergency OFV campaigns followed in 2010 and regular OFV campaigns were carried out in 2011. Rabies decreased to only 18 recorded cases in the second half of 2010, out of a total of 209. The last rabid fox was recorded in February 2011. The present study quantified the direct costs related to rabies control activities. Specifically, two scenarios were considered: the base scenario where control was based on fox depopulation until the virus extinction threshold was reached; an alternative scenario based on aerial vaccination. The targets of both scenarios were assumed to be the same, as were the area and season (winter) of intervention. Costs and outcomes were different. Fox depopulation was assumed to be conducted by gamekeepers and the costs required to reduce the population below the threshold were estimated. Vaccination costs incurred for vaccination campaigns from December 2009 to December 2011 were estimated as the sum of expenses for: lab tests to evaluate vaccination efficacy, baits, use of helicopters for bait distribution, transport and bait storage. Some costs were considered for both scenarios such as lab tests for assessing the epidemiological situation and the vaccination of domestic animals. In this analysis, fox depopulation was considered to be the only alternative to aerial vaccination. Since the present work was primarily focused on economic aspects, the importance of ethical aspects related to depopulation was not taken into account.

Poster topic 06**Poster 71****An economic assessment of *Salmonella* control in the pork supply chain**

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Salmonella are a main concern in public health and pig products can be at risk for human infection. This study aims at developing a tool useful for decision making process regarding *Salmonella* control measures throughout the pig supply chain. The main levels considered are farm, transport-lairage and slaughtering process. A mathematical model has been developed in order to determine the influence of control measures implemented at several steps during the supply chain on the *Salmonella* prevalence on carcasses at the end of the slaughtering process. The model is parameterized using the outcomes of epidemiological models as well as expert knowledge. Using economic parameters, mathematical simulations (Monte Carlo simulations) are then performed to determine which measures implemented at which step(s) are the more cost-effective for *Salmonella* control. The performed cost-effectiveness explicitly includes a *Salmonella* prevalence target to achieve at the end of the slaughtering process. To illustrate this approach, a numerical application is given. Simulation results enabled us to highlight the incidence of the heterogeneity of *Salmonella* prevalence between batches of slaughter pigs on the choice of an intervention strategy. For each considered strategy, the probability to overcome the prevalence target can also be assessed. This study enabled us to develop a flexible tool, which can be parameterized to take into account the diversity of field situations (levels of *Salmonella* infection, slaughter processes). It can also be adapted to specific stakeholders' needs for instance by ex ante assessing incentive systems.

A cost-effectiveness model for an on farm rapid-test for *Campylobacter* in broiler chickens

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As part of the drive to reduce human campylobacteriosis, there is a requirement to reduce the levels of *Campylobacter* in UK broiler flocks. *Campylobacter* control programmes are required and may involve several stakeholders; the poultry industry, retail sector, government and scientific researchers. A consultation of stakeholders has shown support for the use of a rapid farm-based test to support the control programme for *Campylobacter* in broilers. Several rapid test methods have potential for farm based testing. However, ideally, any new rapid test should be more cost-effective than current laboratory (culture) tests. This study has developed a mathematical model that could compare the relative cost-effectiveness of different tests for the detection of *Campylobacter* in broiler flocks. The model highlights the potential for savings using rapid tests rather than culture. Culture is only competitively cost-effective in a short-term testing situation (100 flocks over two years), not when a larger number of tests are required. Our analysis suggests that even in the short-term situation the Lateral Flow Device (LFD) rapid test would be more cost-effective than culture. Thus, as the LFD is available now it could potentially offer immediate savings over current culture methods in most testing situations. Further analysis suggests that if a rapid test can be developed that has a sensitivity and specificity of ca. 90%, set up costs of £500 and individual test costs of £12.50, it should prove more cost-effective than culture. However, this is based on the assumption that all model inputs are comparable. The generation of good comparable performance data for testing on farm samples (faeces) by LFD and the other method options are required before we can confirm these findings.

Vaccination to Live, can it be an option to prepare for FMD potential risk in Japan?

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Foot and Mouth disease outbreak in Miyazaki, Japan in 2010 caused about 290 thousand animal culling and the estimated economic loss amounts to 234 billion yen according to the local government. The outbreak has convergent in July 2010 and recovered FMD free status in Feb. 2011 due to the application of vaccination to kill policy as well as collaborative efforts of stakeholders. This prompt recovery has been praised globally however there still remain arguments from the economic or animal welfare point of view. Most economic analysis of FMD that compare the cost effectiveness of vaccination and stamping out emphasize the importance of international market access. However, it is not the case when the feature of Japanese livestock market is taken into account; expensiveness of animal, precious genetic resource, mostly consumed domestically and limited exports. Under this condition, consumer opinion plays key role to identify economically viable policy. Reflecting this, we conducted a web-based consumer survey on attitude toward FMD control measure taken during the outbreak and willingness to accept for meat if vaccination to live strategy is to be applied. A total of 1920 valid response from female aged 20-69 were collected. As a result, 46.4% of respondents revealed the discomfort with destroying animal only for economic reason, 24.8% showed intention to purchase FMD vaccinated meat if the animal were not infected and 15.3% willing to buy FMD vaccinated meat to support Miyazaki. Willingness to pay (WTP) for FMD vaccinated beef and pork compared to non-vaccinated meat were 56.8% and 65.5% respectively. However consumers who want to support the affected area revealed 150% WTP both for beef and pork if the animals were tested to be uninfected. Though the technical issue remained to assure the vaccinated animal to be uninfected, the results indicate the vaccination to live strategy could be an option to prepare for the future outbreak.

Methodological framework for a participatory study to evaluate the socio-economic factors impairing the efficacy of animal health surveillance systems

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The need to set up efficient, sustainable surveillance networks of animal diseases is a major issue for worldwide animal and public health management. In developing countries the need to assess the efficiency and sustainability of surveillance systems is of primary importance because of major sanitary issues and limited economic resources. So far, only the economic component of the sustainability concept has been subject to scientific interest, leaving out the social aspects. We present here a methodological framework for an assessment of social and economic issues faced by local actors involved in surveillance systems. This multidisciplinary approach consists of two major steps: first, the identification of the pathways of sanitary information diffusion through formal and informal social networks, and second the characterization of the socio-economic factors involved in these information sharing behaviors. Two methodologies can be implemented to develop models of the social network involved in sanitary information flow: (1) individual structured interviews based on prior identification of the actors involved; and (2) participatory methods, including observation and workshops. The development of the two models allows for comparison between their outcomes and their respective relevance. Stated preference methods, widely used in the field of economics to assess non-market values can then be applied to identify and quantify the social goods at stake in sanitary information flow. Due to the social and interactive nature of the targeted decision-making, stated preferences were elicited using participatory tools as well as role-playing games.

Prevalence of antileptospiral agglutinins and anti-*Neospora caninum* antibodies: a first step to economic evaluation of dairy herds in Minas Gerais, Brazil, 2010

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The economic losses related leptospirosis and neoporosis are unknown in Brazil, the prevalence estimate is the first step to achieve a quantification of the lost value and thus what effects control measures should be propose with economically efficiency. The study aimed to evaluate the prevalence of anti-*Leptospira* agglutinins and anti-*Neospora caninum* antibodies in dairy cows, located in properties in the microregion of Sete Lagoas, Minas Gerais, in the year 2010. The state of Minas Gerais is the largest milk producer in Brazil, producing more than 5.6 billion liters of milk annually. A total of 2,915 serum samples were collected from the lactating cows of 151 properties in eleven municipalities. The technique used was the microscopic agglutination test (MAT) for leptospirosis agglutinins and a commercial ELISA kit for anti-*N. caninum* antibodies detection. As a result, 20.7% (CI 95% = 17.1-24.3%) at animal level and 80.8% (CI 95% = 73.8-87.7%) in herd level were positive to anti-*Leptospira* agglutinins. The most prevalent serovars were hardjoprajitno at 19.4%; hardjoprajitno strain Norma at 17.4%; and hardjo-bovis at 17.4%. The prevalence of anti-*N. caninum* antibodies were 21.9% (CI 95% = 18.9-24.9%) at animal level and 98.5% (IC 95% = 97.0-99.9%) at herd level. The agglutinins anti-*Leptospira* and antibodies anti-*N. caninum* are widely distributed in the properties of the microregion of Sete Lagoas, Minas Gerais. The next step of the project is to analyze the risk factors and estimate the economic losses by these two diseases in the dairy cattle. Thanks to CNPq, FAPEMIG and INCT-Pecuária for funding this project.

EPIC Scottish government centre of expertise on animal disease outbreaks: new horizons in the research policy interface for animal disease control

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EPIC is the new Scottish Government Centre of Expertise on Animal Disease Outbreaks. The Centre is designed to provide access to high quality advice and analyses on the epidemiology of animal diseases that are important to Scotland and to best prepare Scotland for the next major disease incursion, by: (1) delivering timely and accurate advice to the Scottish Government; (2) developing the coordination of research, analysis and interpretation across disciplines, leading to high quality, world leading research; (3) stimulating innovative thinking in support of policy development and implementation; and (4) developing a programme of knowledge exchange in order to ensure the effective underpinning of policy as well as the wider dissemination of knowledge. These aims will be delivered through a series of five linked modules: Module 1 – Communication and Contingency; Module 2 – Risk Modelling; Module 3 – Disease Control; Module 4 – Forecasting and Horizon Scanning; and Module 5 – Knowledge Exchange. EPIC is a consortium project involving SAC, University of Glasgow, University of Edinburgh, Moredun Research Institute, BioSS and James Hutton Institute, providing an exceptional concentration of expertise spanning veterinary epidemiology, economics, social science, molecular biology, disease modelling and biomathematics, and a unique opportunity to combine these disciplines to achieve outputs that are meaningful and relevant. This project builds on a previous award to an ‘EPIC consortium’ project focused on surveillance, and aims to build a sustainable model for the control of animal disease outbreaks for Scotland.

Identification of health problems affecting livestock of the Aymara ethnic group in the region of Arica and Parinacota, Chile

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The Aymara ethnic group live in the Altiplano, which is an area of inland drainage laying in the central Andes. This zone includes part of Chile, Bolivia and Peru. Their population is estimated in about two million people. The Aymara’s livelihood is closely related with the livestock they breed, which is mainly composed by South American camels ‘llamas’ (*Lama glama*) and ‘alpacas’ (*Lama pacos*). The main products they get are meat and fiber to produce clothes. Those products are for their own use or for trade. Also, llamas and alpacas represent part of the particular Aymara’s view of the world. To keep a good health status of ‘llamas’ and ‘alpacas’ is a key element for Aymara’s subsistence. Nevertheless, there is a lack of studies addressing this issue. This study therefore focuses in the identification of the main health issues that affects the livestock of South American camel of the Aymara group that live in the Chilean region of Arica and Parinacota, through participatory epidemiology. Personal and group interviews are being conducted during January and March 2012. The results of this study can be of great interest for the Chilean animal health authorities and for the governmental agricultural extension services, to develop agricultural policies according to the Aymara needs.

Developing evidence-based recommendations for food safety and animal health: an evaluation of the GRADE approach

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In food safety and animal health it is critically important that evidence-based recommendations for interventions are made in a manner that is transparent, i.e. the rationale for the recommendation is clear. In human clinical medicine, the GRADE system has been developed over the past 10 years as an approach to facilitating transparent recommendation making. According to the GRADE working group website 'The Grading of Recommendations Assessment, Development and Evaluation (GRADE for short) Working Group provides a framework for grading quality of evidence and strength of health care recommendations that is explicit, comprehensive, transparent, and pragmatic.' The GRADE system is increasingly being adopted by organizations and professional societies worldwide including WHO and CDC. Although judgment is still required to interpret the data, GRADE aims to transparently document, what factors are included in the decision making. The GRADE approach suggests that panels making recommendations explicitly consider the following factors: (1) the quality of evidence; (2) the balance of benefits and harms; (3) certainty about values and preferences and 4) resource implications. This presentation will illustrate the basic principles of GRADE using examples from animal health (autogenous *Moraxella bovis* vaccines for Infectious Bovine Keratoconjunctivitis) and food safety (Vaccination and antibiotics for *Salmonella* in pork) where the GRADE approach was used. Further, the presentation will include a discussion of the potential for the GRADE process to be used in food safety and animal health settings.

A dynamic simulation model for cost-benefit analysis of paratuberculosis control strategies in dairy farms

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Efforts to reduce prevalence of paratuberculosis can be jeopardised if farmers don't enrol in control programmes. For these decision-makers, the expected efficiency of the programme in the situation of their own farm is paramount. Methods to compare the costs of a programme and its expected benefits should account for the goals and constraints of the farm management. The objective of this study was to evaluate the costs and benefits of control programmes in infected dairy herds, taking into account the production goal and the constraints on replacement, assuming it varies with the frequency of other health disorders. A stochastic dynamic herd model was developed. Parameters for horizontal transmission of *Mycobacterium avium paratuberculosis* (Map) were issued from an epidemiological model where the contamination of the environment and the contact structure in the herd are explicitly represented. Herd dynamics and management were detailed. Inputs and outputs were estimated to calculate the gross margin. Different scenarios of Map control were simulated (systematic test-and-cull versus passive surveillance, improving hygiene of calf rearing) and compared to a do-nothing scenario. A sensitivity analysis was carried out with high or low levels of mastitis and infertility. When culling for infertility or mastitis was high, Map infection and Map control programme resulted in an annual herd milk yield below the production goal of the farmer, and in reduced gross margin for all scenarios. When it was low, several scenarios of Map control were beneficial after 7 to 13 years. This model shows that the efficiency of Map control can be reduced, and enables to identify the conditions for positive return on investment of a control programme in a variety of production contexts representative of goals and constraints of dairy farms.

A post-import quarantine survey of infectious diseases in breeding animals

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The study objective was to present the evidence through evaluation of tests performed on animals during the post-import quarantine. This study examines data presented on the introduction of animal infectious diseases of the breeding animals through international trade during 2007-2011 in the post-import quarantine period. Tests were performed in order to reconfirm the negativity as stated in the veterinary certificates that accompany the imported animals. Total of 202 bulls/heifers and 526 boars/gilts from 4 study sites underwent testing by OIE recommended serological tests on paraTB, tuberculosis, brucellosis, leptospirosis, FMD, leucosis, bluetongue, IBR/IPV or, PRRS, brucellosis, leptospirosis, FMD, CSF and tuberculosis, respectively. Imported animals originated from the EU. Two heifers imported from Germany were positive on leptospirosis. Five boars imported from Germany were positive on leptospirosis and two boars imported from Poland were positive on PRRS and leptospirosis. One boar imported from Germany was positive on brucellosis. At the same time, Germany reported presence of diseases to the OIE. Our findings contributed to the fact that despite the veterinary certificates that accompany all imported breeding animals stating for diseases-free status in the region or herd and/or animals diseases-free, the quarantine of breeding animals consigned to the Centers for production of semen is essential and should be a priority. Taken together, our findings confirm that there is need for post-import quarantine for breeding animals in addition to examination performed prior consignment is consigned. Post-import quarantine is a risk-based approach that facilitates safe trade of animals. It is necessary because detection, control and eradication of introduced and spread zoonoses are usually very difficult and costly. Due to biological complexity, it is not easy and often impossible to identify how and when an infectious disease was introduced if discovered after quarantine period.

Perceptions of Finnish livestock producers regarding the costs of biosecurity

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Studies show significant differences between farms regarding the biosecurity measures applied on farms. If proper biosecurity measures are not implemented, costs due to a contagious animal disease can soar. It is therefore of critical importance to know how the implementation of biosecurity measures can be promoted. One important reason for not to implement a biosecurity measure can be that it is considered too costly. This study contributes to the literature by analysing how the characteristics of a livestock farm and producer affect perceptions about the costs of implementing biosecurity measures. A questionnaire enquiring about biosecurity measures was mailed to 4,000 Finnish livestock farms (3,000 cattle and 1000 pig farms) in early 2011. The overall response rate was 44%. Perceptions about the costs of implementation of seven different biosecurity measures were enquired, relating to the use of protective clothing, purchases of animals, and characteristics of livestock house. The results were classified into groups and logistic regression was used to estimate how farm and producer-specific characteristics were associated with producer perceptions about the costs of implementing a biosecurity measure. Previous experience about using the biosecurity measure tended reduce perceived costs significantly, and it was the most important single factor associated with the cost perception. Small farms tended to estimate somewhat lower cost of implementation than large farms. In some cases female and higher educated respondents and producers with a production contract also tended to perceive lower costs of implementation. Hence, results suggest that the uptake of biosecurity measures could be promoted by sharing information and increasing the awareness about (positive) experiences regarding biosecurity.

Quantifying economic losses of FMD based on data obtained during an outbreak: a simulation study
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Decisions to mitigate foot and mouth disease (FMD) are taken under imperfect information, since the actual size of outbreak is unknown until all infected farms have been detected. Our goal was to estimate whether data obtained in the beginning of an outbreak could signal the potential for economic losses and help to target prevention. An epidemiological Monte Carlo simulation model was used to produce 100,000 FMD outbreaks. There were data about each cattle and pig farm in Finland. The model used large datasets to describe farm population and farm networks such as animal transportation registry to describe the spread of FMD via animal contacts. Outbreaks were started from each farm. A partial-equilibrium model simulated economic losses of FMD to Finnish producers, consumers and taxpayers. It took into account foreign trade distortions and their price effects. Regression models estimated which characteristics of an outbreak explained losses the most. Explanatory characteristic included the properties (size, location, local herd density) of the primary infected farm (PIF) and outcomes of an outbreak (size, spatial spread, duration). Data about outbreak magnitude and duration was more informative than the data about PIF. For instance, outbreak duration was important, because foreign trade and business interruption losses were related to it. The properties of PIF were associated with losses. Infections in dairy farms resulted in the most costly outbreaks. To anticipate losses caused by an outbreak, higher economic weights per observation must be used in the very beginning of an outbreak than at later stages. Since losses could be mitigated only partly after the detection of FMD, it is important to identify the cases where further losses are accumulated. In practice the potential to reduce losses by adjusting mitigation policy after PIF has been detected is very limited.

Is there demand for animal disease insurance?

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The European compensation policy for animal disease damages has recently been questioned. It has been suggested that instead of merely compensating for damages from the public funds, policies should provide incentives to reduce the risk of disease damages and that producers should be co-financing the compensation scheme. The aim of this study was to examine the views of producers on animal disease insurance and their interest in participating in various types of insurance arrangements. We sent a postal survey to all Finnish pig and poultry farms (about 2,700). The questionnaire included questions regarding the disease history, use of biosecurity measures, perceptions on the risk of animal disease, and the willingness to buy insurance. Response rates were 21% and 24% for swine and poultry farm, respectively. As much as 96% of the respondents reported to have some insurance to cover their livestock production and 81% reported to have insurance for animal diseases. The most common types of insurance were business interruption insurance (68% of the respondents) and *Salmonella* group insurance (67%). The mean annual premium for animal disease insurance was 630 euro, and for other livestock-related insurance 1150 euro. The willingness to expand livestock insurance coverage was on average relatively low. The most popular option to arrange insurance cover was group insurance arranged by the slaughterhouse or the egg packing company. There was positive attitude towards premiums that vary according to the risk of the farm, and less so for premiums that vary according to the risk at the regional level. The larger the farm, the more positive the respondents were towards insurance. The respondent's education also affected the level of insurance cover that they had, but the age and gender had no statistical effect. Results suggest that there is demand for group insurance specifically designed to take the farm risk level into account. Instead, in the current good animal health situation there is no need for a broad insurance reform.

Movement restrictions in a farms' network for the control of the porcine reproductive and respiratory syndrome virus

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Introduction The transmission of the PRRSv (porcine reproductive and respiratory syndrome virus) between farms occurs because of infected neighboring farms or purchase of infected animals. Because it is difficult for a farmer to know the individual status of purchased animals, there is a need for a collective management based restriction of animal movements after assessment of farm status. We propose to assess the effectiveness of this strategy compared to the constraints it imposes. **Materials and Methods** We used recorded data of between-herds animal movements. The resulting network consists in real movements of different types of animals (8 kg and 25 kg piglets, reproductive gilts) between farms. We constructed a stochastic epidemiological model where herds can be susceptible or infected. The risk of infection due to trade in animals depends on the origin, the number and the type of animals purchased. The risk of infection by neighboring farms depends on the prevalence of the disease in the area. We modeled movement restrictions (based upon the farm's last test result) that respect the animals' flows to and from farms. **Results** The effectiveness of the restrictions of movements depends on the time between successive status assessments Halving the interval between tests (6 months to 3 months) induces a 50% decrease in risk of infection by trade. The constraint due to the increase in the number of movements and changes in the network structure depends on the prevalence in the area. **Conclusion** This model, highlighting the trade-off between constraints (increase in the number of movements, cost of the tests) and effectiveness (reduction in prevalence) of movement restrictions, can be a tool for decision makers to implement and monitor collective management of PRRS.

Spatial equity of the no cost spay/neuter program of dogs and cats in a developing country: the case of Bogotá, Colombia (preliminary results)

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The stray animals surplus is a global threat, observed in different countries. This surplus is also dependent on factors such as urbanisation level, public health, garbage management and cultural traditions. Neutering programs towards domestic animals, when accomplished permanently with adequate geographic distribution, has decreasing costs throughout the time and are effective in diminishing stray populations. The present study used the concept of spatial access ratio (SPAR) derived from the enhanced 2-step floating catchment area (E2SFCA) method to explore the spatial accessibility created by the no-cost neutering program to dogs and cats in the city of Bogotá, DC, Colombia. In particular, the equitable distribution of accessibility patterns is explored in relation to neighbourhood socio-economic strata.

Capacity building for animal disease risk modeling and related decision support systems in Liberia
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The authors present developments in the infrastructure for veterinary services in Bong County, Liberia, explaining the values of the installed capacity of Trans-boundary Animal Disease Information (TAD-info) system, a Decision Support System for national veterinary services. The role of epidemiological stations established in four zones of the country in feeding data from animal population, clinical observations and specimens collected for confirmatory diagnosis at the Central Veterinary Laboratory in Fendal is provided. TAD-info was first installed at the Central Agricultural Research Institute (CARI), Bong County in April 2010, with support from the United Nations Food and Agriculture Organization. In spite of technical challenges in manpower development, it has since contributed reasonably to national statistical record gathering on animal health and disease modeling. The potential use and improvements in manpower development for optimal use of this information gathering and processing facility is presented in this poster. There is need for training and retraining of users to fully utilize the potentials of the facility for the country in order to achieve the desired developmental goal. Emphasis has been placed on the training on geo-referencing and laboratory diagnostic support at the Central Veterinary Laboratory. The growing relationship between this facility and a consortium of Universities for control and prevention of endemic, emerging and neglected human-animal diseases in West Africa is discussed.

Cost advantages analysis of vaccination of laying hens against EDS adenovirus. A case study in Algeria
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The egg drop Syndrome (EDS) due to Adenovirus has recently been observed in laying hens in Algeria, and many farmers would to assess the economic value of vaccination against this virus. The profitability simulation study of the vaccination against EDS has showed an interesting result about the financial advantages. This profitability depends of several factors such as the price of the egg, the size of the farm and the percentage of egg drop. The advantages costs ratio of this vaccination depends of the price's egg, which is ranged between 9.72 and 13. Depending on the size of livestock, the variation of the ratio was 6.82 to 10.81. Finally, it was eventually found that vaccination is at least six times more profitable in case of viral infection to EDS, whatever the size of the farm, the price of the egg or the percentage of egg drop.

A comparative risk assessment of screw worm fly (*Chrysomya bezziana*) in tropical Queensland

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Screw worm fly (*Chrysomya bezziana*; SWF) is a threat to the Australian livestock industries; especially the northern Queensland extensive cattle industry. This risk assessment compares the small land holders (SLH) and the commercial cattle producers (CCP) who would initially be affected by SWF entering Queensland (QLD). Nine incursion pathways by which SWF might enter QLD were considered, and the two considered most likely were entry into QLD via a cattle vessel returning from a neighbouring country in which the fly was present; and entry with infested cattle entering overland from the Northern Territory (NT). The first incursion pathway necessarily involves initial exposure of cattle within 100 km of the coast, and the second cattle in western QLD. A survey of cattle producers, using a questionnaire administered by telephone, together with a review of the literature on SWF, produced qualitative and quantitative inputs into the risk assessment exposure and consequence pathways. The results of the survey were assumed to be equally applicable to cattle properties in western QLD. The likelihood of exposure following entry at the coast was higher for SLH than for CCP, and following entry from NT it was higher for CCP than for SLH. In the consequence assessment outbreak scenarios involving local spread, spread via saleyards, and spread to other properties were considered, and for each type of spread the likelihood was greater following exposure of animals on a CCP than animals on a SLH. Overall, the combined likelihood of exposure and spread was greater for SLH than for CCP, for all spread scenarios. However, given the greater number of cattle on CCPs than on SLHs, even in the coastal strip, initial exposure and subsequent spread is more likely to involve cattle on a CCP than cattle on a SLH. Extension effort needs to be directed to both SLH and CCP.

Evaluating food safety management performance in a milk pasteurising facility using a microbiological assessment scheme

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The performance of a food safety management system (FSMS) in a milk pasteurisation establishment was measured using a microbiological assessment scheme (MAS). The MAS consists of multiple sampling locations along the process consisting of high-risk raw materials, the processing environment, process water and finished product. Nine microbial parameters were assessed. Results were benchmarked against legal, industry and best practice norms. 100% (n=233) of raw milk samples met the EU TBC standard of $<10^5$ cfu/ml, however, *Listeria innocua* was isolated in 3% (n=134) of raw milk samples. *Listeria* spp., *Salmonella* spp., *Staph. aureus*, *Enterobacteriaceae*, *Bacillus cereus* and *Escherichia coli* were not detected in any end products (n=539). *Listeria welshimeri* (a poor hygiene indicator) was identified in 2% (n=153) of environmental samples. *Salmonella* was not isolated in any of the 63 environmental sample. 6% and 1% of operator hand swabs (n=100) had TBC and *Enterobacteriaceae* counts respectively in excess of best practice norms of 10^2 cfu/cm and 10^1 cfu/cm respectively. One (2.2%) water sample (n=46) had a coliform count of 201 cfu/ml whereas five samples (11%) had TBC counts above acceptable norms. Enterococci were not isolated from any water sample. The results indicate that the FSMS is producing a safe product. The MAS is an effective risk assessment tool to assess the overall performance of the FSMS allowing a more targeted use of resources to implement improvement. Satisfactory end product microbiological results indicate that cold chain control, post pasteurisation contamination from dry ingredients (e.g. buttermilk cultures), packaging or unsanitary pipe work are not issues for this plant. The prerequisites of environmental sanitation, raw material supply and control, water treatment and storage and staff hygiene are the areas within the FSMS that pose the greatest risks.

Prevalence of *Salmonella* isolated from water used in retail goat meat shop of Kathmandu valley and Rupandehi district

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To know the prevalence of *Salmonella* spp. isolated from water used in retail goat meat shop of Kathmandu Valley and Rupandehi district. Design: Cross-sectional study Samples: 200 retail meat shops (100 from each site) were randomly selected. Each sample was cultured on Nutrient agar, MacConkey's agar and BGA and incubated at 37C for 24 hrs. Pale colonies on Mac Conkey's agar and Pink on BGA were stored in nutrient broth containing 20% glycerine after Gram's staining for confirmation by biochemical tests. Biochemical reactions of *Salmonella* in TSI, MIO, Simmon's citrate agar, MR-VP, along with catalase, oxidase, KOH tests were used for identification of Salmonell spp. Total plate count were performed to know the bacterial load in water. Out of 100 samples of each site, 96 and 66 water samples of Kathmandu Valley and Rupandehi district respectively were positive for one or more bacteria. The prevalence of *Salmonella* spp. in Kathmandu Valley and Rupandehi district were 18% and 11% respectively. In Kathmandu Valley 15.21% of tap water and 26.82% of tube well samples were positive for *Salmonella* whereas 8.04%, 25% and 40% of tap water, tube well and river water samples respectively were positive for *Salmonella* in Rupandehi district. Water jar and tanker water samples of both places aware free from *Salmonella* organism. Total plate count revealed 94% and 64% water samples of Kathmandu Valley and Rupandehi district respectively exceeded the WHO guideline value (<10 cfu/ml drinking water). It can be concluded that there is greater chance of human Salmonellosis and other bacterial infection through meat contaminated by dirty water. Hence appropriate water sanitizer should be used to reduce the human zoonosis.

Epidemiology of brucellosis and Q fever in rural, northern Togo

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Brucellosis is one of the most common zoonoses, with a major health and economic impact. Q fever, also a bacterial zoonosis, is of unknown global public health importance. The epidemiology of these diseases has never been described in Togo, nor in most West African countries. Using a One Health approach, human and livestock sera were collected in June 2011 in rural, northern Togo by multi-stage, cluster random sampling. Brucellosis: All animal sera were tested by ELISA and Rose Bengal agglutination test (RBT), with the Complement Fixation Test in cases of disagreement. All human samples were tested by ELISA and RBT. Q Fever: Randomly selected sub-samples of animal and human sera were tested by ELISA. Sera were obtained from 601 cattle, 692 sheep/goats, and 683 people from 25 villages. Brucellosis seroprevalences were 9.2% (95%CI: 4.7-18.6%) in cattle, 0% in small ruminants, <1% in people. Q fever seroprevalences were 16.1% (95%CI: 11.8-21.5) in cattle (n=243), 16.2% (95%CI: 11.1-23.0%) in sheep (n=207), 8.8% (95%CI: 4.3-16.9%) in goats (n=201), 38.9% (95%CI: 33.2-44.8%) in people (n=304). There were no associations between human seropositivity and contact with livestock, drinking unpasteurised milk, or general health. Most African brucellosis data were collected in northern countries, where *B. melitensis* is the predominant circulating species. In contrast, the serological picture in northern Togo suggests *B. abortus*. Vaginal swabs are currently being collected from recently aborting cows for culture. If successful, this would be the first reported isolation of *Brucella* from Togo. Exposure to Q fever is common, but the significance is not yet known. The indirect fluorescent antibody test is being performed on the human Q fever sub-sample to verify ELISA results.

Transport-associated fomites: estimation of the potential risk for African swine fever introduction into European Union

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The spread of African swine fever (ASF) without control in Russian Federation (RF) has increased the concerns about the potential introduction of ASF into EU. As imports of pigs and their products are banned since the notification of ASF in RF, the role of illegal imports, fomites or wild boars are of chief importance for potential ASF introduction. The study here was aimed to estimate the relative risk for ASF introduction into the EU through three transport-associated fomites (TAF) which were classified as (1) livestock trucks returning from affected areas; (2) waste from boats; and (3) waste from planes. A novel semi-quantitative model based on a knowledge driven approach was used for this purpose. Several parameters were selected as proxies for each pathway and standardized into six risk categories. The weighted combination of these proxies, which weights were obtained in an expert opinion elicitation, produced a final estimator for each TAF pathway and for each EU country. An extensive sensitivity analysis was performed to evaluate the impact that changes on those weights have in the model outcome. Results of the model indicate that the overall risk for ASF introduction through TAF pathways in EU is low, although some countries concentrate high levels of risk, being the returning trucks the TAF that posed the highest risk. The countries at highest risk in each TAF pathway were Poland and Lithuania for returning trucks, Denmark and Spain for waste from boats and, Germany, UK and France for waste from planes. The model proposed here provides simple and easy to interpret results allowing the identification of the most critical TAF for each country and the countries that concentrate the highest relative risk for ASF introduction. Methods presented are particularly useful when data is scarce and may be useful for developing target surveillance strategies to reduce the risk of ASF introduction into EU.

Prerequisites for HACCP in poultry processing in Maputo, Mozambique

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Poultry is a major component of the diet and a valuable and affordable source of protein for all levels of society. It is unknown whether poultry meat consumption contributes to diarrheal diseases, an important cause of mortalities. This study used participatory risk analysis to investigate the value chains for poultry processing in Maputo, indicating possible stages at which there was a risk of microbiological hazards that could influence safety of the final product. The method included semi structured interviews, various focus group discussions and observation of poultry processing in both formal abattoirs and informal slaughter (farms and live bird markets). The magnitude of the risk of microbiological hazards was estimated using laboratory analysis, specifically 3M™ Petrifilm™ Plates for E coli Type I, Coliforms and plate count as indicators of contamination to assess the compliance with GHP and GMP, relevant pre-requisites for HACCP. 330 samples of poultry carcass were randomly collected from abattoirs, live bird markets and farms. The contamination rate with *E. coli* Type I was significantly higher in markets (63%) than abattoirs (39%) and farms (40%). Suggesting a higher likelihood of risk in poultry meat from live bird markets than those from the abattoir or direct from the farm. All three value chains were, however, contaminated with the faecal derived organism, which has the potential to cause food born disease in consumers. Prerequisites such as lack of processing infrastructure, inadequate waste management and poor hygiene were observed in markets. In the formal abattoir, disinfection of surface and utensils, ablutions or hand disinfection and chilling system was found to be inadequate. A hygiene assessment system is proposed with a focus on those CCPs suggested by the research and participatory risk communication strategy has been developed for all those involved in the poultry chain to improve hygiene and safety of poultry meat.

Key messages from the Safe food Fair food project: food safety in informally marketed livestock products in sub Saharan Africa

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In sub Saharan Africa (SSA), 85 to 90% of livestock products are distributed through informal marketing systems which are not always effectively regulated by state services. Food borne diseases (FBD) are potentially serious public health problems but rigorous implementation of food safety measures is difficult due to the limited resources and adverse effects on the livelihoods of actors along value chains. The Safe Food Fair Food project funded by Germany was conducted in 8 SSA countries between 2008 and 2011 to develop capacity in participatory risk assessment to improve food safety while enhancing market access by smallholder farmers. The main activities were food safety country situation analyses, participatory risk assessments and national stakeholder workshops. In total, 21 risk assessment studies were conducted for a variety of livestock products and hazards. Key messages from the project included (1) the realized importance of informal food chains in African economy; (2) risks were less serious than previously perceived; (3) participatory methods were found useful in risk assessment in resource poor SSA countries; and (4) necessity for trans-disciplinary research and action along value chain. In the next phase starting shortly, Safe food Fair food II, involvement of decision makers, integration of multiple-pathogens and socio-economics into risk assessment are hoped to make important changes in addressing food safety issues in sub Saharan Africa.

True seroprevalence of *Coxiella burnetii* in sheep at Ksar Boukhari region (Algeria)

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Q fever is a zoonotic disease caused by an intracellular bacterium *Coxiella burnetii* and is shed mainly by domestic animals like sheep and goats. Despite of its worldwide endemic situation, the prevalence has not yet been studied in Algeria. That the reason why a seroprevalence survey of *C. burnetii* infection has been conducted in the area of Ksar Bukhari (highlands located 150 km south of Algiers) on randomly 18/250 villages, corresponding to 97 sedentary mixed herds sheep / goats. 144 sera samples from unvaccinated young sheep were collected and tested for the detection of antibodies against *Coxiella*, by a 0.88 sensitive and 0.99 specific test, the indirect ELISA CoxLS, with a cut-off value OD>0,4. Among the results, considered representative of the region and relatively accurate for attended prevalence value, 10 villages (68 herds) were tested positive to *Coxiella*, with a true prevalence rate (60±24)% at herd level and (19±06)% at individual level. These results clearly confirm the recent and wide distribution of *C. burnetii* over Ksar boukhari region, which is the crossroad of many transhumant flocks. The level of prevalence is discussed in comparison with the prevalence in neighbouring Maghreb countries.

Quantitative assessment of the risk of acquiring campylobacteriosis from consumption of ready-to-eat beef in Arusha municipality, Tanzania

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Worldwide, thermophilic *Campylobacter* is one of the most important causes of food borne illness. We carried out a risk assessment for campylobacteriosis acquired through consumption of ready-to-eat beef in Arusha, Tanzania. Between January and March 2010, 18 beer bars serving ready to eat beef were surveyed: 45 roast beef (nyamachoma in Swahili language) and 42 skewer beef (mishikaki) were collected and cultured for thermophilic *Campylobacter*. The number of customers and average sales per day were also assessed. A second survey was conducted in September 2010 to obtain the most probable number (MPN) of thermophilic *Campylobacter* and 30 roast beef and 10 roast chicken samples were examined. A risk model was developed based on public and survey data and dose-response relationship was modeled using medical records obtained from a separate study and literature. Monte Carlo simulation was run for 5,000 iterations and sensitivity analysis was run for 500 iterations. Bayesian inference from two surveys showed that the contamination rates of nyamachoma and mishikaki were 7.7% (90%CI: 4.3%-11.8%) and 34.7% (90%CI: 21.3%-49.1%) respectively. The MPN was 0.37 (95%CI: 0.07-1.0). Every day, 1.4% (90% CI: 0.8-2.3%) of customers consuming either nyamachoma or mishikaki in pubs in Arusha was estimated to develop campylobacteriosis. The annual incidence was 248 (95%CI: 127-406) per 1000 people among whole population of Arusha Municipality and one forth of people was estimated to become sick once a year. The most sensitive factors were contamination rate of ready-to-eat beef and the MPN. From observation, beef was well roasted and the high prevalence could be due to post-roast contamination. Hygiene training focused on such contamination could reduce the incidence greatly.

Identification of influenza virus circulation in backyard poultry and swine in the central zone of Chile

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Influenza virus (IV) infection is considered a threat for both public and animal health worldwide. Influenza pandemics usually occur after periodic exchanges of genes among the viruses of humans, pigs, and wild and domestic birds. Pandemic influenza virus H1N1 2009 caused the first pandemic of the XXI century (its genetic composition indicates that the virus is a quadruple reassortant, with gene segments from human, swine and avian IV). IV that affects animal species can cross the species barrier, causing disease in humans. For instance, the H5N1 highly pathogenic avian influenza epidemic is still considered a threat to the public health, causing hundreds of deaths in humans since its inception in Asia in 2003. The Chilean poultry and swine sectors had improved their production and quality standards by the early 1990s; however, other kinds of animal production exist. Backyard productive systems (BPS) also breed swine and poultry, being recognized as an important component of small farmers' livelihoods. BPS have been generalized as production units having severe biosecurity deficiencies, the animals and their by-products are usually consumed by their owners, sold locally and used as gifts. It has been proposed that pigs can act as mixing vessels and play a key role in the reassortment of human, swine and avian IV. In this context, BPS could play a major role, because its management conditions facilitate the interaction among poultry, pigs and humans, which may result in the emergence of new strains of IV. This research is going to identify IVs circulating in BPS in the central zone of Chile, using the ELISA test, and will evaluate the risk factors associated with the IV circulation, based on the BPSs biosecurity, management and trade conditions. Results from activities performed between March and May 2012 will be presented.

Evaluation of prevention, surveillance and control activities for priority zoonoses in Chile, under the ‘One health’ approach

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The interconnection among humans, domestic and wild animals, and the environment, coupled with elements such as the human population expansion, globalization and climate change, create conditions for disease (re) emergence. Humans and animals usually share resources and environment, but also many pathogens can be transmitted between them (zoonoses). The OIE recognizes the ‘One Health’ approach as a collaborative and all-encompassing way to address animal and public health, and promotes its use at the national level to get a more engaged and sustainable political support for the coordinated prevention of high public and animal health impact diseases at the human-animal interface. In Chile, human health and animal health authorities depend on different Ministries. As an example, during the period of 2000 to 2010, 566 human cases of hantavirus were reported, but there is a lack of data to assess the prevalence of hantavirus in wild rodents, the virus reservoir, during the same time period. This situation suggests that activities focused on priority diseases differ when they are related to human or animal health. The aim of this study was to assess, under the ‘One health’ approach, prevention, surveillance and control activities, for priority zoonoses in Chile, through multidimensional scaling analysis. Results of this study show differences in the efforts performed for prevention, surveillance and control activities, depending on whether the effort was intended to address human, domestic animals or wild animal health, demonstrating that policies for priority diseases were different for the public health and animal health authorities. Also, noted in this study was the absence of official activities focused on wild animals. These results suggest that policies for priority zoonotic diseases in Chile, do not yet follow the ‘One Health’ approach.

Human rabies mortality estimation in rabies endemic southern Bhutan

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We estimated the human rabies deaths in two rabies endemic areas of southern Bhutan and compared the estimates to the reported data using decision tree analysis. The anatomical distribution of dog bite in humans and the probability of developing rabies were used to estimate the human rabies deaths using a decision tree model. This model consists of 10 probability steps (P1 to P10). P1 is the rabies recognition probability in dogs, and the P2 to P5 is the distribution of bites on various body parts: head (P2); arms (P3), trunk (P4) and legs (P5). P6 to P9 are the probabilities of developing rabies following dog bite to the head (P6), arms (P7), trunk (P8) and legs (P9) (a). P10 is the probability of receiving post-exposure prophylaxis (PEP) following bite from a suspected rabid dog. The probability of death ($P_{death} = P1 \times ([P2 \times P6] + [P3 \times P7] + [P4 \times P8] + [P5 \times P9]) \times (1 - P10)$). Then the total number of deaths per year = $(I \times Q \times P_{death} \div 100\,000)$, where I is the incidence of suspected rabid dog bite per 100,000 people/year; Q is the total population at-risk. The mean annual number of reported human rabies deaths in the two rabies endemic areas of southern Bhutan were 1.5 (95% CI 0.75-3.00), equivalent to an annual incidence of 3.14 (95% CI 1.57-6.29) deaths/100,000 people. The decision tree model predicted 2.23 (95% CI 1.20-3.59) deaths/year, equivalent to an annual incidence of 4.67 (95% CI 2.53-7.53) deaths/100,000 people, indicating that no serious under-reporting of rabies exists in Bhutan. In the absence of PEP, 19.24 (95% CI: 13.69-25.14) deaths/year was predicted, equivalent to an annual incidence of 40.31 (95% CI 28.70-52.68) deaths/100,000.

The Belgian animal health barometer: an instrument to measure livestock population health on a yearly basis

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The Scientific Committee of the Belgian Food Safety Agency (FASFC) developed three barometers to measure the safety of the food chain in Belgium on a yearly basis: a food safety barometer, an animal health barometer, and a plant health (phytosanitary situation) barometer. The animal health barometer consists of a set of 13, carefully selected, indicators measuring different aspects of the general health of the animal population including: the primary animal production chain, the various species, process controls and a preventive approach (self-checking/mandatory notification/traceability). A weight was attributed to each indicator after consultation of the stakeholders of the food chain. The status of animal health was represented in a relative manner by comparing results of the current year versus the previous year. Data from 2007 till 2011 have been analysed. In the presentation more information will be given about each indicator, about the concept and about the general evolution of animal health since 2007 in Belgium. The animal health barometer is a practical instrument giving an indication of the evolution of the general health status of livestock in a country. The barometer could be used for benchmarking countries or regions provided that data are available.

A cost benefit analysis for *Salmonella* in British pigs: a risk assessment approach

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The EC has initiated the setting of targets for *Salmonella* in pigs at the Member State (MS) level. Each MS will have to produce a National Control Plan (NCP) to indicate how it will achieve the prescribed target. Two recently completed Cost-Benefit Analyses (CBAs) for control of *Salmonella* in breeding and finishing pigs within the EU indicated that there was no positive cost-benefit for on-farm interventions for the EU as a whole. However, in certain intervention scenarios, the opposite was shown for the UK as an individual MS. We have modified and parameterised a risk assessment model for *Salmonella* in pigs (originally developed for EFSA) in order to run several intervention and sampling scheme scenarios which would inform the development of the UK NCP for *Salmonella* in pigs. To inform the NCP further, we also conducted a preliminary UK CBA for both on-farm and abattoir interventions for *Salmonella* in pigs, using data from the updated risk assessment model and various published and industry sources. Anal bunting achieved the highest effectiveness of any intervention investigated and was also the cheapest. Therefore it also had the most advantageous cost-benefit ratio, but even this intervention meant that there was more money spent on intervention than was saved in human illness costs. A carcass swab target would be likely to reflect a change in lymph node prevalence as prescribed by the EU, but also allows MSs to use abattoir as well as on-farm interventions to achieve their targets.

a risked-based evaluation of the Sudanese standard and regulation for importation of chicks

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Based on the OIE standards, this study was aimed to assess the quality of the Sudanese standard, and the sanitary measures in place for the importation of chicks via the Khartoum international airport. For this purpose, a risk assessment was used as described in chapter 2 of the OIE terrestrial animal health code-2009. Data were collected from the Federal Ministry of Animal Resources and Fisheries FMARF, the Sudanese Standards and Metrology Organization SSMO and from the World Animal Health Organization OIE. The results showed that total of (11,241,209) day-old chicks, were imported into the Sudan during the period 2005-2009 from 10 countries, which may comprise potential risk of introducing Highly Pathogenic Avian Influenza HPAI and many other diseases into the country. In viewing the poultry health status in the exporting counties, the HPAI is endemic in Egypt, which represented the main exporting country of day old chicks in 2005. In 2006 about 18.3% (out of 235,626 susceptible population) were infected with HPAI and 43.2% were destroyed for the same reason. Moreover, the Sudanese standard of importation of chicks had not been set according to risk estimations recommended by the OIE standards, and the sanitary measures in place were less stringent to achieve the appropriate level of protection. Therefore, a multidisciplinary scientific risk analysis following OIE standards are recommended for the importation procedures and setting the Sudanese standards.

A retrospective survey of hydatidosis in slaughtered animals in 22 slaughterhouses in Tehran province capital of Iran 2009-2011

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Hydatidosis is a zoonotic disease that also cause considerable economic losses all over the world. Cystic hydatid disease is considered endemic in Middle East region and is common in all herbivorous animals in Iran. We survey the annual prevalence of hydatid Cyst in slaughtered animal and its trend for 2 years. This retrospective survey covering a period of 2-year from 21 march 2009 to 21 march 2011. Condemnation records for cattle and sheep slaughtered in 22 industrial abattoirs in the Tehran province, capital of Iran, were used as the source data to determine the prevalence rate of liver and lung condemnations due to hydatidosis. A total of 526,034 cattle and 2,833,142 sheep were slaughtered in this period, 79,916 (15.19%) livers and 87,533 (16.64%) lungs of cattle were condemned whereas 273,138 (9.64%) livers and 322,627 (11.38%) lungs of sheep were condemned. Hydatidosis was responsible for more than 19.52% of liver condemnation and 30.53% of lung condemnations in cattle and sheep. The prevalence of liver and lung condemnations due to hydatidosis was increased from 1.70% to 2.01% and from 2.80% to 4.02% for sheep respectively whereas this prevalence was increased from 3.28% to 3.40% and increased from 5.58% to 6.50% in liver and lung of cattle respectively during 2009-2011. Our data indicated that 3.32% of livers and 6.00% of lungs in cattle and 1.81% of livers and 3.30% of lungs in sheep were infected with hydatid cyst. High prevalence of hydatidosis in Iran can be a result of conventionally slaughtering in sheep and goat and easily available carcass wastes and offals for scavenging stary dogs and other wild carnivores and close relation between shepherd dog and sheep and goat.

The efficacy and effectiveness of Q fever vaccines in high-risk groups: a systematic review and meta-analysis

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Q fever causes significant morbidity in high-risk, occupationally exposed groups including veterinarians. Vaccination is recommended as effective means of preventing clinical disease. To assess the available evidence and derive a pooled estimate of vaccine efficacy (VE), a research synthesis approach, including comprehensive and replicable scoping study, systematic review and meta-analysis was undertaken. Primary research of VE of whole-cell and acellular vaccines to prevent clinical Q fever in exposed high-risk individuals was identified, appraised, summarized or synthesized when appropriate. Sixteen electronic databases and grey literature were searched for potentially relevant publications. Abstract-level initial classification relevance screening, full-paper primary and secondary review, data extraction and assessment of study risk of bias (RoB), were performed by two independent reviewers on included control trials (CT) and cohort studies (CS). From twenty-four potentially relevant publications, eighteen were excluded because non-relevant vaccine strains (n=2), lack of comparison groups (n=15) or non-relevant outcomes (n=2) were reported. As our aim was to assess the public health and clinical vaccine effect, studies only reporting antibody or T-cell assays were excluded. Clinical cases in abattoir employees, shearers, and farmers were extracted from CT (n=1) and CS (n=5). Risk ratios were calculated from published raw data and varied according to study design, case definition, and length of follow-up. A fixed-effect meta-analysis of pooled RR resulted in an overall whole-cell Henzerling phase I VE of 90% (95%CI:82-94%). Assessment of heterogeneity will be conducted. RoB revealed unclear to high risk of bias across most design categories. Available evidence of Q fever VE in high-risk groups needs to be interpreted with caution due to the low number of studies and observations, and limited methodological reporting that could potentially bias the outcome.

Framework to evaluate the cost-effectiveness of rabies control on Flores Island, Indonesia

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Rabies is a zoonotic disease caused by the rabies virus. Because of the human losses on the island of Flores (Indonesia) and the associated economic consequences because of expensive post exposure treatment, since 2001 different control programs have been applied to control this virus. The programs included different measures: (1) applying mass vaccination in the dog population, (2) culling stray dogs, (3) sterilizing dogs, (4) putting imported dogs in quarantine, and (5) applying post exposure treatment in human. Unfortunately, the cost-effectiveness of these programs is yet unknown. Therefore, the objective of this paper is to present a framework to evaluate the cost-effectiveness of various rabies control programs on Flores Island. The framework consist of 5 parts: (1) effectiveness; and (2) costs of programs in dogs; (3) effectiveness; and (4) costs of programs in humans; and (5) cost-effectiveness of programs in dogs and humans. Effectiveness of programs in dogs is defined as how effective the programs in reducing of number of rabies infected dogs. Effectiveness for the human population is defined as the number of (disability adjusted life years) DALYs prevented. This effectiveness depends strongly on the rabies control in dogs and on the right application post exposure treatment (PET) in humans. The costs of the programs both in dogs and humans will be calculated using a cost-benefit approach. The most preferable programs are those that show the lowest net cost for one DALY saved. Although we apply this framework on control of rabies on Flores island, it provides an approach that can be used for a wide range of zoonotic infectious diseases.

Prevalence of *Salmonella* on commercial layer farms in Barbados, 2009-2010

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During January-March 2009, an outbreak of *Salmonella* was detected in four commercial layer farms in Barbados. During the outbreak, a total of 511 layers died, and 3,257 layers were voluntarily culled from one affected farm. *Salmonella Enteritidis* was identified in avian tissues (ovaries, liver, uterus), and egg samples submitted to the Ministry of Agriculture, Food, Fisheries, Industry and Small Business Development (MAFFI) Veterinary Services (VS) Laboratory by managers of the affected farms. As a result of this outbreak, MAFFI VS conducted a survey to investigate the prevalence of *Salmonella* on commercial layer farms in Barbados. In addition, the relationships between farm-level exposure factors and diagnosis of *Salmonella* were examined. This paper describes the results of this survey.

Dispersal of animal products and waste from traditional abattoirs in the Far North region of Cameroon

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A study was undertaken in the Far North region of Cameroon to describe the factors which could contribute to dispersal of pathogens for both animals and people through traditional abattoirs. Eight traditional abattoirs (Maroua municipal, Kongola Djidé, Kongola Djolao, Makabai, Mbalmaré, Kousséri and Yagoua) located in three area cities were selected to lead the first, descriptive, phase. In this phase the possible exits of contaminated agents were identified. The categories of agents were men who attended the abattoir, animal products (meat, skins, meat offal, etc), waste water and animals in lairage prior to slaughtering. Maroua municipal and Yagoua were selected for the second, analytical, phase of this study. To this end a questionnaire was administered to those present at the slaughterhouses. In addition, GPS was used to follow circulation of products, waste water and animals in lairage (which includes grazing) prior to slaughtering. On average 28.5%, 14.5% and 18.0% respectively of butchers, workmen and others at Maroua abattoir kept ruminants, while in Yagoua the results were respectively 75.0%, 46.5% and 67.4%. The meats coming from Maroua's abattoir were followed on twelve routes. Times between leaving the abattoir and sale points varied from 4 to 15 min with more half of the ways including contact with at least 5 ruminants, which is a potential route for transmission of diseases like foot-and-mouth disease. In Maroua in the rainy season the waste water spread into the pastures, while in Yagoua they were poured in the Danay River, site of watering for many animals.

Small landholders: risks to national biosecurity?

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It is generally thought that small landholders pose risks to Australian animal biosecurity, through ignorance and poor biosecurity practices. The nature and magnitude of such risks have not previously been defined or evaluated, however. We set out to identify and assess some of these risks, and in so doing to provide information which might inform decisions concerning deployment of biosecurity effort within Australia, in particular in the prevention and management of exotic animal disease incursions. It is evident that owners of small numbers of livestock do indeed pose risks, but are they significant relative to the overall levels of risk? In this project we compared risks to Australian livestock biosecurity associated with small landholders with those associated with commercial livestock producers. We conducted 7 separate risk assessments, covering different livestock species (cattle, pigs, poultry, bees, meat-producing species), geographic regions, and hazards (exotic diseases: screw worm fly, foot and mouth disease, virulent Newcastle disease, avian influenza, *Varroa destructor*; also chemical residues). Methods were quantitative or semi-quantitative, using stochastic models of relevant pathways, and covered the exposure and consequence likelihood assessments of the OIE's Import Risk Analysis framework. Step probabilities in exposure and spread pathways were estimated using surveys of producers, or in one case, a formal expert opinion elicitation process. Criteria for categorising producers as 'small' or 'large' varied among assessments, as did the specific findings. Overall we concluded that the practices and locations of small landholders render them more likely than commercial producers to expose their animals to hazards. However, the trading practices of commercial producers, together with their much greater stock numbers, mean that most of the risk for establishment and spread of hazards is associated with commercial producers.

Adding Bayesian disease mapping and co-factor analysis to the PAZ project in the Lake Victoria Crest, Kenya

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The PAZ Project (People, Animals and their Zoonosis lead by E. Fevre, <http://www.zoonotic-diseases.org/home/Research/paz>, funded by the Wellcome Trust) and its consecutive projects utilize innovative cross-disciplinary data analysis derived from Numerical Ecology to map, prioritize and deliver interventions against infectious zoonotic diseases in people and their domestic animals. The interventions will be tailored to the risk-driven needs of spatio-temporal clusters. The PAZ Project is undertaking a community based cross sectional survey of humans and their livestock in a mixed crop-livestock farming system in the Lake Victoria Crescent in East Africa. Comprehensive economic, social and disease – including HIV, Malaria, Bovine Tuberculosis, blood and GI parasites – data are collected at the household and individual animal and human level together with prevalence data of six neglected zoonoses. Diseases do not exist in isolation. Ignoring interactions between multiple diseases, co-factors and reservoir species, results in the misinterpretation of infection pressures and miscalculation of effects of interventions. Therefore, designing intervention packages that are specifically targeted to clusters of disease and their co-factors, ensures that the interventions are relevant, targeted and cost-effective. The data from the PAZ Project will be analyzed using (1) Principal Component Analysis (PCA); (2) Cluster Analysis (CA); and finally (3) Bayesian Disease Mapping (BDM) methods. The proposed oral presentation will describe the project and strategic plans for and the preliminary outcomes of the data analysis.

Illegal import of meat including bushmeat into Switzerland by private air travel

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Illegal imports of meat can present substantial risks for public health and for the introduction of exotic animal diseases. Studies conducted in different European countries have estimated the volume of meat imports including bushmeat from non-EU countries into Europe by private air travel at a few tonnes weekly. The objective of this study was to estimate the amount of meat illegally imported into Switzerland by private air travel. Because meat from wild animals (bushmeat) has a great potential for the introduction of exotic diseases, the amount of illegally imported bushmeat was estimated separately. Data were obtained by participating in several intervention exercises at the two international airports of Switzerland where meat imports are regularly seized, and by analyzing data on seizures from the last four years. A stochastic model with the software @Risk was then applied to estimate the total amount of illegally imported meat. A wide array of animal species including domesticated and wild species were imported into Switzerland. The total weight of annual meat seizures was estimated at 5,500 kg from which 1.3% was bushmeat. The main contributors to illegal meat imports from domestic species were Eastern European countries and for bushmeat Western African countries and particularly Cameroon. The total annual inflow of illegal imports was estimated by the model to be 1,013 tonnes (95% CI 166-5,494) for meat and 8.6 tonnes (95% CI 0.5-88.5) for bushmeat, respectively. This study only addressed the entry for illegal meat import via private air-travel and did not look into the other channels like air or sea freight or road. To get a broader picture of the magnitude of illegal meat imports into Switzerland and to obtain an accurate risk estimate of these products for public health, a larger study is recommended which would cover all possible modes of entry.

Risk assessment scenarios to understand the persistence of Rift Valley fever in Comoros (Indian Ocean)

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Rift Valley Fever (RVF) is an arbozoonosis identified for the first time in Kenya in the 1930s. In 2000, the first apparition of the virus out of Africa was described in the Arabian Peninsula with both animal and human cases. Indian Ocean showed animal and human cases in 2008 in Madagascar where the disease was absent during 17 years while the same year the same year the first human case was diagnosed in Mayotte from a young Comorian. Lots of models described climate drivers of RVF outbreaks. These models failed to predict malagasy outbreaks. These recent spreads of the disease are likely to be also linked with animal movements. Forecasting outbreaks and managing rapid control of the disease request adapted and more flexible models. This study assessed two scenarios of risk in the Comoros Islands and compared the results with some surveillance data in order to determine the potential role of the introduction of an exogenous hazard. The first scenario explored the endemicity of the disease through insect-borne transmission and developed the probability for the disease to be spread throughout the island because of infectious mosquito bites. The second scenario developed a model with new legal introduction of cattle from Tanzania and subsequent contact and infection of bovines in Comoros (Grande Comores). A quantitative stochastic approach permitted to include variability as well as uncertainty in this quantitative risk assessment. Advanced analysis of the sensitivity of the models allowed to explore the most probable pathways of transmission and therefore to define thresholds to set priorities in the RVF surveillance and the control measures.

Potential for improvement of biosecurity among cattle and pig farmers

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Biosecurity can prevent disease transmission between farms. With increasing farm size, proper biosecurity on farms is even more important. The aim of this survey was to study the level of biosecurity and the potential to improve it on Finnish farms. This study was based on a questionnaire regarding the use of biosecurity measures and the farmers' thoughts about improvement of the on-farm-biosecurity. The questionnaire was sent to 3,000 cattle and 1000 pig farmers and the response rate was 44%. The questionnaire included several different on-farm-biosecurity measures. Some were considered to have higher improvement potential than others. Naturally, the majority of improvement potential was recognized on those farms that did not already have these measures in use. In general, biosecurity was better implemented on pig farms. The measures which were reported to have highest improvement potential were already in use by 33-62% of the pig farmers and 12-66% of the cattle farmers. The farmers reported the following biosecurity measures as the ones that could be improved on their farm (% of respondents that did not already have the measure in use): Pig farmers: (1) control of rodents and birds (45%); (2) a barrier that separates the clean and dirty areas (43%); (3) a separate loading area (43%); (4) a carcass collection container outside the stables (41%); (5) keeping doors locked (40%). Cattle farmers: (1) use of protective clothing and boots by visitors to the farm (46%); (2) control of rodents and birds (44%); (3) keeping doors locked (29%); (4) a barrier that separates the clean and dirty areas (28%) The cattle and pig farmers favored partly different biosecurity measures based on their improvement potential. Encouraging farmers to improve the biosecurity measures which according to the farmers themselves have the highest improvement potential is a reasonable step towards an overall increase in biosecurity on the farm level.

Risk assessment for animal by-products associated with slaughter of pigs

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In Denmark, products originating from slaughter of pigs that have passed *ante mortem* inspection, and where carcasses or parts of carcasses are rejected at *post mortem* are currently categorized as 2 materials and hence subjected to pressure sterilisation – a costly procedure. In 2011, new EU regulations came into force supporting a risk-based approach to allocation of animal by-products (ABP) into the various categories depending on their risk. A risk assessment was conducted to assess the risk associated with ABP not intended for human consumption. Information was found in Danish slaughterhouse statistics, literature, and from contact to experts within pathology and rendering processes. A list of possible hazards was identified. It was evaluated whether potential hazards were pig-specific or could cause disease in other animal species or humans. It was identified which lesions were found – and how often – in finisher pigs. Next, hazards related to lesions found were identified, and difference in risk between carcasses with and without observable lesions was assessed. Finally, effect of the present heat treatment was evaluated. Denmark has a unique zoonosanitary status and surveillance programmes in place enabling early detection of notifiable diseases. Other hazards might be present in live pigs and, hence, on and in carcasses that are accepted for consumption. Most of such hazards are swine-specific, but some might result in disease in other animal species or humans. Among the latter, most are not food/feed-borne but occupational. The exposure risk associated with parts and carcasses that are rejected at *post mortem* – originating from pigs accepted at *ante mortem* – seems not to be substantially higher than the exposure risk related to products from pigs accepted for human consumption. Therefore, such ABP can be allocated to Category 3. At current, main part of ABP of pig origin in Denmark is heat-treated. This process was also assessed and showed elimination of any hazards possibly present.

Sheep production as a link between production sectors in Finland

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Sheep production has marginal economic importance in Finland. There were approx. 2,700 sheep flocks in 2009, but the mean flock size was only 24 ewes. Professional sheep farms (≥ 100 ewes, $n=177$), constituted 49.8% of the total ewe population. Sheep farming may play a role in disease outbreaks if it is frequently connected with other production sectors. Joint production of sheep with cattle and pigs was studied through the official Finnish animal registry. Altogether about a quarter of the sheep farms also had other animals: cattle (21.3%), pigs (1.5%) or cattle and pigs (0.9%). Mixing with other production types was less common among professional sheep farms (16%) than on semi-professional (28%) or hobby farms (22%) (Pearson $\chi^2=17.019$, $df=2$, $P<0.001$). Presence of other animals on the farm did not affect sheep flock size. There were less cattle and pigs on joint production sheep farms than on pure cattle or pig farms (Mann-Whitney U-test, $P<0.001$ and $P<0.001$, respectively). Mixing with sheep production seemed to be more common in the beef sector (6.4% of beef farms), than in the dairy sector (2.5% of dairy farms) (Pearson $\chi^2=147.564$, $df=1$, $P<0.001$). Beef sector farms which also had sheep production were significantly smaller than pure beef sector farms (Mann-Whitney U-test, $P<0.001$). Joint production farms may act as nodes in several production networks. This may increase the threat of spreading diseases, such as bluetongue or foot-and-mouth disease, between animal production sectors. Finnish sheep production is mixed especially with the beef sector. However, a comforting fact is that the beef sector seems to have lower potential to spread diseases than the dairy sector and that professional sheep farmers were less frequently connected with cattle and pig than other sheep farmers.

Exposure assessment to cephalosporin resistant *E. coli* through consumption of broiler meat in Belgium

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Acquired resistance of *Escherichia coli* to cephalosporin antimicrobials is a major issue in intensive broiler farming. In Belgium, about 36% of the *E. coli* strains isolated from live broilers are resistant to cephalosporins while over 60% of the broilers are carrier of these cephalosporin resistant *E. coli* (CREC). A model aimed at estimating the exposure of the consumer to CREC by consumption of broiler meat was developed. This model consists of different modules that simulate the farm to fork chain starting from primary production, over slaughter, processing and distribution to storage, preparation and consumption of broiler meat. Input data were obtained from the Belgian Food Safety agencies' annual monitoring plan and results from dedicated research programs or surveys. The model estimates that the probability of exposure to 1000 cfu of CREC or more upon consumption of a meal containing broiler meat is ca. 1,5%, the majority of exposure being caused by cross contamination in the kitchen. The prevalence of CREC (within the total number of *E. coli*) at primary production and the overall contamination of broiler carcasses or broiler parts with *E. coli* are dominant factors in the consumer's exposure to CREC. The risk of this exposure for human health could not be estimated given a lack of understanding of the factors influencing the transfer of cephalosporin antimicrobial resistance genes from these *E. coli* to the human intestinal bacteria and data on the further consequences of the presence of CREC on human health.

Diseases of honey bees: a new challenge for veterinary epidemiology and risk assessment for international trade

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The WTO Sanitary and Phytosanitary (SPS) Agreement, which came into force in 1995, represented a significant change in philosophy in that trade can now not be prohibited without good reason, such as protecting human, animal and plant life or health. Prior to this, countries could – and did – impose barriers to imports on sometimes dubious health grounds with the burden being on potential exporters to prove that such barriers were not justified. The SPS Agreement now requires that any import restrictions that are imposed must be supported by scientific evidence, and be based on a risk assessment or international standard. It is impossible for any country, even remote island nations, to isolate itself from all risks of imported pests or diseases. Zero risk is unattainable, and a key concept under the SPS Agreement is the acceptable level of risk, which member countries must apply consistently in different situations. The World Organisation for Animal Health (OIE) is mandated under the SPS Agreement as the international organisation responsible for the development of risk-based international standards for safe trade in animals and animal products. The OIE has developed a number of standards covering diseases of honey bees. Where international standards do not exist, or when a country requires a level of protection that is higher than an existing standard, the import conditions chosen must be based on scientific evidence and this entails carrying out a risk assessment. When risk assessments are carried out, they must be done properly, following accepted international guidelines to ensure transparency. The OIE has developed a standard for carrying out animal disease risk assessments for trade of animals and their products, and some OIE member countries have applied this to honey bees. Most risk assessments are qualitative. For the majority of honey bee diseases the level of information available means that fully quantitative assessments are not possible. The risk assessment process will be outlined, using example diseases of honey bees.

Analysis of african trading partners' food safety measures effect on beef export outputs

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In the past decade the average annual value of African beef export was approximately sixteen million dollars. The annual value of the beef export outputs increased haphazardly leading to an average annual downward trend and declined by three percent. A major contributor to this is market access restrictions due to strict food safety measures imposed by the European Union and other African trading partners on beef exports. A trend analysis was done from time series data of notifications by hazard categories of beef export consignments from annual reports of the European Union rapid alert system for food and feed. The result shows an average market access restriction imposed on one hundred and fifty four consignments. The following hazards contributed about seventy percent to the market access restrictions: potential pathogenic microorganisms, bad controls, organoleptic changes, veterinary residues and food additives. In order to create sustainable growth of African beef exports, competitive value added beef products should be exported.

***Toxoplasma gondii* infection in Swedish wild boars**

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Toxoplasma gondii is a common intracellular protozoan parasite of both animals and humans in Sweden. In Europe, approximately half of the infections in humans are estimated being attributed to consumption of undercooked meat from infected animals. Moreover, in both 2007 and 2011 *T. gondii* was ranked by the European Food Safety Authority (EFSA) as a significant disease causing agent in Europe, which should be monitored in domestic food producing animals as well as in game such as wild boars. The Swedish wild boar population has increased dramatically in recent years, with a corresponding increase in consumption of wild boar meat. The present study investigates the prevalence of antibodies to *T. gondii* in Swedish wild boars, with a perspective of improving the risk management of *T. gondii* as a food-borne infection from wild boar meat. During 2001-2011, serum samples from hunted wild boars were collected as part of a surveillance program for infectious diseases organized by the National Veterinary Institute, Uppsala, Sweden. The animals originate from most parts of the country but the majority are from the southern parts corresponding to the distribution of wild boars in Sweden. A total of 1209 serum samples will be analysed for antibodies to *T. gondii* by an in-house ELISA. The current prevalence will be calculated and a trend analysis will be performed to evaluate changes in prevalence over time. The serum samples are currently being analysed, and for that reason no results are presented in this abstract. The results will be presented and discussed at the conference.

Survey of liver flukes in slaughtered animals in 21 Tehran abattoir of Iran during 2008-2011

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Fasciolosis and dicroceliosis are parasitic zoonosis caused by the liver fluke and results in liver disease and limits the milk and meat production of infected cattle and sheep worldwide. we survey the annual prevalence of dicroceliosis and fasciliosis in slaughtered animal as well as their trends for 2 years. This survey covering a period of 2-year from 21 march 2009 to 21 March 2011. Condemnation records for cattle and sheep slaughtered in 21 industrial abattoirs in the Tehran province, capital of Iran, were used as the source data to determine the prevalence rate of liver condemnations due to liver flukes. A total of 526,034 cattle and 2,833,142 sheep were slaughtered in this period 79,916 (15.19%) cattle livers and 273,138 (9.64%) of sheep livers were condemned. Fasciliosis was responsible for 19.42% and 15.66% of total liver condemnation in cattle and sheep, respectively, whereas dicroceliosis was responsible for 32.31% and 41.65% of total liver condemnation in cattle and sheep, respectively. The prevalence of liver condemnations due to fasciolosis was increased from 2.58% to 3.37% for cattle and increased from 1.33% to 1.75% for sheep. The prevalence of liver condemnations due to dicroceliosis was increased from 4.32% and 3.30% in 2008-2009 to 5.59% and 5.02% in 2009-2010 for cattle and sheep respectively. Dicroceliosis was more prevalent than fasciolosis in cattle and sheep.

Ranking potential disease control measures using MCDA: an example from *Salmonella* control in Canadian pork production

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Formal decision analysis tools can help support stakeholders in making decisions in complex problems. They increase transparency, identify clearly the information supporting decisions and provide a framework for exploring key components driving a decision. Multi Criteria Decision Analysis (MCDA) is one such tool. The objective of our study was to develop data sources and explore the use of MCDA in ranking interventions for *Salmonella* control on-farm. Key interventions were identified through expert consultation and preliminary literature review. A non-exhaustive list of interventions with potential efficacy was selected. Important criteria were identified through expert consultation. Data sources for each criterion were identified. Data for input to the MCDA was collected through the following activities: a systematic review, a cost modeling exercise, a producer survey and an expert consultation. An exercise to determine relative importance of different criteria to one group of stakeholders was conducted using a standardized approach. The systematic review identified published clinical trials for each intervention, though not all with the same outcome measure. Meal had the highest evidence of effect from the conducted meta-analysis. Addition of organic acids had the best modeled cost. Meal feed had the best practicality score. Little difference between interventions was identified relating to consumer perception. Stakeholders were divided on weighting consumer perception or evidence of effect as the most important criterion. A key element of decision making processes is the adequate engagement of stakeholders. In each of two formal engagement activities, stakeholder interest in the decision making framework increased. This highlights the importance of early and regular communication with stakeholders. The availability of adequate data is an important factor for supporting decision making.

Decay of *Mycobacterium bovis* during cheese ripening

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Brazilian legislation allows the use of raw milk to produce ripened cheeses, when the ripening period is over 60 days (at 5 °C or above). However, there is not solid scientific evidence that the ripening process inactivates enough amount of *Mycobacterium bovis*, from the food safety perspective. In addition, there is no official methodology for micobacteria counting in food matrix. So, this paper proposes a protocol to study the decay curve of *M. bovis* during cheese ripening. Two batches of parmesan cheese were made with pasteurized milk artificially contaminated with a strain of *M. bovis* isolated from slaughtered cattle in the state of São Paulo. The cheese was ripened at 18 °C and analyzed weekly until the 63th day. The samples were submitted to quantitative culture for micobacteria. The average of Decimal Reduction Time ($D_{18\text{ }^{\circ}\text{C}}$), weighted by uncertainties, was 37.5±5.3 days. This is a preliminar result and we need to run more samples to generate more accurated data about this parameter. The Decimal Reduction Time associated with ripening step is an important data to input risk assessment models of cheese-born tuberculosis.

The effect of thermal stress on *Salmonella* shedding in dairy cattle

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Salmonella is a major food borne pathogen that can cause disease in both animals and humans. Fecal contamination of meat during harvest is one of the main sources of human salmonellosis and in a recent survey, 14.9% of culled dairy cows at U.S. markets were *Salmonella* positive. In order to identify methods to decrease the risk of food borne illness the objective of this project was to investigate the association of thermal stress and *Salmonella* shedding in dairy cattle. In this project, one commercial freestall dairy herd was selected. Pooled fecal samples were taken from 8 lactation groups (1) close-up adult cows; (2) heifers prior to calving; (3) fresh cows, fresh heifers/ hospital area; (4) adult cows within 1 month post-calving; (5) heifers within 1 month post-calving; (6) cows in early-middle lactation; (7) heifers in early-middle lactation; (8) cows and heifers in late lactation). Pooled samples were collected once monthly for nine months. Temperature and relative humidity of the barns were monitored using commercial data loggers. A total of 360 pools were collected. The overall proportion of positive pools was 10.8%. The two lactation groups with the highest proportion of positive pools overall were the heifers prior to calving and the fresh cows, heifers/ hospital pen groups (22% for each). No positive pools were detected from middle to late lactation cows group. The proportion of *Salmonella* positive pools was greatest during the months of August, September and October (47.5%, 12.5% and 15% respectively). At the time of submission, analysis of thermal environment data is pending.

Development of a risk assessment methodological framework for potentially pandemic influenza strains (FLURISK): a project description

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The emergence and worldwide spread of the swine-origin pandemic A(H1N1)pdm09 virus was unexpected by the scientific community and highlighted gaps in our pandemic preparedness. To address some of those gaps, the European Food Safety Authority (EFSA) awarded a grant in December 2011 for the implementation of the project described herein. The objective of the FLURISK project is the development and validation of an influenza risk assessment framework (IRAF) capable of assessing the risk that influenza viruses emerging from animal reservoirs may cross the species barrier and become potentially involved in a new pandemic. The project consortium which is led by IZSVe (IT) consists of European veterinary and human health institutions, namely: Animal Health and Veterinary Laboratories Agency (UK), Royal Veterinary College (UK), National Institute of Public Health and the Environment (NE), Institut Pasteur (FR) and the University of Ghent (BE). FAO and the Center of Disease Control (CDC) complete the consortium as external consulting partners. The Influenza division of the CDC, which is in the process of developing its own tool to evaluate influenza A viruses with pandemic potential, will collaborate in the IRAF development. The CDC tool will be used as a model for building the IRAF. Systematic reviews on the etiology and epidemiology of influenza viruses along with the assessment of current surveillance strategies in animals and humans will contribute to the identification of risk factors for the emergence of pandemic strains and the identification of drivers of geographical virus spread. Risk pathways integrated with risk models will enable the system to weigh the pandemic risks associated with selected viruses. A gap analysis will contribute to the identification of gaps in our knowledge on influenza viruses etiology and epidemiology and will produce recommendations for improving data sharing and promote future research priorities.

Evaluation of real-time PCR without enrichment for quantification of *Salmonella* in swine feces

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Quantification of *Salmonella* in asymptomatic carrier pigs can be used to assess the contamination pressure and to implement effective control measures to reduce contamination in swine herds and introduction of *Salmonella* in the food chain. The objective of this study was to quantify the fecal *Salmonella* load in naturally infected pigs by means of quantitative real-time PCR (q-PCR) without enrichment and compare to the 'gold standard' (fecal culture). Individual pig fecal samples detected positive (n=443) and negative (n=1,225) by standard culture methods were submitted for q-PCR targeting the *invA* gene. The diagnostic sensitivity and specificity of q-PCR was compared with the 'gold standard' by means of receiver-operating characteristic curve (ROC). The threshold cycle (Ct) cut-offs were compared based on sensitivity (Se), specificity (Sp) and likelihood ratios. The area under the curve was 0.94 (95% C.I. 0.871-0.978). Based on a Ct cut-off of 36.8, which optimizes the sensitivity (0.942) and specificity (0.92) a total of 99.84% (1,223/1,225) of the *Salmonella* culture negative were q-PCR negative. Of the culture positive samples, 14.67% (65/443) were detected by q-PCR, but only 3.38% (15/44) of the samples were detected in triplicate and within the quantifiable range ($\geq 10^3$ copies of the *invA* gene). Of those samples within the quantifiable range, the bacterial concentration ranged from 1.06×10^3 to 1.73×10^6 *invA* gene copies/g feces. The majority of pigs in this study shed *Salmonella* at low concentrations below the detection limit of q-PCR. Real-time quantitative PCR without enrichment could be a good alternative to the traditional quantitative culture-dependent methods for detection of high fecal concentrations, but is not applicable for quantification of pigs shedding low concentrations ($< 10^3$ copies of *invA* gene/g of feces).

Spatial distribution of Q fever infected dairy cattle herds in western France

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Coxiella burnetii is the infectious agent responsible for Q fever, a world wide spread zoonosis. Q fever infection occurs mainly after inhalation of infectious aerosols generated from excreta of domestic ruminants, which are considered as the main source for infection. Therefore, any measure which aims to control *C. burnetii* spread among ruminants will result in reducing the zoonotic risk and the within/between herd transmission. The propagation of *C. burnetii* between ruminant herds may result from its passive transport through wind and/or the introduction of infected animals in free herds. However, the relative impact on *C. burnetii* spread between farms of the air-borne dispersion, compared to movements of possibly infected domestic has not been quantified yet, whereas this knowledge could enlighten the type of control measures to be implemented in herds at the regional level and their effectiveness. The present study aimed at investigating the spatial distribution of infected herds in a limited area, to further infer about the relative roles of transmission routes in the *C. burnetii* dispersion. Our hypothesis is that transmission by contiguity (e.g. wind) does not lead to distributions resembling those correlated with the animal movement network. Especially, if some clusters of infected herds are observed after adjustment for animal movements, the role of wind could be indirectly confirmed. To do so, Bulk Tank Milk was systematically collected in more than 2,600 (geolocalized) dairy cattle herds located in a department of Western France and tested using an ELISA based on a ruminant antigen (LSI, Lissieu, France) for detection of antibodies against *C. burnetii*. Spatial statistics (using SaTScan) was used to highlight putative clusters. The prevalence of infected herds in the area was large (around 60%) and highly varied between cantons. Clusters of infected herds were identified, suggesting the main role of wind in the *C. burnetii* dispersion. Characteristics of clusters (meteorological conditions, topography, herd density) were studied.

Learning stakeholder attitudes through an interactive workshop: a case study on *Salmonella* control in GB pigs

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Approximately one quarter of pigs in GB carried *Salmonella* at slaughter and some human cases of salmonellosis may be attributed to this source. A national control programme to meet EU requirements is anticipated and research has been commissioned to provide a scientific evidence base for developing interventions. Adoption of an intervention at any level in the pork food chain requires behaviour change by operators. Success can be defined as a reduction in the number of human cases of salmonellosis attributed to GB pig products, which demands a consensus amongst stakeholders for co-ordinated action throughout the pork food chain. Therefore, scientific advances and technical advice are necessary but not sufficient if the strategic aims of policy-makers are to be realised. In order to investigate the perceptions of stakeholders, we conducted a one day workshop in which research results were presented to an invited audience and their views were captured using interactive methods including delegate messaging tablets and individual voting devices. These enabled immediate feedback and stimulated further discussions. Over 70 delegates attended, representing farmers, processors, veterinarians, retailers, risk managers and researchers. A brainstorm session yielded 10 possible interventions, which delegates later ranked according to impact and difficulty in implementation. Interventions in the abattoir and processing were highly regarded as both effective and relatively straightforward to implement. However, delegates also believed that a combination of measures from 'farm to fork' were required as there was no 'silver bullet'. The workshop was well received and proved a highly effective means of stakeholder engagement. Funded by DEFRA; thanks to LiveGroup Technology for facilitation.

Poster topic 07**Poster 40****Rabies vaccination coverage, *Echinococcus* and *Leishmania* prevalences in the dog population of Bamako, Mali**

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Within the research program Integrated Control of Neglected Zoonoses (ICONZ), we investigated prevalences and risk factors of canine echinococcosis and leishmaniasis as well as dog rabies vaccination coverage in urban Mali. The results will assist in developing a targeted elimination program. Through two surveys of 2,940 households in Bamako, 372 owned dogs were identified. Blood, fur and faecal samples were collected for analysis including microscopic, immunodiagnostic and molecular methods. To obtain basic dog demography data, 277 dog keeping households are followed if possible through telephone interview every 4 months for two years. Out of 101 collected samples analysed to date, one intestinal *E. granulosus* and 28 *Taenia* infections have been identified, but specific anti-*Leishmania* antibodies have not been detected. A total of 28 dogs (17%) have been vaccinated against rabies. Out of 18 sera tested, 11 demonstrated sufficient antibody titres. The 22 reported human rabies cases in Bamako from 2004 through 2009 indicate that rabies is likely the most important zoonosis of urban dogs. The observed vaccination coverage of about 17% is insufficient to interrupt transmission. A concerted mass vaccination program complementing the efforts of private dog owners would be needed to eliminate dog rabies in Bamako.

Assessment of exposure to *Vibrio* in shellfish consumed in Abidjan, Côte d'Ivoire

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The consumption of shellfish contaminated with *Vibrio* spp. is a cause of serious food borne diseases (FBD) and a concern in Abidjan where shellfish are mostly purchased on informal markets. This study assessed the risk of exposure to *Vibrio* spp. via the consumption of shellfish in Abidjan using stochastic modelling. Parameters were derived from 3 studies: *Vibrio* spp. prevalence in shellfish (n=322) at markets, household survey (n=120) and focus group discussions (n=8) on consumers' practices. Both non-parametric bootstrapping and parametric distributions were used to represent uncertainty. The model was implemented in ModelRisk, using Monte Carlo simulation with 5,000 iterations. The incidence rate of consumption of shellfish contaminated by *Vibrio* spp. at the time of purchase was 5 per person year [90% CI=2.7; 7.3]. The prevalence of *Vibrio* spp. in shrimp and crab were 10.5% and 6.9%, respectively. The main parameter influencing the exposure was *Vibrio* spp. prevalence in crab, followed by the daily rate of consumption of shellfish. Shellfish consumption was daily for 11.7% of households, occasional for 45.8% and rare for 42.5%. Hazard and risk characterization are ongoing to estimate the risk of FBD associated with the consumption of contaminated shellfish. Results from the household survey showed that 7.5% of respondents reported symptoms of food poisoning. Shellfish are consumed boiled (96.7%) or fried (3.3%); reported cooking times varied from 5-15 min (6.8%) to more than an hour (64.2%). Although shellfish cooking practices seem to limit the risk of FBD, findings from focus group discussions suggest cross-contamination of vegetables and other food items consumed raw might happen.

A Norwegian risk assessment of diseases in production animals

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The purpose of this risk assessment is to assist the risk managers by evaluating which diseases should be the responsibility of the national food authorities and/or the responsibility of industry. It thus includes the following main elements: (1) hazard identification; (2) hazard characterization; (3) exposure assessment; (4) impact assessment; and (5) risk characterization. The estimated risk is expressed as exposure multiplied by impact. A total of 71 different disease conditions have been considered. The disease or relevant agent where assisted at 7 different points. The risk assessment was conducted such that every individual expert appointed to the group gave a score, based on a carefully defined scale from 1 to 10, for every point for each disease, with a score of 1 representing the lowest risk and a score of 10 the highest risk, according to the opinion of that individual member. Each individual provided their score for each point independently of the other members of the panel. When the scoring had been completed, the scores were entered into a spread-sheet and processed using the @RISK computer programme to create a graphical distribution, and to calculate the mean and distribution of the scores for each point. The results of this process will be illustrated graphically. The results of the current risk assessment will be demonstrated for three points of exposure and 4 points for the impact assessment. Lastly, the risk was assessed as a product of both exposure and impact. In this assessment the following conditions were ranked as highest: (1) salmonellosis; (2) swine influenza; (3) canine distemper; (4) paratuberculosis; (5) BVD; (6) glanders; (7) *Mycoplasma bovis* infection; (8) methicillin-resistant *Staphylococcus aureus* (MRSA) infections; (9) Q fever; (10) American foulbrood. This assessment has been conducted by Panel 8 (Animal Health and Animal Welfare) of the Norwegian Scientific Committee for Food Safety.

Impact and significance of the recent outbreak of Q fever in Western Europe: feasibility for future control programmes

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Following the 2009 outbreak of Q fever in the Netherlands, the European Food Safety Authority was requested to assess the significance of the occurrence of Q fever in the European Union (EU), to provide a better understanding of the scale and distribution of both the disease and *Coxiella burnetii* infection (the causal agent of Q fever), with the focus on farm animals and humans. An assessment of the magnitude and distribution of infection and disease in domestic ruminants and in humans was conducted after considering diagnostic tests for *C. burnetii* infection and surveillance in different member states (MS). Impact and significance was assessed, based on expert opinion. Several methods were used to clarify risk factors for maintenance of infection in ruminants and spillover of infection from ruminants to humans, including the development of a simple conceptual model, a critical review of available literature, and several country case studies. Infection with *C. burnetii* is endemic in domestic ruminants in most, if not all, EU MS. Although infection is common, observed disease is rare. The overall impact of infection on the health of domestic ruminants in EU MS is limited. In humans, *C. burnetii* infection is present in most, if not all, EU MS. Q fever is a zoonotic disease with limited public health impact in the EU, however, in certain epidemiological circumstances and for particular risk groups the public health impact can be significant. Control options for infection in domestic ruminant populations were evaluated, following the development of a generic framework for the control of infectious diseases, and based on available data about individual control interventions. Criteria for evaluation were: efficacy to reduce animal infection and spill over to humans, feasibility and sustainability. A range of control options are possible and should be used in combination.

Characterization and spatial distribution of scorpion sting accidents in Belo Horizonte, Minas Gerais, Brazil, 2005 to 2009

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A retrospective epidemiological study was done to characterize scorpion sting accidents occurred in Belo Horizonte, between 2005 and 2009. Notification data were used from the National System of Notifiable Diseases (SINAN), Epidemiological Surveillance System (SISVE) and also from the clinical records of Sector of Toxicology of João XXIII Hospital (HPSJ XXIII). For spatial analysis, the programs MapInfo 10.0, Hotspot Detective and SatScan were used. Between 2005 and 2009 occurred in Belo Horizonte 2769 cases of scorpionism, which represents an accumulated incidence of 114.7 cases per 100,000 inhabitants. There was a decreasing trend during the years and a higher rate of cases between August and January. The species *Tityus serrulatus* was responsible for most accidents. There was no statistical difference between men and women affected and people aged between 55 and 64 years had a higher risk to scorpionism. Most of the cases were attended within one hour after the sting. Local symptoms were more frequent than systemic manifestations. Ninety-six percent of the patients achieved cure and there were two deaths, both on children. Among 1924 georeferenced scorpionism cases, the highest incidence was observed in the Northwest Sanitary District (DS), followed by the Northeast DS. It was also observed large concentration of cases in the regions of the city cemeteries. Using the Technique of Kernel Density, there were concentrated points of scorpionism cases in three DS and it was also detected two clusters in the period, one in 2005 and another between 2006 and 2007. It is suggested to consider the determinants of scorpionism to the planning of control and focus on priority areas.

Leptospirosis infection in sheep and cattle in a New Zealand abattoir: sero-prevalence, shedding and diagnostic test comparison

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In New Zealand, leptospirosis is the most common occupationally acquired zoonotic disease. We present cross-sectional data from animals slaughtered at a mixed-species abattoir that reported a leptospirosis incidence of 3 cases from 20 staff in 2009. We compare the results from real time PCRs (RT-PCR) and microscopic agglutination tests (MAT) between research and commercial laboratories. Serum, urine and kidney samples were collected from 399 sheep and 146 cattle during nine weeks in 2010. Sero-prevalence was 44% (175/396) for sheep and 62% (90/146) for cattle. Sero-prevalence from six suppliers ranged from 20% to 83%. Twenty nine percent (115/399) of sheep and 21% (30/146) of cattle kidneys were RT-PCR positive, with a range of 4-68% for sheep suppliers and 14-22% for cattle suppliers. The shedding rate (based on urine RT-PCR results) was 31.4% for sheep and 21.2% for cattle. In total, 26.6% (73/274) of urine samples were tested positive by Massey RT-PCR, and 27.4% (75/274) by the commercial lab. The agreement between RT-PCRs from two labs was almost perfect (Kappa=0.93, 95% CI: 0.88, 0.98). At the MAT cut-off titre of 1:96 was chosen, the agreement was almost perfect for serovar Hardjjobovis (Kappa=0.92, 95% CI: 0.88, 0.95), and substantial for serovar Pomona (Kappa=0.70, 95% CI: 0.62, 0.78). Sero-prevalences and shedding rates detected in this study were higher than those previously reported. The risk of transmission to meat workers and animal handlers was therefore high. Feedback to the abattoir, stock suppliers and their veterinarians reinforced the need for control strategies such as livestock vaccination and the use of personal protective equipment. Despite that different sample handling, DNA extraction and RT-PCR protocols were applied by the laboratories, there was almost perfect RT-PCR and high level of MAT test agreement between the research and commercial labs.

Where to draw the line: challenges of undertaking one health sero-epidemiological studies in developing countries

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A practical objective of the One Health approach to zoonotic disease is to objectively determine the burden of infection and disease in animal and human populations. For many zoonotic diseases, infection in domestic and wildlife results in no (or sub-clinical) disease, and therefore no diagnostic tests or protocols exist to measure exposure. This usually leads, in the first instance, to the use of tests developed for human populations, which are then subsequently assessed, and where necessary modified for the animal population. The challenge arises when the test validation has either not been done or else on very different animal populations. In 2011 we undertook an integrated public and animal health study in two provinces in Laos with the aim of determining, inter alia the burden of exposure to two pig related zoonotic viral diseases, Hepatitis E and Japanese Encephalitis. As the ELISA tests for JeV and HeV had not previously been used in pig samples in Laos, we needed to determine appropriate cut-off points. For both tests we used standard exploratory data analysis (EDA) methods – box-plots and histograms – to determine data outliers and the appropriateness of the recommended cut-off values. This EDA approach indicated that the threshold was set too low, i.e. that the test had a sub-optimal specificity. To determine the effect of this on our principal study objective – to determine risk factors and ‘hot spots’ – we systematically varied the cut-off values, reclassifying those samples being suspected of being false positives as ‘inconclusive’. Incorporating this data-mining approach into an algorithm has considerable potential as an interim and cost effective approach to overcome the problem of test validation in developing countries where complete ‘gold standard’ assessments are not feasible.

Q fever in Switzerland: Seroprevalence in small ruminants and risk assessment for humans

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Q fever is a zoonotic disease caused by the intracellular bacterium *Coxiella burnetii*. Humans become infected mainly through inhalation of contaminated aerosols generated by birth products and various other excreta shed by infected cattle, sheep and goats. Starting in 2007, the Netherlands experienced the largest outbreak of Q fever ever reported in literature and was linked to episodes of abortion in large dairy goat farms. The dimensions of goat and sheep farms in Switzerland differ substantially from those in the Netherlands. However, the likelihood for a larger outbreak of Q fever in Switzerland is not known. The aim of this project was to study the seroprevalence of Q fever in sheep and goats and to assess the risk for a larger outbreak in humans. Prevalence was determined from a representative sample of 72 goat farms and 100 sheep farms respectively. Samples collected for the 2011 nationwide cross-sectional survey to document freedom from *Brucella melitensis* were analyzed by ELISA. Herd level prevalence ranged from 5% in sheep to 11.1% in goat flocks. At animal level, prevalence was 1.8% in sheep and 3.4% in goats, respectively. In addition, we quantified the bacteria in aborted material using PCR, in order to obtain information on the extent of environmental contamination following abortions. Furthermore, these samples will be used to identify virulence factors, as well as the genotypes present in Switzerland. A literature search on Q fever epidemiology was used to identify risk pathways and to generate a qualitative risk assessment for human infection. A sensitivity analysis will reveal which factors have the greatest influence on the probability of larger outbreaks of Q fever in humans. These results form an important basis for future prevention and control strategies for Q fever.

Specification of data collection on animal diseases to increase the preparedness of the Animal Health and Animal Welfare Panel (AHAW) of the European Food and Safety Agency (EFSA) to address questions from risk managers

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Risk assessment is a core part of EFSA AHAW panel tools used to address questions from risk managers. The lack of accurate quantitative data and a standardized methodology to collect data for risk assessment may delay the production of accurate scientific opinions and limit the use of formal and structured quantitative risk assessments. Therefore, the aim of this project was to develop a methodological framework stating how to specify the data needs in accordance with the type of risk questions and the relevant risk assessment methods. To do so, we started by reviewing AHAW opinions adopted between 2004 and 2010 (WP1). This review permitted identification and categorization of the most recurrent risk questions, the related list of data needs and the suitable risk assessment methods. Subsequently an inventory of the possible sources of needed data and assessment of their availability and accessibility and description of their format were performed (WP2). A metadata model for data collection and documentation was then proposed (WP3). The outcomes and conclusions from the three first work packages was used to propose a structured approach to data collection in regard to the expected future risk questions. Based on four case studies related to *Echinococcus multilocularis*, *E. granulosus*, Porcine Reproductive and Respiratory Syndrome and Venezuelan Equine Encephalitis, we conclude that this approach will lead to more efficient preparatory data-collection, and will therefore enable more rapid response to new risk managers questions.

Evaluating a group based intervention for improving meat safety in a Nigerian wet-market

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Developing countries have rules and regulations for assuring food safety; yet food-borne disease remains a major cause of sickness and death. Approaches based on collective action and capacity strengthening could complement traditional inspection and enforcement. We evaluated a participatory training intervention to improve food safety among meat processors and retailers (butchers) in Bodija Market, Ibadan, Nigeria. Butchers are traditionally self-organised into groups. An interactive training workshop was held for group representatives who were selected to pass on information and training to their group. Meat hygiene knowledge, attitude and practice was assessed before attending the workshop and afterwards (n=63). It was also assessed for those who did not attend the workshop (n=68) but were intended recipients of training through their group. Microbiological quality of meat was assessed before and after the workshop (n=400 samples). After the workshop, participants significantly improved knowledge, attitude and practice in key food safety aspects; specifically, understanding sources of contamination and food-borne diseases, use of bleach and disinfectant and hand-washing. Participants also shared information with an average of 18 other group members and improvements were seen in group members who did not attend the workshop but received training through their group. Microbiological quality of meat sold also significantly improved after the intervention. The intervention cost \$8.82 per butcher reached and was estimated to reduce risk of diarrhoea (costing patients \$4.46 on average) by at least 5%. In conclusion, participatory, group-based methods targeted at meat processors and retailers can improve meat hygiene knowledge, attitude and practice as well as the microbiological quality and hence safety of meat.

One Health Hubs in Asia: building a sustainable platform for conducting interdisciplinary regional epidemiology activities

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The basis for 'One Health' activities is joint consideration of the human and animal health aspects of zoonoses, and implications for development of disease control programs. However, a challenge faced by national disease program managers who have embraced the One Health paradigm is maintaining their enthusiasm long enough to effectively institute change in their organisations. To meet this challenge, we have designed a two-phase One Health training program using a blended teaching model that incorporates web-based and face-to-face delivery modes. The program consists of two phases: phase one provides Masters level training in epidemiology, and phase two establishes interdisciplinary professional networks through an activity-based collaboration platform. Phase 1 has been completed in 7 South Asian countries with coordinated training of doctors and veterinarians that used shared learning resources. Approximately 65 health professionals have completed the training in English, with a second cohort from Central Asia starting in 2012 in Russian. Phase two of the One Health training is designed to actively reinforce skills learned by the graduates of phase one. 'Country groups' identify an important zoonosis that can be investigated through application of their newly acquired epidemiological skills. Projects are implemented to achieve tangible benefits in management of a zoonotic disease. For many of the zoonotic diseases (HPAI, brucellosis, rabies) cross-border and cross-discipline cooperation is essential for effective control. National 'One Health Hubs (OHHs)' are virtual entities operated by the country groups and have the endorsement of relevant health ministries. Underpinning all OHH activities is 'HubNet' – a regional professional network that provides powerful web-based tools for communication, collaboration and resource sharing, within and between the OHHs.

***Mycobacterium avium* subsp. *paratuberculosis* in pasteurised milk: a quantitative exposure assessment**
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Mycobacterium avium subspecies *paratuberculosis* (MAP) causes paratuberculosis or Johne's disease (JD); a chronic granulomatous enteritis which mainly affects ruminants. A potential role of MAP in the pathogenesis of Crohn's disease and development of type I diabetes has been suggested. However evidence to support these links is inconclusive. The potential contribution of milk to human exposure is still a debatable topic. Using available published data and the results of expert elicitation, a stochastic exposure assessment was developed to estimate the likelihood of human exposure to MAP via pasteurised milk. The assessment consisted of two modules: the 'farm module', detailing the amount of MAP reaching bulk milk tanks and the 'pasteurisation plant module', which estimated the level of exposure in pasteurised milk and the frequency with which positive samples would have been detected (using a detection limit of 0.023bacteria/ml). The potential impact on MAP concentration following different farm-level control measures and different \log_{10} reduction cycles due to pasteurisation were evaluated. Given our settings, we estimate that the maximum MAP concentration in pasteurised milk was 1.1×10^{-6} cells per ml (minimum 1.82×10^{-11} ; median 1.5×10^{-9}). Our assessment suggests that, at the farm level, removing heavy shedders would be the most effective control measure to reduce human exposure to MAP via consumption of pasteurised milk. At processing plant level, \log_{10} reduction due to pasteurisation would need to be 2 fold reductions to detect positive samples. We hypothesised that placing milk from positive farms into the skimmed milk process, using microfiltration, could be a feasible alternative to reduce human exposure via pasteurised milk.

Consumer phase risk assessment of a ewe raw milk traditional cheese (Serra da Estrela)

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The goal of this work was the development of a *Listeria monocytogenes* (LM) risk assessment for a traditional ewe raw milk traditional cheese (Serra da Estrela cheese). The assessment focused on the phase from retail to consumption and it aimed to: estimate the consumer exposure to LMs; estimate the probability of infection resulting from that exposure; identify the impact on the risk of the different consumer behaviors in the conservation and consumption patterns and identify critical data gaps to characterize the risk of LMs infection in this product. To model the exposure the following parameters were included in the model: prevalence of contaminated cheeses, level of contamination, serving sizes and time-temperature of storage profiles before consumption. On a previous study at the retail level, Serra da Estrela had a prevalence of LM 39.6% IC95% [30.1-49.8%] of the sampled cheeses positive and with a concentration that ranged from <10 cfu/g to 4.9×10^3 log cfu/g. A sensitivity analysis was done with a variance based method and first and second order indices were estimated to evaluate the impact of the input variable uncertainty in the risk estimate. The estimated marginal risk per portion ranged from 2.1×10^{-9} to 2.1×10^{-6} depending on the optimum growth rate assumption and corresponding to an expected number of LM cases resulting from the consumption of this cheese from 0.002 to 1.7 per year. Only the initial concentration at retail had a small main order effect on the output with considerable total effects from aW, temperature, maximum storage time and pH and initial concentration. The results of this risk assessment, suggest that this product can be the source of a non-negligible risk to the consumer and that the storage behavior has a strong impact on the risk of *L. monocytogenes* infection. Nevertheless, there is a considerable uncertainty on the estimates, resulting from data gaps on the specific optimal growth rate in matured Serra da Estrela Cheese.

Increased biofilm formation of *Campylobacter jejuni* isolated from slaughterhouse

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Despite numerous investigations and programs established to control *Campylobacter* during broiler processing, poultry meat remains the major source of human campylobacteriosis. Therefore the main routes of broiler carcass contamination during slaughtering are important to investigate. With this aim we have traced the changes of *C. jejuni* genotypes within one broiler flock from the beginning of rearing to the final product at the slaughterhouse. Genotyping of 345 collected isolates of *C. jejuni* revealed ten different flaA genotypes of *C. jejuni* along the broiler meat production chain. Broiler fillets were mainly contaminated with genotypes found on the surfaces of slaughterhouse equipment and in the scalding water after cleaning and disinfection. All twelve genotypes were further tested for biofilm formation and their phylogenetic relationship. Interestingly, the results showed a correlation of the origin and the phylogenetic relationship of the *C. jejuni* isolates and their ability to form biofilm. Only two strains were not able to develop biofilm, while most of the *C. jejuni* isolates originating from meat and surfaces of the slaughterhouse formed biofilm after both 24, 48 and 72 hours of incubation. Interestingly, these biofilm forming strains were phylogenetically related to each other. Furthermore, two strains that were isolated after disinfection developed significantly more biofilm after 24 hours of incubation than the remaining strains. A comparative genomic analysis using DNA microarrays showed genetic differences as the gene content of strains that efficiently formed biofilm were different from those that did not.

the veneto region information system: introduction to gesvet, the procedure used by the veterinary services

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Following the food crisis that hit Europe in the '90s, data collection and sharing along all the steps of the food production chain ('from farm to fork') have become fundamental to guarantee food safety and transparency for consumers. Since 1994 the Veneto Region has established the Regional Data Bank (RDB) of livestock holdings and related industries, which also constitutes an informative base to be used for survey purposes. In late 2000, in order to comply with the European legislation on food chain safety, several satellite procedures were joined to the RDB, thereby setting up the current Regional Information System (RIS). The aim of this paper is to highlight GESVET, a computerised program for the recording and management of activities performed by the Veterinary Services (VS) of Local Public Health Units. The system is based on internet technologies (HTTP, SOAP, XML, Web Services) with a strong logic of integration (common master data). Access is controlled by user authentication. The internet application is implemented in Delphi 2010 (object-oriented language). The Web Server used is Apache 2.2 (Apache © Software Foundation). GESVET is organised in different modules: outbreaks of infectious diseases; slaughterhouse inspection; inspection & surveillance; registration of food industries according to Regulation EC 852/2004; animal transport. The system is designed to record and manage VS activities and it also allows the printing of each required document and the management of computerised registers (e.g. slaughter register). The current number of GESVET users amounts to 381; a specific call-centre has been activated also to check for data quality. The GESVET procedure constitutes a suitable operational tool for uniform recording and functional planning of Public Health activities. Data quality is the main crucial point in RIS effectiveness and every effort is made to avoid mistakes in the archives.

Using an interdisciplinary approach to investigate food-borne disease in Thailand

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Thailand has undergone an enormous economic development over the last 20 years, and public awareness of food-borne disease (FBD) risk has increased with urbanisation and tourism. The true impact of FBD is unknown due to significant underreporting. The cultural diversity, economic variation and tropical environmental conditions result in a highly complex system where traditional western food safety approaches to risk management are not effective. Instead expertise from multiple disciplines is needed to understand the drivers of the system which influence the occurrence of FBD. Given the scarcity of data, extensive use is needed to be made of qualitative data. As a first step, scientists from the social, anthropological, medical, economic and veterinary sciences developed a conceptual diagram of the key factors involved in the underlying system. As a second step, the existing knowledge in relation to the relevant system components was summarised, and information gaps were identified. Then baseline data was collated on FBD occurrence based on official reports as well as available literature. Recognising the data limitations, focus group discussions were used to obtain further data on disease risk perception and relevant risk behaviours. Livestock population data was obtained to describe spatial and temporal trends in productivity. Demand and consumption of animal-derived foods was characterised using national data. Expert opinion was collated on the processes along the livestock value chain, including food processing and selling, such as through street food vendors. The outcome of the research was a synthesis of the knowledge from different disciplines generated as part of this work, and will be used to inform further research and risk management, specifically in relation to human behaviour change.

Heavy metals epidemiology in livestock

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The National Plan for the Control of Residues and Contaminants (PNCRC) is a Brazilian governmental program that oversees chemical hazards in several food production chains. Relying on certified laboratories, the Plan's results are representative for all target species due to its systematic probabilistic sampling based on the binomial distribution, which enables detection of violations in arguably low-prevalence scenarios. As such, the PNCRC depicts the levels and the distribution of residues and contaminants in several foods on a nationwide basis. Between 2006-2010, the PNCRC database was divided according to three categories as applied to bovine tissue samples collected at abattoirs under Federal Inspection, with inferences being mainly related to the last rearing farm. Categ. 0: Results < quantitative limits (QL) Categ. 1: QL ≤ results < maximum limit (ML) of Brazilian law Categ. 2: Results ≥ ML For the case of heavy metals (As, Cd, Pb, Hg), a national distribution given the three categories is displayed on a thematic map. In addition to the fact that map results suggest that non-compliant results are rare, the plan's robust surveillance rationale ensures safe levels of consumer exposure to heavy metals associated with beef products. Specifically, a control optimization is proposed for the orange spotting to further reduce observed levels to 'as low as reasonable achievable' by using ever-stricter good agricultural practices (GAP). As contamination of food producing animals with heavy metals is mostly due to environmental rather than deliberate sources, conduction of descriptive epidemiological studies based on thematic maps is of key importance to initiate bona fide risk assessment and management protocols.

Epidemiology of bacterial infections in livestock and their human keepers in Western Kenya

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We report on the results of work on three bacterial zoonoses arising as part of a large project dealing with zoonotic infections amongst livestock and the farmers who keep them. Domestic livestock are an important source of zoonotic infections to humans, particularly in rural parts of Africa. Understanding the interactions between people and their domestic animals, and the transmission of zoonoses between them, is of vital importance in creating the evidence-based disease control policies that are required to protect both human and animal health. The wider project addresses the impact of co-factors (a condition that influences the effects of another condition) on the epidemiology of, and burden imposed by, these diseases. We describe the results of an analysis of three bacterial infections of major public health significance (q-fever, brucellosis and tuberculosis), with a focus on infection in both domestic cattle and humans. In particular, we explore the spatial distribution of these infections in Western Kenya, and explore patterns of infection at the household level in both species (n=450 households). In addition, using multivariate methods, we examine non-zoonotic co-factors as explanatory variables for the individual pathogens, and quantify the risk of co-infections with multiple bacterial zoonoses. We use our wealth of ancillary risk factor data to explain the patterns observed.

Analysis of the baseline survey on the prevalence of *Salmonella* in holdings with breeding pigs, in the EU, 2008: factors associated with *Salmonella* pen positivity

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A European Union-wide *Salmonella* baseline survey was conducted in 2008 in holdings with breeding pigs. A total of 1,609 randomly selected holdings housing and selling mainly breeding pigs (breeding holdings) and 3,508 holdings housing commercial breeding pigs and mainly selling pigs for fattening or slaughter (production holdings) were sampled. In each selected holding, pooled fresh faecal samples were collected from 10 randomly chosen pens of breeding pigs over six months of age, representing the different stages of the breeding herd, and examined for the presence of *Salmonella*. Analyses at country-level demonstrated a strong positive association between the prevalence of *Salmonella*-positive breeding holdings and the prevalence of *Salmonella*-positive production holdings, suggesting a vertical dissemination of *Salmonella* between the holdings. Based on the combined results from breeding and production holdings, multivariable regression analysis showed that the odds of *Salmonella*-positive pens with pigs increased with the number of breeding pigs in the holding and with the following pen-level factors: flooring systems other than slatted floors or solid floors with straw, presence of maiden gilts, number of pigs per pen, feed of commercial compound origin or pelleted feed. Methodology, results and conclusions will be presented.

Practicality of on-farm interventions for *Salmonella*: a survey of pork producers' perceptions

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Control of foodborne disease is of importance to all in the food production chain; multiple points exist along the chain where interventions can be considered. How practical an intervention is to implement effectively on the farm should be considered. As part of a larger project on ranking different interventions for *Salmonella* control, a survey of pork producers was developed. The objective was to develop a 'practicality' score for six interventions with potential effectiveness for controlling *Salmonella* on-farm. In 4 provinces in Canada, a questionnaire was delivered to 100 randomly selected producers. Questions asked related to demographics, issues in using interventions and ranking the interventions in terms of practicality. The interventions asked about were the use of antibiotics, acid in feed or water, disinfection, meal instead of pellets, wet feed and vaccination. 220 surveys were returned. Respondents capacity for finisher pigs ranged from 120 to 290,000. The use of different interventions varied with disinfection being used most commonly (201/220) and vaccination being used least commonly (25/220). Producers were asked about the labour, equipment, paperwork and 'problems' associated with each intervention. They were also asked to rank the interventions with respect to their practicality. The summary practicality score was a reasonable predictor of producers ranking. Users of specific interventions gave lower practicality scores ($P < 0.01$). For those who used interventions: 'Meal' had the best (lowest) practicality score ($P = 0.003$). The most realistic assessment of the practicality of an intervention is likely from those who implement the intervention. This survey allowed us to get input from a wide variety of pork producers and will provide a numerical estimate for practicality for use in a larger decision analysis project.

Detection of dioxins in meat chickens in slaughterhouses submitted federal inspection service in Brazil

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Dioxins are chemical compounds biphenyls, most resistant to chemical and biological degradation by most microorganisms, it is human carcinogen, can be found in various environments such as soil, vegetation, air, water and marine sediments. It is estimated that 90% of human exposure is by ingestion of contaminated food, having a cumulative effect especially in high-fat foods such as beef, dairy, milk, chicken, pork, fish and eggs. A tolerable daily intake for dioxin is 1-4 pg/kg body weight /day by World Health Organization. Brazil is the leading exporter of chicken meat and the national legislation complies with the parameters set by the European community. This study aimed to detect dioxin in chicken meat derived from regulated abattoirs for export. Was collected from 500 g of fat cavitation lots coming from slaughterhouses 41 randomly selected, totaling 253 samples in the period between 2009 and 2010, whereas incidence of 1% and confidence interval of 90%. The detection of dioxins was performed by gas chromatography and mass spectrometry, high-resolution limit of quantitation of 1 pg/g of the main dioxin congeners found in foods. All samples were negative for dioxins. The spatial distribution of the slaughterhouses was plotted on maps by MAPINFO program and geographical coordinates were obtained by the finder global positioning Google Earth, to the address provided by the Brazilian Ministry of Agriculture. It is concluded that the chicken slaughterhouse submitted to the Brazilian Federal Inspection Service meets international demands for export. Funding: INCT-Pecuária

Consumer conservation practices and consumption habits: the case of Serra da Estrela Cheese in Portugal

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Despite their increasing concerns on food safety, consumers fail often to apply good practices in food handling, storage and preparation which may increase the risk of food borne outbreaks. This work aims at characterizing consumer practices related to conservation and consumption of Serra da Estrela cheese (a traditional matured soft sheep cheese). Consumers were approached in shopping areas of Oporto (north), Lisbon (center) and Algarve (south), during the period May to July 2011, when buying Serra da Estrela cheese or similar and provided with explanation of the study objectives. A kit was prepared including a temperature recorder (Thermochron® 1921G) in a cardboard support covered with vegetal paper, a questionnaire, a pre-stamped envelope and a promotional pen. Enrolled consumers were asked to conserve the cheese on the support, in contact with the thermometer, and record the rate of consumption, aspects of family composition, people consuming the cheese and place of storage. After a week spent at consumer's home, both questionnaire and thermometer were to be returned to researchers in postage-paid envelope. The number of consumers willing to participate were 51 and 39 returned the information (related to 107 persons), resulting on a response rate of 76%. Results indicated that only 2% belong to the pregnant/immunodepressed group, 13% were children, 21% over 60 years old and the majority, 64%, had between 15 and 59 years old. Average portions had 40.2 g (SD 57.1) and daily consumption per person was 106.5 g (SD 148.7). The refrigerator is the preferred storage in the warmer months (60%) and cheese is left at room temperature in the winter months. Data obtained from temperature data loggers varied between -0.5 °C and 34.5 °C (average of 17.0 °C). This study allowed the collection of quantitative data at consumer level, important for microbial risk assessment and for the understanding of possibilities of risk management at this level.

Prevalence of hepatitis E virus antibodies in serum samples of Austrian domestic pigs

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The ubiquitous nature of the Hepatitis E virus (HEV) in domestic pigs and the genetic similarity between porcine and human isolates of the genotype 3 supports the potential to be a zoonotic disease (1) The high seroprevalence of HEV antibodies in domestic swine from many Asian, North-American (2) and some European countries (3) has already been reported, indicating a worldwide distribution in swine herds. In Europe, the seroprevalence of anti-HEV antibodies (HEV-Abs) in domestic pigs ranges from 30% to more than 90% (4). For our study, serum samples from a total of 1,367 pigs out of 154 different farms were collected from different slaughter houses in Austria. The sample range varied between 1 to 34 animals per farm, giving an average of 8.9 tested pigs per herd. The samples were tested by PrioCHECK® HEV Ab porcine Kit (Prionics) to detect HEV-Abs, following the instructions recommended by the manufacturer. From 1,367 tested pigs, 630 (46%) were HEV-Ab positive. Concerning the 154 tested farms, in 118 (77%) of these farms a minimum of one animal was positive for HEV-Ab. On the other hand, in 36 (23%) of all tested farms no HEV-Abs were detected. In 16 of the 36 negative farms a minimum of 16 animals was tested, indicating a relative high percentage of Austrian farms being HEV-Ab negative. HEV-3 has been recently described in Austrian domestic pigs (3). The results obtained in this preliminary study lead to the assumption that the prevalence in Austria may be lower than reported in other countries like Spain (98%) or the USA (100%) (4).

Building a foundation for ‘One Health’: an education strategy for capacity development in epidemiology and biosecurity

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The emergence of diseases such as SARS, H5N1 and H1N1 influenza from animal source populations has exposed a global shortage of capacity in dealing effectively with such threats, and has been a driving force behind the ‘One Health’ movement. The likelihood of emergence of novel infections is the highest in the developing world, which is paradoxically where this capacity shortage is most acute. Capacity development is urgently required, and education is a key element of this. In 2010, Massey University established a predominantly distance-taught degree programme for public health doctors and veterinarians, with a focus on epidemiology and disease control. Two degrees were established: a Master of Public Health (Biosecurity), and a Master of Veterinary Medicine (Biosecurity). The programme was first offered to 70 participants from Afghanistan, Bangladesh, India, Nepal, Pakistan and Sri Lanka. The teaching model was determined by two fundamental considerations. Firstly, the courses were designed specifically for online delivery, so that the candidates could remain in their functions. The courses adopted ‘best practice’ in e-learning techniques; they emphasized effective collaboration, problem-based learning, small-group activities and facilitated discussion. Secondly, the courses were designed to contain relevant subject matter. The curriculum consisted of one block of basic epidemiology courses, which was taken by all candidates, followed by a block of veterinary and public health specialty courses. The attrition rate over the 15-month duration was low, and the courses were positively evaluated by the participants. A positive outcome was the forging of linkages between veterinarians and public health professionals, as well as between professionals from different countries. To strengthen such collaborations, further activities, which aim to develop a regional ‘One Health’ professional network, are currently underway.

Impact of intervention failures and vaccination on beef carcass *E. coli* O157 contamination

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Substantial progress has been made in decreasing the contamination of beef with *Escherichia coli* O157. Previous efforts have focused primarily on slaughter interventions to decrease contamination. Still, occasional contaminated lots of meat are detected and outbreaks continue to occur. These contaminated lots are hypothesized to occur during ‘event’ days when several control failures converge to produce the contaminated lot of meat. This may be due to a combination of increasing quantity of O157 entering the slaughter facility on cattle, increased transfer from hides to carcasses, or the failure of control methods within the slaughter facility. Recently, vaccines have emerged as a tool in pre-harvest O157 control. Data indicate vaccines decrease prevalence and shedding concentration however they may also impact hide prevalence and concentration. Utilizing @Risk in Microsoft Excel we incorporated data from published scientific literature into a Monte-Carlo framework to estimate the prevalence and concentration of carcass contamination with *E. coli* O157 with and without vaccination and following a series of slaughter control failures. Vaccine efficacy was modeled based on published scientific literature. Additionally, the model examined the impact of a possible vaccine effect on hide prevalence and concentration of O157 on arrival at the slaughter facility. High hide to carcass transmission of O157 and low efficacy of carcass intervention in the slaughter process were modeled as control failures. Slaughter control failures markedly increased and vaccination decreased carcass O157 prevalence and concentration however the majority of the decrease was related to the potential impact on hide prevalence and concentration. These results indicate the need for research to evaluate the full range of vaccine effects in the value of vaccination to pre-harvest beef production.

Risk factors and control of *Salmonella enterica* in Danish broiler flocks 2001-2011

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The objective was to identify risk factors and to evaluate the effect of legal orders during the study period. The study was based on data from the Danish *Salmonella* database. Sock samples from the litter of 37428 broiler flocks were collected 3 weeks before slaughter and tested for the presence of *Salmonella enterica*. The exposure variables comprised hatchery, number of flocks and houses per farm, season, year, geographical region and number of flocks per house per year per farm. The data were analysed in multivariable logistic regression with random effect of farm and with the broiler flock as the response unit. All cases were considered incidents as parent stock tested negative for many years. The overall incidence risk was 1.36% with 509 test positive flocks during the period. The annual incidence risk varied from 1% in 2001 to 2.1% in 2005 followed by a general decrease from 2005 to 2011 with only 0.6% flocks infected. The final model included all exposure variables except hatchery. The odds ratio (OR) increased with decreasing number of flocks and increasing number of houses per farm, and when number of flocks per house per farm year was ≥ 3.5 . The OR was higher during summer and autumn compared to winter and spring. The OR varied significantly among regions and among years. Danish poultry producers initiated a voluntary control program by 1992 and since 1994 nine legal orders have been issued; 5 of these were enforced during the study period in 2003, 2005, 2008, 2009 and 2010. Major intervention points have been implementation of sock sampling 3 weeks before slaughter; request of farm eradication plans; longer empty periods between flocks and public supervision in positive farms. Concurrently there has been a declining trend in the incidence risk since 2005. The results indicate there is an effect of legal orders, and that infections of broiler flocks take place in the rearing units, most likely due to insufficient biosecurity procedures.

A relational study between *ante-mortem* findings and *post-mortem* condemnations in three beef abattoirs

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All cattle presented for slaughter undergo *ante mortem* (AM) examination and are categorised into 3 groups: (1) casualty animals accompanied to the slaughterhouse with a veterinary certificate; (2) remarkable animals that present without certification but have defects identified at AME; and (3) apparently healthy animals (AHA). *post mortem* (PM) condemnation of meat is regarded as the ultimate definition that an animal or part of is unfit for human consumption. This study examines certification, AM and PM data in 3 beef abattoirs over a 3 year period. 216 certificates were examined. 763 animals had all or part of their carcasses condemned at PM. Casualty animals accounted for 14.5% of all condemnations and 11.3% of full carcass condemnations. AHAs accounted for 69% of full carcass condemnations. Emaciation, oedema and toxic conditions accounted for 80% of full carcass condemnation from AHAs and therefore went undetected at AM resulting in high risk animals being slaughtered amongst truly healthy animals and are a potential source of cross-contamination. Such findings highlight the need for enhanced AM detection of these conditions in the development of a more risk based meat inspection system. The present study prompts research into the practical application of body condition scoring and the development of rapid detection methods for acute phase proteins and serum albumen levels to aid enhanced AM.

What the eye doesn't see: 'visual' versus traditional inspection of 'free-range' fattening pigs

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Modernisation of *post-mortem* inspection regulations in the EU means that, if certain requirements are met, fattening pigs reared under controlled housing conditions in integrated production systems since weaning need only undergo visual inspection. This does not involve palpation and incisions and may reduce the risk of cross carcass contamination. Uptake by the UK pig industry has been low because slaughterhouses accept a mixture of indoor and outdoor reared pigs throughout the day; the latter still have to be inspected by traditional means. A qualitative risk assessment of the comparative risks to public and animal health from visual inspection of indoor and outdoor pigs concluded that the risk was negligible for all pigs. However, there were insufficient data to assess if there would be a reduction in food-borne risk due to reduced microbiological carcass contamination. Our study is a field trial of visual versus traditional meat inspection of fattening pigs from non-controlled housing conditions. Field work is on-going until April 2012. Batches of such pigs are inspected by both visual and traditional methods and carcass sponge samples are taken from a subset of pigs on the slaughter line after each of the inspection points. The microbiological work includes total aerobic plate counts; Enterobacteriaceae counts, and the isolation of *Salmonella* and *Yersinia*. Obstacles to the implementation of a risk-based visual-only inspection system are also being investigated. The data generated from these investigations will be used to inform a comparison between the two inspection methods, to re-assess the risks to animal and public health and to determine the impact of implementation of a risk-based visual-only inspection system for all UK pigs. We present the outcomes from this study.

Active surveillance for MRSA in the environment and canine patients of a small animal teaching hospital

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Infectious disease prevention and control programs are critical for managing pathogens such as Methicillin Resistant *Staphylococcus aureus* (MRSA) in veterinary hospitals. To understand the molecular epidemiology and ecology of this bacterium in the hospital environment, an active MRSA surveillance program was established at the OSU Veterinary Medical Center. Molecular epidemiological analysis was performed on environmental and canine-origin MRSA isolates. Antimicrobial susceptibility testing, SCCmec typing, PFGE typing, and dendrographic analysis were used to characterize and analyze these isolates. Overall, 13.7% of the surfaces sampled were contaminated with MRSA through the year. During this time, 91.4% of the environmental isolates collected were SCCmec type II and 88.9% USA100, which is consistent with HA-MRSA. This reflects a low diversity of MRSA strains circulating in the hospital. One unique PFGE pulsotype was the most prevalent for 5 consecutive months, circulating among different surfaces and hospital locations. It was later replaced by a combination of several different strains, some of which were only detected once on one surface, and others that were found up to 4 consecutive months in different locations and surfaces. The molecular analysis of isolates also suggested that incoming MRSA positive dogs were capable of introducing a new strain not previously seen in the hospital environment. Based on these results, it is evident that once a MRSA strain is introduced into the hospital, it can be easily spread and maintained in the environment over time. This information has been used to develop biosecurity and biocontainment protocols with the goal of decreasing student and personnel occupational exposure to MRSA, in addition to protecting our patients and their owners from potential nosocomial or zoonotic transmission of this pathogen.

Leptospirosis Incidence and Risk Factors in Meat Workers in New Zealand

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Leptospirosis is an endemic bacterial disease of sheep, beef cattle and deer in New Zealand and currently the most important occupational zoonotic disease in meat-workers and farmers. Apart from dairy cattle and pigs, livestock are rarely vaccinated. A study in meat workers revealed a sero-prevalence against *L. interrogans* sv *Pomona* (P) and/or *L. borgpetersenii* sv *Hardjobovis* (H) of 10-31% in 4 sheep, 19-17% in 2 deer and 5% in 2 beef plants. The objectives of this study were to determine the incidence of leptospirosis infection in meat workers, to estimate the relative risk of putative causes of infection with *Leptospira*, and to evaluate the proportion of workers in the population with flu-like disease attributable to new infections. We conducted a cohort study in 8 abattoirs slaughtering sheep, cattle or deer. Sera were collected twice from 592 participants in 2008-2009 or 2009-10 and tested by the Microscopic Agglutination Test for P and H. Information on risk factors including personal data, workplace, lifestyle and clinical history were recorded and analysed by multifactorial logistic regression. Forty-nine of 592 (8%) participants seroconverted to either P and/or H. Forty-seven of the newly infected persons worked in sheep plants. In sheep plants, the annual meat plant specific infection risk was 12%. In workers of plants processing other species, the incidence was 0% (deer) and 1.2% (mainly beef cattle). Risk factors for new infection in sheep plants were worker position and time worked in the meat industry. The average annual risk of experiencing flu-like symptoms due to infection with *Leptospira* was 2.7%. The seroconversion demonstrated significant exposure to the two tested *Leptospira* serovars in sheep meat workers. Estimates of the contribution of *Leptospira* to 'flu-like' illness and days away from work are helpful for estimating the economic impact of leptospirosis. The identified risk factors and possible control measures will be discussed in detail.

Meta-analysis to evaluate efficacy of a three-dose regimen of type III secreted protein vaccine at reducing the presence of STEC O157 in the feces of feedlot cattle

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Pre-harvest control of *Escherichia coli* O157:H7 (STEC O157) might prevent human illness by decreased carriage by live cattle and reduced transmission to carcasses or the environment. Immunization of cattle with a type III secreted protein (TTSP) vaccine inhibits colonization of cattle. Our objectives were to perform a meta-analysis to estimate efficacy of a three-dose regimen of TTSP vaccine at reducing the presence of STEC O157 in the feces of feedlot cattle, and to test for heterogeneity of vaccine effect. Pen-level data (n=182 pens, 1,462 cattle) from four natural exposure randomized controlled vaccine trials conducted from 2002-2008 at the University of Nebraska-Lincoln were analyzed. Factors explaining the probability for a positive fecal sample were tested in a generalized estimating equations (GEE) logistic regression model adjusting for clustering of repeated test-periods within block. Clustering or potential confounding by study was accounted for by treating study as a fixed effect. Relative risk was estimated from a log-binomial GEE model. STEC O157 was detected from 661 of 5,451 post-vaccination samples. The probability to detect STEC O157 post-vaccination was 8.4% and 15.8% in vaccinated and unvaccinated cattle, respectively. Interactions between vaccination and (1) study; (2) prevalence of control pens within each time-place cluster; and (3) days from vaccination were not significant or had poor model fit. Adjusting for study, cattle in pens receiving three doses of vaccine were less likely to shed STEC O157 (OR=0.46 P<0.0001). Model adjusted vaccine efficacy was 48% (95% CI, 0.38-0.58). We concluded that a three-dose regimen TTSP vaccine reduced the probability to detect STEC O157 in the feces of cattle, and vaccine efficacy was not modified by factors we measured.

The parasitic phase of *Ostertagia ostertagi* and *Cooperia oncophora*: quantification of life history traits using systematic review and meta-analysis techniques

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Ostertagia ostertagi and *Cooperia oncophora* are the two most common gastro-intestinal (GI) nematodes of cattle in temperate climate regions and pose important constraints on animal productivity. These nematodes have a direct life-cycle, consisting of a free-living and a parasitic phase. During the parasitic phase, three parameters that determine the parasite density within the host are the establishment rate, adult mortality rate and fecundity rate. Transmission models and nematode control will benefit from more accurate estimates of these life history traits and their variation. The aim of this study is therefore to quantify the three main life history traits of the parasitic phase of *O. ostertagi* and *C. oncophora* and to assess factors affecting these traits. A literature search was conducted using a systematic review protocol to find experimental trials in which cattle were infected with *O. ostertagi* or *C. oncophora*. Using general keywords a first search resulted in 5,266 potential publications. Next, a title-based selection generated 400 infection trials. An article-based selection resulted finally in only those trials which contained the needed data on infection mode and dose, number of animals used, host age, faecal egg counts and intestinal worm burden. Summary estimate data of the different trials were used to compute overall estimates of the life history traits by inverse variance weighting. Subsequently, these data were compared to data from 8 infection trials conducted in our own laboratory. Finally, probability density functions were fitted to the data and a set of regression models was used to evaluate the influence of host age, infection mode and dose, number of infections and duration of exposure.

Use of simulation to calculate sampling unit probabilities to be in the sample

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Data analysis from surveys should consider design features to make parameters population estimations, so it being necessary to know the probability of each sampling unit entering the sample. Many times these probabilities cannot be determined exactly and must be calculated approximately. Simulating, a large enough number of random samples, it is possible to calculate the relative frequencies of inclusion of each unit in the sample. The objective of this study is to show a simulation routine as an effective tool to determine these probabilities compared with the exact probability. As example was used a sampling design for the primary sampling units (PSU) proportional to population size (PPS): in 21 slaughter plants, taking samples of size 5. The population size variable was the volume exported by the different plants. 10,000 replicates were used and the simulation results were compared to those obtained using the exact probabilities, generating the sample space and calculating the exact probability of each sample. All routines were done in Intercooled Stata v.12. The simulation results suggest that the inclusion probabilities of each unit may be determined by simulation of the sampling routine. The methodology proposed by simulation is simple and can be applied to any sample regardless of its complexity, to be precisely matched to the design used.

The use of log-linear capture-recapture modelling to estimate turkey farm population in Canada

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Countries with incomplete farm registries also conduct surveillance to confirm freedom from diseases therefore they need additional options to present the surveillance results. The log linear capture-recapture (CR) modelling approach was originally proposed by Feinberg in 1972 and has been used to estimate parameters of biological populations. The Log linear CR modeling approach has been used for multiple systems estimation, which involves more than two sampling lists of the members of a population. One of the major advantages of log-linear models is to adjust for sampling lists dependencies. The purpose of this paper was to estimate the turkey farm population size in Canada based on series of poultry farm population samples, collected by the Canadian Notifiable Avian Influenza Surveillance System (CanNAISS) pre-slaughter component, from 2009 to 2011. From CanNAISS pre-slaughter component we have three farm sampling lists (k) 2009, 2010, and 2011 with 227, 256, and 330 turkey farms respectively. A list consisted of all turkey farms sampled during a given year. Log-linear CR modelling was applied on three turkey farm sampling lists. In this approach, data are on a form of 2k contingency table for which the cell corresponding to individuals uncaptured by any of the k sampling lists is missing. With three lists, there were eight different possible CR log-linear models, each associated with a distinct estimate. We used the Akaike Information Criterion to select the best model fitting the data. The 95% confidence interval of the estimated number of farms was calculated in SAS using the profile likelihood method. The use of log-linear CR modelling approach was appropriate for estimating the number of turkey farms in Canada.

Modeling the observed population dynamics of *Ixodes ricinus* in Europe depending on weather variables

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The hard tick *Ixodes ricinus* is a Europe-wide major vector of animal and human diseases. Like all arthropods, *I. ricinus* populations are subject to large fluctuations during the different seasons. These variations are due in part to the climate variability and the circadian rhythm. A better understanding of the relationship between abiotic variables and observed tick abundance allows a better prediction for the periods of high or low tick abundance, hence a possibility of a better risk assessment. The objective of this work was to obtain a statistical model describing the population dynamics of *I. ricinus* from astronomical and meteorological variables. A campaign of collect ticks in open environments (mainly forests) has been implemented in France, Belgium and the Netherlands, based on the principle of collecting ticks every two weeks for a full year. In different sites, the observed data have resulted in a population dynamics of *I. ricinus*. Furthermore, for different sites, it was possible to get rainfall, temperature, relative humidity and day length data. We then built a first generalized linear mixed model to estimate abundance of ticks *I. ricinus* where the site is taken as a random variable. The equation of the model is: -Natural logarithm (number of (*I. ricinus* 1)) = f(weekly maximum temperature, minimum relative humidity weekly, monthly precipitation, day length). With f() representing a function. A Spearman correlation coefficient of 0.517 significant (P<0.001) was obtained for the comparison between the simulated data obtained by the statistical model and the observed data collected on sites that did not serve to build the model.

Development of a critical appraisal tool for cross sectional studies

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Evidence based medicine is highly dependent on the ability to critically appraise available literature. There are currently numerous critical appraisal (CA) tools available for observational studies such as cohort and case control studies; however there seem to be limited tools for cross sectional studies. With this in mind we aimed to develop a CA tool specifically for cross sectional studies. Areas that needed to be included in the critical appraisal tool were identified by the authors. A first draft of the tool was created using previously published CA tools for other types of study as a template. STROBE, reporting standards for observational studies, was also used as a guideline as to what should be included in the CA tool. The CA tool was trialled with colleagues within the Centre for Evidence-based Veterinary Medicine, the Population Health and Welfare group within The University of Nottingham, and the Centre for Veterinary Epidemiology and Risk Analyses in University College Dublin. The trials were conducted using different research papers of varying quality that used cross sectional study design methodology. The CA tool was also distributed to an online forum of experts in evidence based veterinary medicine. The analysis identified 30 components that needed to be included in the critical appraisal of cross sectional studies. From each component, one question was created by the research group. The resulting instrument was judged to have good measure of inter-rater agreement, but this seemed to be dependent on the quality of the study. A CA tool for the 'assessment of cross sectional study design' (ACSSD) has been developed. Continued work is required to verify the tool with a focus on the reproducibility of ACSSD in a wider community of researchers.

Documenting livestock movements in the Far North Region of Cameroon

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The goal of our project is to understand the epidemiology of infectious diseases in the ecological context of networks of host movements. Specifically, we want to know how livestock movements affect the epidemiology of Foot-and-Mouth Disease (FMD) in the Far North Region of Cameroon and how the FMD virus (FMDV) behaves in this endemic setting. The region is characterized by relatively high cattle densities ranging from 25 to over 100 animals per square kilometer and a total population of approximately 650,000 animals managed by both mobile and sedentary pastoralists. Regional and international livestock trade routes intersect with the seasonal transhumance routes and pastures used by pastoralists in the region. Although the government collects data on the number of animals vaccinated and sold on the markets, there is no data on the seasonal movements of mobile pastoralists or the trade cattle moving through from Chad to Nigeria. In order to document these multiple and overlapping networks of livestock movements we use a combination of GPS technology and ethnographic methods, including surveys, observations, and semi-structured interviews. In this poster we discuss our methods for data collection and analysis as well as the products and how these help us to understand the ecology of Foot-and-Mouth Disease.

Characterization of cattle transit in the states of Paraná and Santa Catarina, Brazil, 2008

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The international trade rules and the requirements of commercial partners of Brazil in the beef market makes animal defense organisms provide greater accuracy in control of their health products. This work aims to inform research institutions and market chain meat through a methodology of an epidemiological study based on GIS, which aims to characterize the movement of cattle in the States of Parana and Santa Catarina in 2008. The need for the state of Parana become free without vaccination and the state of Santa Catarina maintain their free status without vaccination for FMD, and thereby both increase the area of performance in the export of meat products, demonstrates the importance of knowledge of these regions to encourage programs of prevention, control and eradication of disease in general. The characterization of the geographic areas was divided into three stages: descriptive analysis, spatial analysis and networking flow analysis. These studies were generated through a database provided by the Ministry of Agriculture, Livestock and Supply. The State of Paraná showed some regionalization of flow between the regions of bovine origin and the poles of slaughter, both focused on the north and northwest. The State of Santa Catarina has been focused its slaughter poles in east and southbound, but animals' origin are from different regions of the State. The methodology of this study intends to contribute as an exploratory tool for implementation of strategic actions in systems of surveillance. Funding: CNPq, FAPEMIG and INCT-Pecuária.

A community resource for spatial, temporal and food chain epidemiological modelling to assess risks in bio-terroristic or agro-terroristic crisis situations

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The intentional contamination of food chains with bio-terroristic or agro-terroristic agents is a significant and non-negligible threat. In 2009, the European Commission implemented the CBRN action plan obligating all EU member states to improve preparedness and response capabilities with respect to such threats. As part of the EU-funded AniBioThreat research project, an epidemiological community resource for governmental and scientific bodies applicable in crisis situations (including natural disease outbreaks) is proposed. Freely available at <http://www.eclipse.org>, the Spatiotemporal Epidemiological Modeler (STEM) provides a fully developed open-source software infrastructure for model generation, parameter estimation, simulation and documentation. This framework is extended by a library of animal and human disease models from scientific literature. Maps of administrative boundaries, transportation networks and associated data (e.g. discrete transportation events) can be imported, enabling the integration of real-world commodity flow data into simulations. The generic structure for representation of epidemiological data, transport processes, disease models and contamination scenarios supports an efficient information exchange between stakeholders involved in crisis situations. The framework allows the execution / simulation of user-defined intervention scenarios which could support decision making by risk managers. As a proof-of-concept, the distribution of *Salmonella* from animals to humans via consumption of contaminated meat has been modelled. Simulation results are discussed in the context of available epidemiological data on *Salmonella* prevalence on farm level and human salmonellosis cases in Germany.

Qualitative risk model to estimate bovine rabies occurrence in Brazil

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Bovine rabies is still considered endemic in Brazil and despite the control efforts, the disease still spreads in an insidious way and the main vector is the vampire bat, *Desmodus rotundus*. This project aimed to create a predictive model to estimate the probability of bovine rabies outbreaks in each municipality of 21 out of 27 Brazilian States. The risk was estimated using concepts of receptivity and vulnerability. Questionnaires were sent to the Local Veterinary Units of each State and covered a number of questions related to the surveillance of possible risks, such as: bovine outbreaks, active roosts, bats positivity and spatial changes. The bovine density and geomorphologic features were obtained from national registries and geographic information systems. The risk results were compared with the 417 bovine outbreaks in 2010 distributed throughout the municipalities. Out of 5,016 municipalities accessed, 217 (4.3%) were rated as having a high risk for the virus spread, 1,277 (25.5%) as medium risk, 2,045 (40.8%) as low risk, and 544 (10.8%) as negligible risk. In 933 (18.6%) cases the risk was unable to be determined because the lack of information. From 417 municipalities presenting herbivores outbreaks in 2010, 183 (43.9%) were rated as high risk, 196 (47.0%) as medium, 23 (5.5%) as low and in 15 (3.6%) the risk was not determined. The results showed that places with outbreaks were skewed towards areas with higher risk for the virus spread. In the future, these models could allow the targeting of efforts, adoption of control measures directed to certain locations, optimization of the control team's transit and a better understanding of rabies spread. Additionally, efforts need to be made to stimulate the continuous surveillance of risk and reduce areas with lack of information.

Poster topic 08**Poster 10****Modelling foot and mouth disease transmission in a wild-pig-domestic cattle ecosystem**

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The role of wild animal species in outbreaks of important exotic diseases, such as foot-and-mouth disease (FMD), is a concern in many countries. Disease models have been used to understand disease transmission in wildlife, but to date much of the modelling has been limited by methodological issues and lack of quality data. In Australia, wild pigs are considered to be particularly important because of their widespread distribution and contact with domestic livestock. To assess the potential role of wild pigs in an FMD incursion a good understanding of many factors is required including: wild pig distribution and densities; social organisation and group structures, movement distances, distribution and densities of other susceptible species; and seasonal effects. In this presentation we will describe the development and application of a stochastic spatial simulation model for studying FMD in a wild pig-domestic cattle ecosystem in the Kimberley region of Western Australia. The study region covers a remote, sparsely populated pastoral area (15,000 km²) in northern Australia and contains approximately 80,000 cattle on 6 pastoral leases, and 3,500 wild pigs. The model (coded in the MapInfo/MapBasic® geographical information system software) takes into account important ecological, behavioural and geospatial relationships, such as interaction between the different host species, and the distribution, density and connectivity of the wild pig and cattle populations. It has been underpinned by detailed surveys and data collection in the field.

Assessing surveillance: impact of time to detection on size of foot and mouth disease outbreaks

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Australia is a significant exporter of livestock and livestock products. This trade is assisted by a favourable animal health status. However, increases in international travel and trade, and domestic factors such as land use changes, have resulted in greater risks of exotic and emerging diseases, while public sector resources available for managing risks are static or declining. The need to develop a more consistent national approach to surveillance that allocates resources, according to regional risk profiles has been identified. A study was done to identify and describe risk of occurrence of significant diseases, with Australia divided into 12 livestock production regions on the basis of environment, geography, livestock production and marketing systems. The effects of time to detection on the size of an outbreak of foot and mouth disease (FMD) were assessed through disease modelling. For each of the regions, 1000 model iterations were run, over a period of five weeks without controls, with the index farm and time of year selected randomly to allow for variation depending on where and when FMD is introduced. Information was collected on whether the disease established, mechanisms of spread, number and type of infected farms and spread to other regions, enabling the relationship between outbreak size and time to be quantified. The study found considerable heterogeneity in size of potential outbreaks between regions. There was minimal spread in northern Australia (regions 1-4), but in the more intensive southern areas (regions 7-12) FMD spread rapidly, indicating that delays in detection would have serious ramifications. The work has highlighted the importance of taking regional and seasonal factors into account when assessing disease risks and has provided valuable information to assist preparedness planning in terms of resources required for managing FMD outbreaks in different parts of the country.

Simulation model for the spread of bovine tuberculosis within France cattle herds

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France obtained the bovine tuberculosis free status in 2001 by the European Union. However, the disease incidence recently increased in some departments like the Dordogne, since 2004, and the Côte d'Or, since 2007. Several hypotheses were formulated about the factors supporting the persistence of the disease in this current form (characterized by a low number of animals infected by herd) like the herd type, beef herds being predominant in the Dordogne and Côte d'Or. We built in this work a model of the within herd transmission of bovine tuberculosis, with an aim of understanding the impact of herd management practices on the dynamics of the disease. The model is a discrete time deterministic model. Four health states are considered: susceptible (S), infected without visible lesion but positive with the tuberculin (PPD) intradermal test (I1), infected with partial seizure of the carcass (I2) and infected with offals or total carcass seizure (I3). Several parameterizations were elaborated and compared according to the Akaike's information (AIC). The best parameterization used the frequency-dependent transmission function, and two estimated transmission parameters (β_2 and β_3 , corresponding to the transmission from animals I2 and I3, transmission from I1 animals being considered null). A stochastic version of the model was exploited using the estimated parameter values. Two fictive herds dairy and beef were simulated (n=100 animals) to analyze the effect of the yearly culling rate, and of the maximal cows age. Results showed that both variables have a long-term effect on the dynamics of the tuberculosis in beef herds, whereas only the maximal cows age has an effect in dairy herds.

Managing farms that develop welfare problems during an exotic disease response: a modelling and economic evaluation

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An outbreak of Foot and Mouth disease (FMD) in Australia would have devastating impacts on the Australian economy, including the immediate loss of international market access, disruptions to domestic markets, and the slaughter of thousands of animals. Consequently, Australia invests considerable resources in emergency disease response planning. One issue that has been identified as a concern is that movement restrictions implemented to control an outbreak may lead to serious animal welfare problems as animals are prohibited from moving off farm as part of normal management practices. Intensive pig farms are likely to be at high risk of developing welfare problems during an FMD outbreak given their limited capacity to house growing pigs. A modelling study was undertaken to assess welfare compensation issues and costs that may arise during an outbreak of FMD in Australia. FMD outbreaks were simulated in two intensive livestock production regions. For each region, moderate and severe outbreak scenarios, with four control strategies involving stamping out, pre-emptive slaughter or vaccination were assessed. Three welfare management strategies involving full or partial culling or controlled movement to slaughter were evaluated. An economic evaluation was performed to compare the impacts of the various strategies. Key findings from the study were that under moderate outbreak scenarios when resources are adequate there is minimal difference in outbreak size and duration between control strategies, and welfare issues can be managed effectively with minimal impact on the overall response. Under the severe scenarios, alternate control strategies (e.g vaccination) were more likely to be effective in controlling the outbreak and reducing welfare impacts. The majority of the costs incurred during an outbreak were due to export market closures. The results of the study will aid decision makers in disease preparedness planning by identifying effective management strategies that reduce welfare problems.

Fractional polynomials for modelling continuous predictors

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Good modelling practice in epidemiological studies involves evaluation of the linearity of the relationship between any continuous predictor and the outcome in any sort of regression model. If the assumption is evaluated and found to be violated, categorization of the predictor is frequently employed to rectify the situation. However, this involves assuming a stepwise relationship exists between the predictor and the outcome, and this is not usually biologically tenable. The use of a polynomial function of the predictor has the potential to avoid the loss of information associated with categorization. In particular, fractional polynomials may be used to model a wide range of shapes of relationships with only a few predictors, hence balancing the twin objectives of good fit and parsimony. Fractional polynomials are generally more flexible than conventional polynomial, but remain somewhat resistant to local-influences, making them suitable for predictions. The use of fractional polynomials involves identifying the best combination of power terms from a predefined set of power terms (usually: -2, -1, -0.5, 0, 0.5, 1, 2, 3 plus combinations with the log transformation). Models of different degree (number of power terms) can be compared using the Akaike Information Criterion. The use of fractional polynomials will be demonstrated using some synthetic data along with data from 2 recently completed studies. The first is an evaluation of the relationship between ELISA optical density ratios (ODRs) from an *Ostertagia* antibody ELISA (the continuous covariate) and milk production response to anthelmintic treatment in dairy cows. The second example is the use of fractional polynomials to model a number of important confounders in a survival analysis of the effects of *Salmonella* ELISA test status on time to culling in dairy cows.

An experimental and modelling study on the mechanisms of indirect transmission

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Untraced indirect transmission between farms is often witnessed during epidemics of livestock disease. Recent examples include epidemics of avian influenza virus, classical swine fever virus and foot and mouth disease virus. A better insight into the underlying mechanisms of this form of transmission is needed to be able to fight epidemics better. In this study we used a novel experimental setup in which the indirect transmission of two different pathogens between spatially separated broilers was studied. In the centre of an experimental room five broilers were placed together and each animal was inoculated with both *Campylobacter jejuni* and *Escherichia coli*. Surrounding this centre cage ten susceptible animals were placed individually at a distance of approximately 75 cm. The infection chain was thereafter monitored by taking daily cloaca swabs of the susceptible animals. The results of the experiment showed a clear difference in transmission pattern for the two pathogens, possibly caused by a difference in the ability to survive in the environment. We developed a new mathematical model describing indirect transmission by taking both transport and decay of the pathogens in the environment between the infectious and susceptible individuals into account. The model parameters were estimated using the data of the experiment. Our results show that this model proves successful in explaining several key features of the indirect transmission observed here. We believe it is a promising approach to describe indirect transmission in the field, with the possibility to analyse specific bio-security measures by considering their effects on the model parameters.

Epidemic simulation of an FMD outbreak in Minnesota, USA

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Foot-and-mouth disease (FMD) is a trans-boundary disease occurring regularly around the world generating international concern. Currently endemic in many regions, outbreaks of FMD have occurred over the past 15 years in several countries that have historically been FMD-free. The objective of this study was to simulate the spread and control of FMD in Minnesota (MN) using the North American Animal Disease Spread Model (NAADSM). FMD response plans of USDA and MN focus on disease eradication. These plans informed aspects of the model related to disease control including movement restrictions, depopulation, and surveillance. Also, direct and indirect contact rates (MN specific), and airborne spread are used in NAADSM. The simulated FMD outbreaks (1000 model iterations) begin in and are limited to MN. Livestock premises included in the study area were MN dairy, beef, swine, sheep and goat units. These industries accounted for 33% of total state farm receipts in 2010. Farm size and locations were supplied by the MN Board of Animal Health. The simulated outbreaks began in central MN in one of two major livestock sectors (dairy or swine). This study describes the range of epidemiological results associated with the spread of FMD in MN. Summary statistics include mean number of infected herds and animals, mean duration of outbreak, mean duration of active disease spread, and total herds and animals destroyed. The type of herd initially infected influenced the outcome. Preliminary results indicate that when infection starts in a dairy, the mean number of animals infected was about 62,000. The maximum infected over 8 million (85% of susceptible livestock in MN) which occurred in less than 1% of iterations when FMD became endemic.

Impact of emergency vaccination in a foot-and-mouth disease outbreak in Minnesota, USA

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Foot and Mouth Disease (FMD) is a high consequence pathogen. This paper builds on our description of the simulation of FMD spread in Minnesota (MN)(see companion paper). The main goal of USDA and MN FMD response plans is disease eradication. These plans were used to formulate aspects of our MN FMD spread model. Important elements included movement restrictions, depopulation, surveillance, and numbers of MN livestock premises that could be vaccinated. Additionally, we model MN-specific direct and indirect contacts between herds, and airborne spread. Simulated FMD outbreaks (1000 model iterations) begin in and are limited to MN. Vaccine related variables explored included time to deliver vaccine (7, 14 and 21 days), time to develop immunity from vaccine (4 and 7 days), and number of herds vaccinated per day (two levels: 50 (assumption with federal/state veterinarian applied vaccination) and 1,500 (assumption with industry vaccinators under the supervision of accredited veterinarians) herds per day). Our study describes the implications of emergency vaccination and compares the epidemiological results of FMD in MN with and without emergency vaccination. Preliminary results suggest that vaccination has important implications in a MN outbreak and is associated with large differences in disease and outbreak duration and number of animals/herds infected. These results are more striking for scenarios in which disease begins in a dairy. Assuming a dairy herd is initially infected, the mean number of animals infected ranged from 30,000 to 88,000 with 50 herds per day vaccinated and varying delivery and immunity time. However, when vaccination capacity was increased to 1,500 herds per day and other conditions held constant, the mean number of animals infected was consistently below 20,000. Variability around means was also decreased with vaccination.

Stochastic models to evaluate control strategies and freedom from infection for classical swine fever, foot and mouth disease and highly pathogenic avian influenza

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To limit the impact of epidemics like CSF, FMD and HPAI on animal welfare and economics, control measures and final screening should be applied as effectively as possible. We studied this for the Netherlands using a stochastic individual-based modelling approach. The models describe the within-herd and between-herd transmission dynamics. The within-herd transmission is formulated in terms of individual animals, and parameters are estimated from literature on transmission and vaccination experiments. The between-herd transmission is modelled by a transmission kernel, i.e. distant-dependent probabilities of infecting another farm, calibrated by observed outbreak data of the Netherlands. The model is applied to the current situation, using the location coordinates and farm sizes of all farms with susceptible animals in the country. The effect of vaccination is included at the individual level, making a comparison between control strategies possible at the livestock-area level. The results for individual animals indicate how many infected animals escape detection during the epidemic (i.e. in minor outbreaks), making a comparison between final screening scenarios possible. By combined modeling of the individual and livestock area levels, epidemic control and freedom from infection can be studied simultaneously. This approach can support decision makers in forming a deliberate opinion on the expected effectiveness and risks of vaccination strategies against contagious diseases. Results for CSF, FMD and HPAI will be shown. Ring vaccination around detected farms is a good alternative to ring culling for CSF and FMD, but not (yet) for HPAI, due to the fast transmission of the virus compared to the delay to reach full protection in the animal by vaccination. Several end screening scenarios will be shown.

The spatiotemporal epidemiological modeler: an open source framework for modeling food-borne disease

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Globalization greatly increases the potential magnitude of pandemic disease. Global epidemics may result not only from human-human transmission, but also from food-borne pathogens, food-borne mycotoxin, vector-borne, and zoonotic diseases. What can be done to protect populations from emerging disease or to implement better response measures? While the speed of modern transportation and global trade amplifies the threat, the near real time capability of modern information technology provides opportunities for improved predictive capability and proactive containment. The SpatioTemporal Epidemiological Modeler (STEM) freely available through the Eclipse Foundation (<http://www.eclipse.org>) provides a modern 'plug and play' software architecture with a plethora of functionalities facilitating such efforts. STEM represents epidemiological scenarios including all associated information as 'a graph' and additionally offers toolsets for developing sophisticated simulations of disease spread. STEM contains data sets describing the geography, transportation systems, and population for all countries worldwide together with disease models, population models, and tools for model comparison and cross validation. As an Eclipse application, STEM supports a collaborative community in creating a growing library of 'pluggable' data and algorithms to model existing and emerging disease threats, including zoonotic and food-borne diseases. For example, models for malaria and dengue fever are built on top of global mosquito vector capacity models using historic climate data from NOAA and the NASA Earth Observatory for the years 2001-2010 available as STEM 'plugins'. This talk will describe work underway to use the STEM framework to model both food-borne diseases and the global supply chains through which they spread.

Future zoonotic disease incidence informed by climate change scenarios

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The role that climate variability and change play in altering infectious disease risk is a major issue calling for a multi-disciplinary approach. We demonstrate the integration of skills from human and veterinary epidemiology, statistical modelling and climate science in estimating the burden of infectious disease in New Zealand 2015, 2040 and 2090 under three future climate change scenarios. We used baseline weekly data from 1997 to 2007 to model the effect of past climate variation on notifications of campylobacteriosis and cryptosporidiosis. These models produced adjusted regression coefficients that were coupled with the National Institute of Water & Atmospheric Research's climate projections to project the future burden of disease in 2015, 2040 and 2090. The weekly average absolute humidity, rainfall and temperature were positively associated with the probability of campylobacteriosis notification. Campylobacteriosis notifications were projected to increase especially during the summer in the top half and coastal areas of the north island. Cattle density and poor drinking water quality were risk factors for campylobacteriosis notification while Maori ethnicity was protective. Weekly average rainfall and temperature were positively associated with the probability of cryptosporidiosis notification. Cryptosporidiosis notifications were projected to both increase and decrease with season and location. Rural living and poor drinking water quality were risk factors while Maori ethnicity was protective. Disease projection estimates are currently being incorporated into a web-based tool to identify communities at risk and help aid the implementation of informed strategies for disease risk reduction. Our disease projections are our best estimates of the future burden of disease and must be seen in the light of multiple uncertainties including model estimates and future emissions, settlement, land use and policy changes.

Creating a biological context to analyze long term behavior of periodically driven biological systems

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Many biological systems are influenced by a periodic environment, for instance the seasonal or circadian cycle. For an epidemic influenced by a periodic environment, the growth rate is a blend of periodic fluctuations and long term increase or decline. Therefore, it is often not straightforward to determine if an epidemic can expand and persist. To obtain more insight in this matter, the long term behavior should be disentangled from periodic fluctuations. The Floquet theory is a mathematical tool to deal with such problems. However, it is not often applied to biological systems, because a good connection between the mathematical formalism and the biological context is not available yet. We present a biological context, where the Earth's rotation around the Sun or its own axis causes the periodicity of the biological system. Explicitly taking into account the effect of Earth's rotation on the dynamics of the biological environment, paves the way to derive the Floquet theory within this biological context. Since the periodicity of the environment is caused by a known fixed rotation, the biological system can be mathematically transformed so that the long term growth rate can be determined separately from the short term cyclic behaviour. For practical applications, we offer a straightforward recipe for the determination of this growth rate. We will show the application of this recipe to a transmission model of a vector borne infection.

Simulating spread and control of HPAI in Belgium

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The objective of this study was to evaluate the consequences of introducing HPAI into the Belgian poultry sector, using a spatially explicit and detailed stochastic simulation model (Interspread PLUS) and explore the epidemiological consequences of different control strategies. The parameter settings of the model are described in detail. To identify which parameters are the key drivers of the model output, a sensitivity analysis was performed. It showed that overall, the model is stable against perturbations of the model parameters. The greatest influence was caused by the local spread probability. Animal movement probability was also an important factor, but the impact was linear, indicating robust model behaviour. The model predictions for uncontrolled outbreaks were used to visualize five zones with different infectiousness levels. Three different index farms from three different zones (very low, medium and very high infectious zone) were then randomly selected for the simulations of controlled outbreaks. Three non-vaccination and 3 vaccination strategies were evaluated. The results indicated that the type and the location of the index farm have a great influence on the outcome of an outbreak. However, our analysis also showed that currently planned interventions in Belgium, based on pre-emptive culling within 3 km of an infected farm, are likely to control the majority of outbreaks in an efficient way, from the very low to the very high infectious zones and that in the Belgian context, vaccination strategies might not be a feasible or cost-effective option.

Influence of between-group transmission function on a simulated pathogen spread in a structured population

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In a structured population, individuals can belong to different groups according for instance to their age or physiological status. In epidemiological models applied to structured populations, both within- (WG) and between-group (BG) transmission have to be represented. The former has been largely studied, whereas little attention has been paid to the latter, being however pivotal in populations such as herds. Our objective is to compare the pathogen spread in a structured population using different BG transmission functions in a theoretical model. This classical SIR model considers a two-group structure, no demography and a frequency-dependant WG transmission function. Five BG transmission functions, leading to five models, were identified in the literature: equivalent to density (D)- and frequency-dependant, with in the latter case different expressions of the denominator (current group size (FD), other group size (V) and sum (W) or product (G) of both sizes). The transmission rates for each BG function were estimated to give the same fixed R_0 for all models, through the computation of a next-generation matrix. Results from the different models were compared for different values of R_0 , group sizes and respective influence of WG and BG transmission. Different transient behaviours and equilibriums are simulated for the prevalence in both groups, depending on the considered BG function. More particularly, functions FD and G can be distinguished from the three others. A sensitivity analysis with R_0 , population sizes, influence of both types of transmission and transmission function as factors and, prevalence and epidemic size as response variables, was carried out. Results show that, if R_0 acts predominantly on model outputs, the choice of the BG function can not be neglected. The distinct biological meanings and the simulated differences for the considered BG functions give insight into the choice of the appropriate function in epidemiological modelling.

Social network analysis of poultry movements in Argentina during 2009 and 2010

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The poultry production in Argentina is the second largest industry after the cattle, and for that reason, the potential introduction and spread of exotic diseases affecting poultry would have severe socio-economic consequences in the country. In order to allocate surveillance strategies to prevent and rapid control infectious diseases affecting poultry, the characterization of the structure and contact patterns between poultry farms is crucial. However, there are very few studies describing in detail the animal movement contacts between poultry farms and none has been developed in Argentina. The study presented here is aimed to describe in detail the structure and the trade flows among the poultry farms in Argentina using graph theory and social network analysis. Particularly, data on poultry farms (i.e. census, location, etc.) and poultry movements from January 2009 to December 2010 were obtained from the National Service for Agrifood Health and Quality (SENASA). The poultry directed network was constructed using poultry farms as nodes and poultry movements between farms as links. Degree, closeness and betweenness centrality measures and other SNA metrics were computed to identify 'important' nodes that may be at particular high risk for disease introduction and spread. Analyses were performed using R Language v2.10.1 with igraph library and network was visualized using ArcGIS 9.3 (ESRI). The poultry contact network was compounded by 6,330 nodes with 50,374 links for 2009 and, 6,458 nodes with 50,566 links for 2010. Nodes with the highest number of outgoing and ingoing links correspond to a hatched farm and meat production farm, respectively. This is one of the very first studies characterizing the poultry movements and identifying poultry farms, periods and regions at highest risk for potential disease introduction and/or spread, and will be useful for the design of risk-based surveillance strategies and contingency planning of diseases affecting poultry.

FAO TADinfo: the use and constraints

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TADinfo is a unique veterinary data management system designed by FAO for national veterinary services to facilitate national level epidemiological analysis of disease situations and decision making. The FAO developed programme consists of a database (MySQL based) and a mapping component (KIDS). TADinfo has five data entry modules and four database management modules including a function to list diseases, clinical signs, localities, aiming at providing user countries more flexibility in adjusting the database to their own needs. The first software release was based on MS Access linked to ArcView (2002). This version was soon replaced by a Java written database. Today it uses Tomcat, MySQL. Since the last ISVEE in 2009, Durban, TADinfo has been deployed in 13 additional countries whilst 10 countries have received updates. The actual use varies according to the user country's disease data collection system. The deployment is carried out as part of various FAO and other projects, and comprises also trouble shooting/ad-hoc support/advice by FAO HQ once the system has turned operational. Through these projects, FAO has trained some 100 national veterinary staff since 2004 as 'training of trainers (ToT)' on the use and management of TADinfo. The trainers then conduct in-country training involving their colleagues and provincial veterinary staff. Some countries have managed to connect their own computers to their TADinfo installed computer via LAN and use these for shared data entry; two countries are now using internet connection to enter data to secured national web servers. Recurrent computer virus infections and rapid turnover of trained staff are the known major obstacles to sustainability. To assess the actual situation upon deployment including additional practical needs and constraints, a questionnaire is sent to the TADinfo deployed countries. The poster presents the outcome of the questionnaire, and seeks to analyse relevant trends in animal disease database systems.

A qualitative model to assess effectiveness of meat inspection

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The meat inspection (MI) system in place in the EU Member States is currently at the centre of a debate: could this system be rendered more targeted and cost effective without compromising its original mandate of protecting public health (PH), animal health (AH) and animal welfare (AW)? We developed a model to qualitatively assess the capacity of each MI task to detect PH and AH and AW hazards ('effectiveness'). The model parameters were set by a panel of experts, including epidemiologists and MI and public health professionals: the final qualitative estimate was the combination of Sensitivity (Se) and Positive Predicted Value (PPV). Se was calculated as the product of the proportion of infected animals showing lesions in a particular organ and the proportion of these animals that can be detected by the MI task. The PPV depended on the Se and Specificity of the MI task and the proportion of infected animals that show clinical signs. The model was validated for seven hazards. Expert elicitation was used to reduce uncertainty of specific estimates and to fill data gaps. The model showed good discriminatory capacity to compare 'effectiveness' between inspection tasks and across hazards. Data to feed the model was scarce in the literature. Model validation revealed that very few of the current MI tasks seemed to contribute to the identification of all hazards. By contrast, most tasks appeared to contribute to the identification of ≤ 2 of the studied hazards and some were essential for identification of certain hazards. Only very few tasks appeared to have no value. The model was simple and robust, representing an interesting tool for discerning between essential and redundant MI tasks. The model allows assessing the relative importance of MI tasks and provides a basis for investigating the impact that alternative inspection scenarios would have on the identification of hazards. The lack of reliable and harmonized data collection during MI is of concern, and may preclude any evidence-based attempt to revise the MI system.

Analysis of cattle movements in Belgium

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This study aimed at analyzing recorded movements of cattle that took place in Belgium in the year 2000. Raw data were extracted from the National Cattle Tracing System and the unit of analysis were pixels of 5 km by 5 km in which the country was divided. Each movement was referenced with the pixel of origin and destination. Social network analysis was applied to these data. In 2000 Belgium had 33,843 farms containing 3 million cattle (the median of farms and cattle per pixel was 23 and 2,153, respectively). A total of 1.1 million cattle heads (39% of the national herd) were moved: 13% within the pixel of origin and 87% to another pixel. The distributions of distances were analyzed only when the pixels of origin and destination differed. These distributions were: 1-10 km 11%; 11-50 km 32%; 51-100 km 24%; 101-200 km 31% and >200 km 2%. The network was comprised of 1,290 nodes and 227,141 directed links. The median out-degree (representing the number of destination pixels) was 162 (range 0 to 413). The median in-degree was 60 (range 0 to 1,208). The highest values for out-degree were in northwestern and southern Belgium. The highest values for in-degree were in the north, in particular the province of Antwerp and also West and East Flanders. The clustering coefficient was 0.98, indicating that almost every node was directly connected to all the others. Assuming that data for year 2000 are representative, we conclude that the pixels in the north, which have high in degree, are susceptible to disease outbreaks, as they receive large numbers of cattle from various origins. In case of an outbreak in other part of the country, the disease would probably be spread to this fattening zone. This should be taken into account to improve surveillance and control strategies.

Modelling *Salmonella* transmission around a typical British pig finishing unit

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Salmonella control on farm is extremely important as *Salmonella* species are an important cause of zoonotic disease. Pork, after eggs and poultry, is considered to be a principal source of human food-borne infections. As field studies are expensive, the development of methods to analyse on-farm control of *Salmonella* is warranted. A stochastic simulation model reflecting the structure of a pig unit was built. The model was developed using a continuous time Markov chain. Pigs were classed as susceptible, infectious, carrying or recovered with regard to *Salmonella* status. Infectious animals were associated with a population of free-living infectious stages. An important finding after simulation of the model was the affect of shedding on herd prevalence. It was found that a presence of ‘super-shedders’ on a unit resulted in high prevalence of *Salmonella*. Although ‘super-shedders’ are known to exist, the extent to which they are found on farm and their role in *Salmonella* epidemiology is unknown. The affect of ‘super-shedders’ was reflected in the estimated basic reproduction number, R₀; approximately 7 when ‘super-shedders’ are present. A further finding of importance related to the impact of the probability of infection after exposure. A 10 times reduction in probability resulted in a decrease in prevalence of approximately 15%. The finding that high prevalence farms could have a number of ‘super-shedding’ pigs is important for the industry. Further research efforts should investigate the frequency and cause of super-shedding and impact of control targeted at these animals.

Detecting communities of animal trade based on Google's PageRank

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Network analysis has become a useful tool to study animal trade. Recent studies applied community detection analysis in animal movement networks, to improve predictive modelling and to help us understand the trade patterns of the animal production industry. We implemented and tested a community detection algorithm that reflects the definition of an animal production zone, providing useful information for researchers and decision-makers, specially to understand animal flow and identify trade regions within an area. We analyzed the State of Mato Grosso database of cattle movements for the year of 2007, provided by INDEA (Instituto de Defesa Agropecuária do Estado do Mato Grosso). This database holds information about 15,844,764 animals moved. We implemented an algorithm that accounts for links direction and weight. It is based on the calculation of LinkRank, a modified concept of Google's PageRank. In this sense, the community is defined as a group of nodes in which a random walker is more likely to stay. We think that this community definition is adequate to find regions of animal production, assuming that a community is a group of premises or counties that an animal is more likely to stay during its life. We found 14 cohesive communities, all of them containing counties that are geographically adjacent to each other. A small group of counties remained in the border of two or more communities, acting as trade borders. Community analysis is an useful tool to understand animal trade within a given area, and therefore to help predictive modelling or the planning of surveys and other veterinary preventive control measures. Also, network community analysis along with Geographic Information Systems can synthesize information in a very revealing way, avoiding one to be overwhelmed by the large amount of information maintained in livestock movement databases.

Immunization strategies on the network of bovine movements of Mato Grosso, Brazil

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The heterogeneity of animals' movements on a farms network can increase the probability of the spread of diseases, making them harder to eradicate. Due to this, it is extremely important to develop immunization strategies in order to minimize the risks of epidemic outbreaks. The aim of this study is to analyze the effects of different immunization strategies in controlling the spread of diseases on the farms network of bovine movements of the State of Mato Grosso (MT), Brazil. Using the Susceptible-Infected-Susceptible (SIS) model, we simulate an acute and a chronic theoretical disease using different immunization strategies, and analyze the equilibrium prevalence level after each strategy. The immunization strategies implemented are the Uniform Immunization, where we randomly choose the farms that will be immunized; the Most Time Infected Immunization, where we choose the farms that stayed infected the most time during the simulation without any control; the Kin Immunization, where we choose the farms with the highest in-degree (number of farms that sell to the studied farm); the Kout Immunization, where we choose the farms with the highest out-degree (number of farms that buy from the studied farm); and the Ktotal Immunization, where we choose the farms with the highest total degree (the sum of the in-degree and the out-degree). All the studied strategies decreases the prevalence of the diseases, however the Ktotal Immunization strategy presents the most effective reduction for the MT network. These results indicates that by surveying just a few farms of the MT network it is possible to reduce the prevalence level of some diseases optimizing their control, a result with both practical and economical impact. We hope that our study may assist in the development of programs to prevent and control diseases in animals.

A description of cattle movement from brucellosis positive and negative farm premises in Mato Grosso, Brazil and the use of PageRank as a parameter for the analysis of the network of animal movements
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An important factor for the introduction and spread of infectious disease in cattle production is the animal movement between farm premises. In this way the network analysis leads to a better understanding of the potential risk for disease spread in a susceptible population and allows one to control and prevent infectious diseases such as bovine brucellosis. In the present study, cattle production premises are the nodes and the movements of animals are the links. We used the data of the survey for brucellosis obtained from 549 farm premises and the data of cattle movement obtained from the records of animal transit in the State of Mato Grosso, Brazil. Descriptive statistics of overall network were calculated using R and a comparison of movements between positive and negative premises was calculated by Mann Whitney test. The analyses of animal movement network were done using 2 parameters: degree and PageRank. The premises' degree was defined as the number of direct links between this premise and all other premises. The PageRank is a method for computing a rank for every web page used by Google that determines the web page's relevance. For this study the PageRank was adapted to indicate an importance of a particular node (premise) based on the links connected to it and the weight of the link. The distribution of herd size in each premises showed a similar pattern between 2004 and 2007. There was no significant difference of degree between positive and negative premises ($P > 0.05$) and the descriptive analyses indicate a large heterogeneity in the Mato Grosso network flow. The use of PageRank in an animal movement network could be an important tool in disease control. Acknowledgement: FAPESP, CNPQ

The use of probability scoring rules to carry out comparison and validation of infectious disease models

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Deardon *et al.* detail a class of 'individual-level models' (ILMs) for infectious disease spread. They have been fitted to data from the UK 2001 foot-and-mouth disease epidemic, and used to model the spread of porcine respiratory and reproductive syndrome and influenza. Fitted in a Bayesian statistical framework using Markov chain Monte Carlo methods, they are an intuitive and flexible class of models that can be used to take into account population heterogeneity via various individual-level covariates. Of course, for a model to be used to inform, for example, control policy for a disease outbreak, it is key to be able to show evidence that the model has a sufficient fit to observed data. Standard statistical methods for doing this (e.g. the chi-squared goodness-of-fit test) fail in systems such as those of infectious diseases, due to the complex dependencies that exist in the data. Here we examine the use of probability scoring rules to both compare, and ascertain the adequacy of fit for, individual-level infectious disease models.

Comparison of different survival models as descriptors for culling distributions in dairy cows

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This paper presents the results of a study to develop and evaluate survival analysis the effect of treated diseases on the culling rate (remove from herd) in dairy cows. Five different models, with and without time-dependent covariates, using Gompertz distribution were studied. Model 1 treated diseases as binary and time-independent covariates. Models 2 through 5 treated diseases as time-dependent covariates. For each observation, we split follow-up time in intervals each corresponding to a different lactation month. In other words, each observation from study entry until culling or censoring was split into several one-month observations by Lexis expansion of the original dataset. Model 2 assumed an animal experience a certain disease from the beginning of the occurrence of that disease by the end of follow-up period. Model 3 assumed cows are at risk from the beginning of the study until the disease occurred (inverse of model 2). In model 4 and 5 an animal was assumed to experience a certain disease for one month if the disease occurred during this period by this difference in model 4 assumed diseases occurred only one time and in model 5 multiple disease occurrences at different months were considered as different episodes. According to Akaike's Information Criterion (AIC) value and Cox-Snell residuals model 5 was the best model. A comparison of culling models with and without time-dependent covariates found that models without time dependency tended to seriously underestimate the risk of a disease on culling.

Decisions on FMD emergency vaccination informed by outbreak data and model predictions

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The choice of whether or not to apply emergency vaccination is one of the most difficult decisions facing the authorities when foot-and-mouth disease (FMD) breaks out in a free country. A simple quantitative tool was proposed in 2006 using the first 14-days incidence (FFI) of outbreaks by 12 regional foci in the 2001 UK epidemic to predict the duration and the cumulative number of outbreaks at the end of the epidemic. We used a modified FFI procedure to analyze data from the FMD outbreaks in Argentina in 2001 with the 17 affected provinces as the units of observation. Output was also analyzed from a series of FMD simulation models with current Danish population data at the national level using a modified DADS model (DTU-DADS). The primary independent variable was the number of outbreaks detected during the first 14 days of the epidemic. Local herd density was also included in the Argentinian analyses. The dependent variables were the number of outbreaks after day 14, and in the Danish analysis also the epidemic duration after day 14 and the area affected at the end of the epidemic. Statistically significant positive correlations were found in all regression analyses of both data sets. The highest values were seen in the Argentinian outbreak data when herd density was also included in the model. The Danish simulation data showed a higher degree of variation. This difference is to be expected, since the Danish data simulated 1000 different epidemics, while the Argentinian data analysed regional variations within one and the same epidemic. Emergency vaccination should be considered if the predicted cumulative size of the epidemic appears alarming. The results indicate that predictions using the number of outbreaks by day 14 and modifications hereof might be useful in informing such decisions.

An integrated web system to support veterinary activities related to the management of information in epidemic emergencies

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The efficiency of management of public health emergencies is improved by quick, exhaustive and standardized information flow of data on disease outbreaks. The efficiency of surveillance systems and disease control or eradication programmes is increased by using specific software for data analysis and collection. In this context, the National Information System for the Notification of Outbreaks of Animal Diseases (SIMAN) was designed and developed to collect and share outbreaks notifications data in real time by using the World Wide Web. The system is part of the e-Government process that involves all public administrations of the European Union (EU) and refers to the use of information and communication technologies for the digital processing of documents in order to obtain simplification and interoperability of administrative procedures through the Internet. EpiTrace is a useful web application based on the Social Network Analysis (SNA) and on network epidemiological models. This software has been integrated in the BDN and gives the possibility of assessing the risk associated to holdings on the basis of their trade patterns and to target better risk management measures in case of an outbreak.

Implications of commuting assumption in multi-scale model

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Compartmental models (CM) were among the first theoretical approaches in epidemiology, proved to be predictive, but the assumption of homogeneous mixing does not meet real contact structure. According to livestock movement databases, the contact structure often follows scale-free distribution, that led to models with contact structure other than homogeneous, i.e. complex network models (CNM). We define a CNM as set of nodes, links and disease transmission dynamics between nodes. In many studies, nodes represent sites that trade animals and links the livestock movement between nodes. Since a node can retain many animals, hybrid models were developed to consider the two scale disease spread. A CM to describe the spread within a node and the CNM deals with the spread through the network. In veterinary epidemiology one common assumption of CMs is that the livestock trade behave as if animals were commuting, which means that animals entering in a node do not change the total number of animals, but influence the spread of a infectious disease and then return to their home node. We build a SI model in which animals do not commute and our objective was to compare it to the SI commuting model to evaluate how this commuting assumption affects the disease spread. We created a structure of three nodes and external compartments to make the two models work in similar fashion and capture the nuances of outcomes. Our results show that the number of susceptible animals are more sensitive to livestock movements in our model than in the commuting model. Moreover, the speed of disease spread within a node is different for the two models. These results are important considering that theoretical models are tools helping identify strategies for prevention, risk evaluation and disease control. We are now further investigating these CMs in theoretical and real complex networks. Acknowledgment: CAPES, FAPESP, CNPq

Antiviral agents to control classical swine fever epidemics

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Classical Swine Fever (CSF) represents a continuous threat to pig populations that are free of disease and vaccination. When CSF virus is introduced, the minimal control strategy imposed by the EU is often not sufficient to mitigate the epidemic. As additional measure, preemptive culling encounters ethical objections, while emergency vaccination leads to prolonged export restrictions. Antiviral agents, however, provide instantaneous protection without inducing an antibody response. The use of antiviral agents to contain CSF epidemics is studied with a model that describes virus transmission within and between herds. Epidemics are simulated in a densely populated livestock area in The Netherlands, with farms of varying sizes and pig types (finishers, piglets and sows). Our results show that vaccination and/or antiviral treatment in 2 km is more effective than preemptive culling in 1 km. However, the instantaneous but temporary protection offered by antiviral treatment is slightly less effective than the delayed but permanent protection offered by vaccination. For this reason, the most effective control strategy is to vaccinate animals when allowed (finishers and piglets) and to treat animals with antiviral agents when vaccination is not allowed (sows). As independent control measure, antiviral treatment in 1 km presents an elevated risk of epidemics running out of control. A 2 km control radius largely eliminates this risk, at the expense of higher control costs. An economic analysis can point out whether the benefit of earlier regaining the freedom of disease status outweighs the costs of treating more animals with antiviral agents.

Estimation of back yard pig (BYP) density in the EU: first step to evaluate the role of BYP in disease transmission

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The presence of backyard pigs (BYP), which are usually managed with low biosecurity measures, is a reality in many EU countries; however there are no official counts or knowledge about their distribution. Although suggested, the contribution of BYP in the persistence of diseases such as classical swine fever (CSF) or African swine fever (ASF) has not been fully investigated. The current situation of CSF in some EU countries, with outbreaks in BYP and wild boars, and the continuing spread of ASF in the Russian Federation, with outbreaks occurring close to the EU borders, has increased the concerns on the potential role that BYP may have in the persistence of such diseases. The study presented here was aimed to estimate the BYP density in the EU as a first step to evaluate its potential role on the persistence of CSF or ASF. Specifically, we estimate the relation between 117 socio-economic and cultural factors and the density of BYP in Romania, Bulgaria and Sardinia, for which BYP counts were available, using a generalized linear model. The model with the lowest AIC and the highest adjusted R-squared was considered the one that best fitted the data and was used to estimate the abundance of BYP in the rest of EU countries. Model revealed that BYP is particularly concentrated in areas where agricultural holdings have mixed livestock and low standard gross margin, farm owners are old (i.e. age 55-66) and labour force is familiar. A BYP density map at NUT3 level for the whole EU has been produced and will be validated using expert opinion. Interestingly, areas with the largest number of BYP have the highest number of CSF outbreaks in the last 10 years. Methods and results of this study would be useful to further evaluate the epidemiological role of BYP and, ultimately, to allocate efforts to prevent CSF or ASF disease spread and/or persistence into the EU.

Pig farm-to-pork: risk factors of *Salmonella enteritica* subsp. *enteritica* contamination in freshly cut pork in northern of Thailand

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The aims of this study were to determine the prevalence and associate risk factors in freshly cut pork in a pig producing compartment of northern Thailand. Samples were collected from fattening pigs at the farm. Samples were also collected from the same individual pigs through the processing line until they were cut in cutting room of a slaughterhouse. A total of 1,982 samples were collected from 194 pigs including 193 feces, 181 Mesenteric lymph nodes, 181 caecal-content, 181 swabs from carcass after splitting, 180 swabs from carcass after washing, 173 freshly cut pork and 173 pork to be delivered to the market. An additional 521 samples were collected from the farm and slaughterhouse environments. A total of 971 (48.9%) samples from the processing line were positive for *Salmonella enterica* using standard method (ISO6579). The lowest prevalence was observed in carcasses after washing (12.9%; 95% CI: 7.0-18.8), the highest prevalence in cecal content (83.1%; 95% CI: 74.5-91.6) indicated that a large proportion of pigs might be infected at the farm. The final logistic regression model with *Salmonella* contamination in freshly cut pork as an outcome variable showed that *Salmonella* contamination on carcass after washing (OR=5.2; P=0.006, RR=1.7; P=0.000), mesenteric lymph node (OR=2.3; P=0.016, RR=1.4; P=0.009), cutting board during cutting process (OR=2.2; P=0.022, RR=1.4; P=0.009) and environmental samples of fecal material (overshoes swab) at farm (OR=2.4; P=0.019, RR=1.5, P=0.008) were significantly associated with *Salmonella* contamination in freshly cut pork samples.

Comparison of different strategies for the control of two highly infectious animal diseases

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Up-to-date knowledge on epidemiologic aspects of infectious diseases is needed to make scientifically-based policy decisions about control strategies. The benefit of emergency vaccination or pre-emptive culling during an outbreak of classical swine fever (CSF) or foot-and-mouth disease (FMD) is widely discussed in non-endemic countries. Simulation models can be used to compare such control strategies, especially when the disease is absent in a country and recent disease transmission experience is lacking. We used a spatially-explicit, stochastic simulation model based on farm contacts to estimate the effect of several control parameters on simulated outbreaks of CSF and FMD in Switzerland. Various vaccination and – only for CSF – pre-emptive culling strategies with different radii around an infected herd and different implementation times, in addition to the basic control strategies (culling of infected herds, tracing and establishing movement restriction zones), were compared. The simulated size and duration of an outbreak depended mainly on detection and control implementation delay of the basic control strategies and less on vaccination or pre-emptive culling. However, if vaccination were conducted on a larger scale (20 km radius) and in an already advanced stage of the epidemic (approximately 50 infected premises), the probability of an epidemic being large (>25% among all epidemics) was significantly reduced. The knowledge gained in this project provides a basis for the evaluation and discussion of control strategies for highly infectious diseases in Switzerland and in countries with similar settings.

Antiviral supplementation to pig feed can contain outbreaks of classical swine fever

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Classical swine fever (CSF) outbreaks results in huge economic losses to countries with densely populated pig areas (DPLAs). The EU minimum control measures require depopulation of infected farms, movement restrictions, zoning and surveillance. Emergency vaccination is authorised for DPLAs although the EU Minimum strategy plus culling in a 1-km ring around infected premises is preferred. Nonetheless, vaccination in a 2 km ring has been found equally effective as 1 km ring culling using stochastic modelling. Alternatives control measures (e.g. antiviral agents, in particular small molecule inhibitors of the CSFV replication) are being explored. Hence, the present study was set up to simulate inter-herd CSFV spread when antiviral molecules are supplemented to pig feed in a 1 km ring around infected farms. The effectiveness of the antiviral strategy for containing CSF outbreaks was compared to six other control scenarios including the EU Minimum strategy, the EU preferred policy for DPLAs and the use of 2 km ring vaccination. The InterSpread Plus model was adapted to the 2006 Belgian pig population and outbreak simulations were performed with a fast spreading CSFV strain entering a DPLA in Belgium. Four out of the seven control strategies resulted in outbreaks that were controlled by the end of the simulation period (i.e. 365 days). Although there were point-estimate differences for the four strategies in terms of the number of infected herds and the duration of the outbreak, the distributions of the outcomes were not different. Nevertheless, the results indicate that CSF outbreaks can be controlled by means other than pre-emptive culling such as antiviral supplementation. Although further studies are needed, antiviral supplementation might be an interesting additional tool to control CSF outbreaks and is a potential alternative to 'conventional' containment measures such as pre-emptive culling and emergency vaccination.

Risk of recurrent cases of bacteria specific clinical mastitis in dairy cows

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The objective of this study was to estimate the risk of a first case and subsequent cases of bacteria specific clinical mastitis (CM) in Holstein dairy cows. The pathogens we studied were *Streptococcus* spp., *Staphylococcus aureus*, *Staphylococcus* spp., *Escherichia coli*, *Klebsiella* spp., and *Arcanobacterium pyogenes*. We analyzed 40,864 lactations (9,873 cows) of which 17,265 were primiparous and 23,599 were multiparous lactations, in 5 large, high milk producing dairy herds in New York State. There were 12,725 first cases, 4,535 second cases and 1,798 third cases of CM. Generalized linear mixed models with a Poisson error distribution were used to study the effects of parity, calving diseases, previous milk yield, season, number of cases of CM in the previous lactation and previous cases of bacteria specific CM within the lactation on the risk of a first case and the conditional risks for second and third cases of bacteria specific CM. The first 2 weeks in milk (wim) and $wim \geq 3$ were analyzed separately as the former analysis focused on calving diseases as a risk factor and previous milk yield was not included. For first case analyses, among primipara, $wim \geq 3$, cows with metritis and or displaced abomasum in their current wim were at higher risk of *Streptococcus* spp. There was higher risk of *Staphylococcus* spp. and *Klebsiella* spp. during the summer months. Among multipara, $wim \geq 3$, as parity increased from 2 to ≥ 4 , risk of bacteria specific CM increased. Cows that had 3 cases, compared to a single case of CM in their previous lactation had a greater risk of a first case of bacteria specific CM in their subsequent lactation. Cows with a higher previous milk yield were generally at greater risk of bacteria specific CM. The risks of second and third bacteria specific CM cases will be reported, as well.

Assessing control measures against MRSA ST398 in a farrow-to-finish pig farm: a modelling approach?
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Since its first detection in 2003 in pigs and pig farmers, the livestock-associated methicillin resistant *Staphylococcus aureus* (MRSA) strain ST398 has become a worldwide threat to humans. Despite the implementation of stringent measures to identify and de-colonise people carrying the bacteria, MRSA ST398 is still spreading in the community. Removing MRSA ST398 from farms is therefore considered as one option to prevent its spread from farms to humans. However, the lack of licensed disinfection products renders difficult the control of MRSA ST398 in farm. In the attempt to provide guidance for the development of new cost-efficient disinfectant product, we developed a stochastic epidemic model coupled with both a model of herd demography and bacterial growth. Using this model, we compared the effectiveness of three different control strategies targeting bacteria on pigs and/or in the environment in a commercial farrow-to-finish pig farm. These strategies were tested in scenarios where preventive or reactive action was taken. When no control activities were implemented, the predicted endemic prevalence was consistent with what has been previously recorded in the field. Removing bacteria from the environment showed little benefit with either preventive or reactive strategies. In contrast, the endemic prevalence was significantly reduced when control activities focused on removing bacteria from pigs. Although applying controls on production stock alone was inadequate to prevent a farm from becoming contaminated or to stabilise prevalence at a low level, elimination may be reached if control activities were consistently applied throughout the breeding and production chains. These findings highlight the difficulties to achieve effective and economical control of livestock-associated MRSA in animal husbandry environments.

Analysis and characterization of swine movement in four Canadian provinces

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Network analysis has increasingly been used in veterinary epidemiology to understand contact patterns among animal herds and to investigate the impact of animal movement on the spread of infectious agents. No model is currently available to represent contact between swine herds in Canada. The objective of this study was to investigate pig movement patterns between farms in four Canadian provinces using social network analysis (SNA) tools and to estimate parameters to be used for modelling the spread of porcine reproductive and respiratory syndrome (PRRS) virus. Swine movement data from a four month pilot pig traceability program were used to construct a directed contact network of the swine industry in these provinces. In the network, each pig farm was represented as a node, while the movement of animals between farms was represented as directed links. Monthly and overall movements were analyzed and patterns of contact between farms were described through the estimation of key network analysis measures. A total of 2043 shipments were recorded in the data set. The resulting network had 158 nodes and 330 links. The medians and (ranges), for in-degree and out-degree of the overall network were 1(0-59) and 1(0-12) respectively. The overall clustering coefficient was 0.122. The network can be characterised as 'small-world'. The distribution of in-degree and out-degree was right skewed; many farms had no or few connections, while a few farms were highly connected. Similar network characteristics have been reported from animal movement studies in other countries. Parameter estimates and characteristics of this network will be used to represent the heterogeneity in contact between swine herds while building a network based PRRS virus spread model.

Comparison of methods to elicit stakeholder preferences for multi-criteria decision analysis in the context of disease prioritisation

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Disease prioritisation is a decision analysis problem; somehow, the differing opinions of stakeholders need to be balanced to reach a decision acceptable to the group. Multi-criteria decision analysis methods offer quantitative, repeatable decision making solutions. By dividing the problem into measurable criteria on which stakeholders base their decision, subjective stakeholder preferences can be modelled as weights of importance for the criteria. Aggregation of weights with objective disease measurements for the criteria provides an overall disease score, weighted to reflect stakeholder preferences. Methods for modeling stakeholder preferences were trialled in a survey to prioritise exotic diseases for the Australian pig industry. The aim of the survey was to define weights of importance for 9 criteria which were measurable disease attributes that affect impact. The survey was presented to stakeholders as an online questionnaire. To increase participation, different approaches to estimate criteria weights were used. The criteria were first presented as a list for ranking and direct elicitation of weights. Four groups of test scenarios were then presented for ranking and indirect elicitation of weights using probabilistic inversion, and also for scoring and indirect elicitation of weights using a logistic regression technique. Finally, participants were asked to rank and score a set of real, but unlabelled diseases, to validate the weights elicited by each technique. Overall, 80 responses were collected for direct weighting, and over 50 for the indirect weighting methods, allowing all three methods to be evaluated. The results of the stakeholder preferences for each method are presented. The advantages and disadvantages of each method are also discussed, particularly with regard to potential improvements for future disease prioritisation.

Evaluating the benefits of vaccination for foot-and-mouth disease as an adjunct to a standard stamping out policy

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Foot-and-mouth disease (FMD) is one of the most feared diseases to countries that rely on the export of live animals and / or animal products, due to the trade restrictions that are applied during and following an outbreak, until proof of freedom can be re-established. Many countries are reluctant to use vaccination during an outbreak due to the challenges associated with proving disease freedom following the outbreak, and the delays involved, despite the fact that vaccination can assist the control and eradication process. This study describes the use of a modelling approach using the InterSpread Plus simulation system to evaluate the benefits of using vaccination as an adjunct to a traditional stamping-out eradication programme. The study population comprised all livestock farms in New Zealand. Three hypothetical introduction scenarios were created, involving single or multiple seed infected farms in different parts of the country. The primary transmission mechanisms included direct and indirect contacts and a local spread kernel. Transmission rates were varied by turning on or off an airborne spread mechanism. Vaccination programmes were varied in terms of timing of deployment relative to the first diagnosis, and size of ring vaccination buffer. Altogether, 65 models were defined, with 100 iterations conducted for each model. Mean and median time to eradication, number of farms depopulated, number of animals destroyed and number of vaccine doses used for the different vaccination programmes were compared to the standard stamping-out approach. Non-parametric regression and classification and regression trees were used to evaluate which variables had the biggest effect on the outcome measures. Findings will be used to review contingency plans for FMD in New Zealand.

Controlling disease outbreaks in wildlife using limited culling: modelling classical swine fever incursions

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Disease modelling is one approach for providing new insights into wildlife disease epidemiology. This paper describes a spatio-temporal, stochastic, susceptible-exposed-infected-recovered process model that simulates the potential spread of classical swine fever through a documented, large and free living wild pig population following a simulated incursion. The study area was in northern Australia. Published data on wild pig ecology from Australia, and international Classical Swine Fever data was used to parameterise the model. Sensitivity analyses revealed that herd density, daily herd movement distances, probability of infection transmission between herds and disease related herd mortality were highly influential on epidemic size but that extraordinary movements of pigs and the yearly home range size of a pig herd were not. CSF generally established (98% of simulations) following a single point introduction. CSF spread at approximately 9 km² per day with low incidence rates (<2 herds per day) in an epidemic wave along contiguous habitat for several years, before dying out (when the epidemic arrived at the end of a contiguous sub-population or at a low density wild pig area). The low incidence rate indicates that surveillance for wildlife disease epidemics caused by short lived infections will be most efficient when surveillance is based on detection and investigation of clinical events, although this may not always be practical. Epidemics could be contained and eradicated with culling (aerial shooting) or vaccination when these were adequately implemented. It was apparent that the spatial structure, ecology and behaviour of wild populations must be accounted for during disease management in wildlife. An important finding was that it may only be necessary to cull or vaccinate relatively small proportions of a population to successfully contain and eradicate some wildlife disease epidemics.

Simulation based models may assist the identification of potentially large outbreaks

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During an outbreak of a highly contagious animal disease, the ability to pin down potential large outbreaks would be valuable for proactive risk management. A simulation model was applied to produce 100,000 different outbreak scenarios for Foot and Mouth disease (FMD). Scenarios were started from every Finnish pig and cattle farm. If the simulated outbreak included more than 17 farms, it was considered a large outbreak. A predictive model for large outbreaks was then developed (GLM, binomial-family, logit-link). The probability of the large outbreaks was predicted in the model by the location, number of contacts within 30 days, production type and size of the primary infected farm (PIF). The most valuable information for the prediction was the number of contacts of the PIF (Wald $\chi^2=3,000.6$; $P<0.001$). Production type of PIF had the second largest effect on prediction (Wald $\chi^2=1,073.1$; $P<0.001$). Size of the PIF did not have a significant effect on the probability (Wald $\chi^2=0.9$; $P<0.357$). Large outbreaks were most probable if the outbreak started from a dairy or sow farm. Location of the PIF in high risk regions increased the probability of a large outbreak (Wald $\chi^2=787.7$; $P<0.001$). Some additional predictive value was achieved also by knowing whether the PIF was located in either of two CVO-districts having the highest farm density (Wald $\chi^2=40.2$; $P<0.001$). By applying a cut-off point of 0.08, the model sensitivity was 55.8% and specificity 15.6%. Properties of the PIF could be applied as one indicator of a large outbreak, although this may have a quite limited value. However, by applying the function we were able to pin down over 55% of large outbreaks, which was ten times more than the expected value for large outbreaks in the country (5.4%). Predictive modeling would be most beneficial when applied in contingency planning before any real outbreaks are on hand.

Modelling the risk for avian influenza viruses in wild birds in the Ebre Delta according to their distribution and behaviour patterns

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The surveillance systems for avian influenza viruses (AIV) in wild birds should be adapted according to predominant species, populations' sizes, migration patterns, and interaction between species. This work presents an individual-based stochastic model for the Ebre Delta based on the Monte-Carlo method. The aim was to build a flexible system to estimate the avian subpopulations that could be at highest risk of AIV spread for different periods in this area. Data recorded between 2007 and 2008 on the wild avian populations, apparent AIV prevalence, behavior, affinity and patterns of movements were incorporated as inputs. The model estimated that, in the breeding season AIV would affect mainly Mallards and Common Terns. And, in the event of having Mallards as primary cases, the main species affected would be Mallards, Coots and Black-headed Gulls, mostly in some specific lagoons. If the introducers were Common Terns, the species at highest risk would be Common Terns and Sandwich Terns in sandy beaches and bays. In the wintering season, AIV would be mainly introduced by Mallards, Shovelers and Common Teals, in areas of sandy beaches, salt marshes, rice fields and bays. And the species most likely affected as secondary cases would be Mallards, Coots, Herring Gulls, Shovelers, Common Teals and Pintails. This approach can serve to optimize the surveillance for AIV in wild birds in specific wetlands and build hypothesis about their plausible spread.

Estimation of the variation that can be attributed to different levels in a clinical trial of a vaccine against *Campylobacter* in broilers

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This presentation is focusing on the interaction between the experimental design of a vaccination trial and appropriate data analysis using a trial of a vaccine against *Campylobacter* in broilers as an example. This study was designed using four rotations with eight isolators per rotation (10 chickens per isolator). Treatment was administered at isolator level on day 14 (vaccine or placebo). The broilers were inoculated with *Campylobacter jejuni* at day 31 and slaughtered at day 42. The numbers of *Campylobacter* (cfu/g) were obtained in the laboratory using selective cultivation methods and log transformed to obtain a Gaussian distribution. Initially, the effect of the vaccine was analyzed using all data in a t-test. Subsequently, the t-test was stratified by rotation. Finally, mixed linear models were used, taking into account the physical hierarchical setup of the trial. Results from the t-test indicate an effect of the vaccine, whereas the result obtained from the complex model indicated high variability between birds and isolators but not significant vaccine effect. The apparent observed differences between vaccinated and placebo groups in the t-tests could be attributed to the variation between incubators. Broilers in the same isolator had more equal numbers of *C. jejuni* compared to chickens in other incubators. It is possible that chickens in the same isolator re-infect each other with *Campylobacter*. In this study, the design effect was considerable, reducing the effective sample size (67 animals instead of the 290 animals included). The clustered design used in this trial was trying to emulate the clustering effect found in broiler flocks and farms.

Quantitative microbiological data analysis of a *Campylobacter* vaccination trial

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Campylobacter jejuni is considered the main pathogen causing human campylobacteriosis and poultry has been identified as one of the main risk factors. Strategies that aim to control *Campylobacter* in poultry such as vaccination strategies could reduce the incidence of human campylobacteriosis. The objective of the present trial was to assess whether or not a vaccine candidate could give a 2 logs reduction of the numbers of *Campylobacter* in broilers. Sample size calculations indicated the use of 400 animals (200 vaccinated and 200 controls). The experiment was conducted in four different rotations using 8 incubators per rotation with 10 chickens in each incubator. The vaccination treatment was randomly assigned at incubator level. Broilers were challenged with *C. jejuni* at day 31 and faecal/caecum samples were collected at slaughter at day 42 and processed in the laboratory. To illustrate the importance of analysing the data in accordance with the setup of the study, the data was analysed both without and with taking the nested design into account. Initially, the effect of the vaccine was analyzed using all data in a t-test. Subsequently, the t-test was stratified by rotation. Finally, mixed linear models were used, taking into account the physical hierarchical setup of the trial. Results from the t-test indicate an effect of the vaccine, whereas the result obtained from mixed linear models indicated high variability between birds and isolators but not significant vaccine effect. The apparent observed differences between vaccinated and placebo groups in the t-tests could be attributed to the variation between incubators. Broilers in the same isolator had more equal numbers of *C. jejuni* compared to chickens in other incubators. It is possible that chickens in the same isolator re-infect each other with *Campylobacter*.

Evaluation of control strategies for bovine viral diarrhoea in Hokkaido, Japan using stochastic modelling

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Infection with bovine viral diarrhoea (BVD) virus in cattle can result in decreased body weight and milk production, reproductive disorders and death. Primary source of infection are persistently infected (PI) animals. In Hokkaido, Japan, all cattle entering common pasture in summer are vaccinated before movement to control the disease. Additionally, these cattle may be tested for BVD antigen and culled if positive. The efficacy of this control strategy remains nevertheless controversial. The aim of this study was to evaluate the efficacy of a test-and-cull and/or vaccination strategy for BVD control in dairy farms in two districts, Nemuro and Hiyama in Hokkaido. The herd size in Nemuro is 126 heads per farm, and in Hiyama 56 heads per farm. A stochastic model was developed in order to compare the different control strategies over a 10 year period. The model is individual-based and follows the dynamic of the disease both within and between herds. Parameters integrated into the model were obtained from literature as well as from the Hokkaido government. Nine different scenarios were looked at in the model: no control, test-and-cull strategy based on an antigen testing either for calves or only for cattle entering common pastures, vaccination strategy either for all adult cattle or only for cattle entering common pastures, and combinations of these strategies. Results comparing the different control measures will be presented. The findings obtained from this model will be the first of their kind in Japan and provide important information for the implementation of BVD control measures in Japan.

Simulated effects of introducing emergency vaccination or depopulation during FMD outbreaks in Denmark

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The purpose of this study was to explore the effects of modifying the control strategy 14 days after the first detection of a simulated FMD epidemic in Denmark. The spread of FMD was simulated using an adapted version of the stochastic and spatial disease-spread model DADS, called DTU-DADS, using Danish data on herd locations and movements. The epidemics were initiated in 1000 randomly chosen cattle herds located in cattle-dense areas. The basic scenario consisted of: the minimum EU control measures, culling of forward-traced herds and a 3-day national stand-still on animal movements. Alternative scenarios included culling, suppressive or preventive vaccination of herds within 1 km. The results show that there may be positive effects of applying additional control measures on the size, duration and costs of a FMD epidemic. The median duration decreased from 56 days in the basic scenario to 46 days in both vaccination scenarios and 40 days in depopulation scenarios. Furthermore, the median number of infected herds decreased similarly, but with fewer infected herds in the protective vaccination scenario. However, the total costs and losses of an epidemic, including export losses, changed from 562 million € in the basic scenario to 515, 539 and 616 million in the depopulation, suppressive and protective vaccination scenarios, respectively. These results suggest that vaccination will often be a more expensive strategy in a country with a large export, like Denmark. Furthermore, the simulated results show that from the economic point of view depopulation in zones is often preferable.

What, where and weather? Integrating open-source taxonomic, spatial and climatologic information into a comprehensive database of livestock infections

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What are all the species of pathogen that affect our livestock? As 7 out of every 10 human pathogens came from animals, with a good number from livestock and pets, it is important that we answer this question. Only 10 years ago, the first comparative list was compiled for humans; we still have no equivalent for animals. Using a new research tool, the open access ENHanCED Infectious Diseases (EID2) database, within this project we aim to further develop the information held within EID2, to build a comprehensive list of livestock and other pathogens. Previously, EID2 has been created largely from DNA and RNA sequences that have been uploaded onto public databases; where such sequences are from a pathogen, they are frequently uploaded with further information on the host, where and when it was obtained, and who by. EID2 takes this information, and draws conclusions; for example, that a certain type of pathogen infects a certain host species, and is/was present in a certain country at a certain time. Similar conclusions have also been drawn and added to EID2 from publications held in other public databases. EID2 also maps pathogens and using incorporated climate data, it can model the climate conditions that determine their distribution. Specifically, the improvements which will be made to EID2 will include: more spatially detailed information for pathogens; improvements to the database's ability to handle records with badly defined host species; the addition of further environmental data to produce better models to explain pathogen distributions and predict them in the future, given climate change; and information to allow users to work at the level of diseases, rather than individual pathogens or groups of pathogens. Finally, we will give users the ability to add certain information of their own.

The implications for population-level spread of within-farm avian influenza transmission dynamics

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Using the example of highly pathogenic avian influenza (HPAI) in Great Britain, we demonstrate how variability in farm-level transmission dynamics has implications for pathogen spread at the population-level. A deterministic S-E-I-R model was used to simulate the within-flock transmission of HPAI, enabling the build-up of infectious faeces within the poultry house to be tracked over time. A measure of the relative transmission potential (TP) was computed for each farm by linking the amount of infectious faeces present each day of an outbreak with temporally explicit catching-team movement data. Larger flocks tended to have greater on-to-farm movement activity. However, where density-dependent contact was assumed, faster detection led to a decreased opportunity for catching-team visits to coincide with an outbreak, and thus maximum TP-levels were found for mid-range flock sizes (~25,000-35,000 birds). When assessing all factors simultaneously using multivariable linear regression, those related to the pattern of on-to-farm movements had the largest effect on TP. However, the most important movement-related factor depended on the mode of transmission. These results highlight the importance of considering cross-scale dynamics at the farm-level, as the joint effect of interacting factors, such as flock size and the bird-to-bird mode of transmission, could not be predicted from the farm-level movement patterns alone.

A metapopulation model framework to explore the value of compartmentalisation for the British poultry industry with respect to avian influenza

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Compartmentalisation is a concept with substantial economic implications for poultry industries worldwide. However, the requirements for achieving compartment status, as stipulated by the World Organisation for Animal Health (OIE), are not specific to an individual country's poultry industry structure, or to the likely inter-farm epidemiological links. For Great Britain (GB), the absence of a large outbreak of highly pathogenic avian influenza (HPAI) to date makes it difficult to achieve evidence-based recommendations for effective separation between subpopulations. We undertook an exploratory analysis of a subset of the British poultry industry using a metapopulation modelling framework. Subpopulations represented multi-site companies, as informed by a network database representing industry-relevant links between poultry farms. By assuming compartmentalisation and zoning control would predominantly inhibit network and spatially-mediated epidemiological links respectively, the relative risk of infection "leakage" through compartmentalisation was quantified by comparing parameter thresholds corresponding to $R_0 > 1$. Overall, R_0 was more sensitive to changes in network-related parameters than to spatial proximity. However, outbreak conditions were identified where spatial transmission under compartmentalisation was relatively more "risky" than zoning control, even at short inter-farm distances of 1 km. This infection "leakage" might have greater consequences for farms external to the compartment, as multi-site farms were more likely to be within close proximity to farms of other companies. With further knowledge regarding the likely mode of spatial spread, such analyses could help inform an appropriate minimum inter-farm distance, for the definition of compartmentalisation in the event of a HPAI outbreak in Britain.

One-health simulation modeling of pandemic influenza H1N1 2009 spread between humans and animals

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Circulation of pandemic influenza A/H1N1 2009 virus (pH1N1) in human and swine populations along with H5N1 virus presents the potential of another pandemic. This study investigated influential parameters for pH1N1 spread at the human-swine interface, and impacts of targeted vaccination and other control measures. It also assessed the suitability of NAADSM (North American Animal Disease Spread Model) for modeling directly spread zoonotic diseases. Data from swine farms (488) and human-households (29,707) categorized as swine workers, rural or urban in a county of Ontario were used for the study. Impacts of 6 different combinations of transmissibility of virus at the swine-worker-swine interface, and vaccination of swine-workers before the outbreak at 4 coverage levels (0-60%) were assessed for human or swine origin of the virus. Furthermore, efficacies of control strategies (speed of detection, zoning, movement control, and ring vaccination) were assessed using 108 scenarios. Results were assessed using epidemic peak day, size and duration. No significant differences in the outcomes were evident between outbreaks of human or swine origin. Lower transmissibility and vaccination significantly delayed epidemic peak by 12-40 days, reduced total units infected by 0.6-60%, and prolonged durations of the outbreaks by 3-41 days. However, vaccination of swine-workers had no effect on epidemic size of urban people. For control strategies, fast and moderate speed of detection with movement controls of infected units alone had significant impact (outbreak ended with 1-8 units infected in 31-42 days) compared with slow detection (16-857 units infected over 60-263 days). NAADSM could model directly spread zoonotic diseases under certain simplifying assumptions.

The efficacy of test-based culling for bovine tuberculosis control in US cattle herds: a modeling approach

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In 2009, the United States Department of Agriculture proposed a new policy for elimination of bovine tuberculosis (bTB) from cattle herds. This included whole-herd test-based culling, using the 2-stage series testing protocol (caudal fold test followed by comparative cervical test), with confirmatory culture and PCR at slaughter. We built a stochastic model of bTB spread within US cattle herds to determine the efficacy of this protocol. An SERI model (susceptible-latent-reactor-infectious) was implemented with slaughterhouse surveillance and pulsed whole-herd testing of herds detected in the slaughterhouse surveillance. The model was validated by comparison of simulated data to 10 real observed outbreaks on US dairy farms in which test-based culling was successful. The number of positive animals observed fell within the 95% prediction interval for all 10 herds. In a second validation simulation study, introduction of 1 latently infected animal to a herd of 276 adult animals showed that 27% of all simulated herds eliminated the infection without detection. For detected herds, median time to detection was 27 months, and test-based culling was sufficient to eliminate the infection within 3 whole-herd tests. Global sensitivity analysis indicated that the model outcome was most sensitive to the herd's culling rate, which is inversely related to the number of animals infected and which is higher in dairy herds than in beef herds. Scenario analysis showed that the number of animals culled was most sensitive to the number of negative whole-herd tests required to declare the herd bTB-free, while the length of quarantine was most sensitive to the interval between whole-herd tests. Overall, the model shows that the recommended test-based culling protocol should be efficacious for eliminating infection from herds.

Combination and comparison of two spread models of highly pathogenic avian influenza (HPAI) in a region of Spain

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Since 2003 HPAI has had devastating consequences for poultry affecting ~400 million domestic birds and causing ~\$20 billion economic losses. Early detection of HPAI cases helps the application of control measures mitigating the impact of the disease. Models are an efficient way to obtain early detection enabling the simulation of epidemics. Until 2006 Spain was free of HPAI, however in the last 5 years 2 cases of HPAI were notified. Because Spanish industrial poultry sector ranked 3rd in Europe, the spread of HPAI would have devastating consequences on the country. Consequently a better knowledge of the dynamic of the spread of HPAI in Spain is needed. A comparison of two spatial spread models is the solution proposed to investigate the variation of HPAI risk in each zone, and the adequacy of using either in control plans. Model I was a deterministic spatial model based on risk factors compiled by multicriteria decision. Model II was a stochastic spatial simulation model carried out using InterSpread Plus. Comparing results of both models in each farm showed a significant correlation (Spearman coef. $\rho=0.825$, $P=0.0$). Results were classified into quartiles of risk (Very High, High, Medium and Low) and compared. Bivariate analysis shows a significant association ($P=0.0$), which was more significant in quartiles 'Very high' and 'Low'. The consistency of results suggests appropriate assumptions in the introduction of parameters in each model. Similar risk farm classification in Very high and Low risk quartiles show that decisions to prioritize or discard control areas, according to risk estimated, would have been similar using either model. These areas identified could be selectively targeted as part of a surveillance program aimed at early detection, which could contribute to improved the control of HPAI. This work was financially supported by FAU2008-001-CO2-01.

Spatial analysis of Newcastle disease spread in Spain

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Newcastle disease (ND) is one of the most significant viral avian disease, which causes devastating losses to the poultry industry. In the last 10 years more than 60 countries have been affected. Understanding how a disease spreads as a function of its risk factors, is useful to determine appropriate surveillance plans to specific areas. The aim of this study was to develop a spatial model to zone the risk of spread of ND in industrial chickens based on risk factors. Four risk factors have been studied on each farm: biosecurity (biosecurity surveys), trade movements between farms (network analysis made using free Pajek software), farm census, and farm density (analyzed by Kernel density method). Risk factors were standardized, transformed into four raster layers, and compiled using Multicriteria Spatial Decision. Results were shown in a risk map and were classified in 4 risk levels (very high, high, medium, and low) for spread of ND. The spatial clustering of high-risk areas of spread of ND was evaluated using Getis-Ord test A sensitivity analysis was performed by Monte Carlo simulation. Results showed that broiler farms in the province of Segovia have a significantly higher risk of spread. We identified 20 high-risk clusters ($SD>5.5$). Trade movements of live birds was identified as the most influential risk factor (regression coefficient =0.4). This work contributes to the identification of high risk areas of spread of ND which enabled applied focus surveillance efforts in these areas. In this way the efficiency of prevention and control systems could improve in terms of cost / benefit. This work was financially supported by FAU2008-001-CO2-01.

Agent-based models for assessing the effects of contact heterogeneity and network structure for spread of influenza H1N1 2009 virus in swine

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Agent-based (AB) models are increasingly being used to study disease transmission and control strategies as they capture complex heterogeneities in individuals' interactions. Social networks and spatial locations can be represented explicitly in these models. Policy interventions can be studied in more detail than that possible with aggregate differential equation models. Contacts between different swine farms types and their behaviors can vary which will influence the way diseases spread and the effectiveness of control measures. The impact of contact heterogeneity and network structure for the spread and control of influenza in swine has not been reported. Therefore the objective of this study was to compare the impacts of heterogeneity of contacts and network topologies (such as random, small-world, scale-free) on the spread and control of influenza A/H1N1 2009 virus in swine using AB network models. Swine population data from a county in Ontario comprising 488 farms (39 sow herds, 137 nursery and 312 finishing farms) were used. Stochastic SEIR (susceptible-exposed-infectious-recovered) AB network models were constructed using AnyLogic®. Each agent represents a farm and contacts between swine farms are incorporated explicitly using different network structures in the models. Effectiveness of targeted vaccination and quarantine measures were assessed. Parameters were extracted from literature. Modeled outcomes were assessed by peak incidence, cumulative incidence, duration and speed of outbreaks. Final results including an assessment of the value of this modelling approach will be presented. Such models could be easily adapted for other infectious diseases of swine (e.g. FMD, PRRS, etc.).

Characterization of swine movement networks in southwestern Ontario, Canada

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The study objective was to characterize swine movements in southwestern Ontario, Canada during the period 2006 to 2007 using social network analysis. The ultimate goal was to use these results for agent-based network simulation modeling of influenza spread in swine. Data describing swine movements between premises (20 sow herds, 69 nursery and 162 finishing farms plus 91 abattoirs-network A) and premises' attributes (farm types, herd sizes, etc.) were extracted from a database maintained by a large swine health and management company. Analyses were carried out separately for the network A and a subset of data with farms only (network F). In the network A, a total of 13,177 movements were observed between 1,150 links amongst 342 premises. The highest movement frequency was observed from finishing to abattoirs (49%), followed by those from sow herd to nursery (28%), and from nursery to finishing herds (12%). Network F contained 5,760 movements between 810 links amongst 245 farms. The average daily movements between swine farms ranged from 0.0027 to 0.3712. The overall medians (ranges) of movement off- and to-premises were 14 (0-409) and 6 (0-3,333) respectively for network A, and were 1 (0-409) and 8 (0-363) for the network F. Both networks demonstrated small-world (presence of local clusters of movements between premises with few long-range movements between clusters) and scale-free properties. Scale-free network indicated presence of few premises with relatively high number of contacts compared to most others. Consequently, heterogeneities of the contacts and network topologies must be considered in simulation models to improve accuracy of predictions of diseases spread and control measures. In conclusion, this study provided useful parameters for modelling diseases spread in swine that was not reported in Canada previously.

Bayesian spatial and temporal distribution of the risk of campylobacteriosis associated with travel in New Zealand

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With increasing travel and trade opportunities, there has been a greater risk of contracting enteric illness across borders. In this study, a hierarchical Bayesian spatio-temporal regression model for travel associated campylobacteriosis was fitted to data about the annual number of reported cases in short term travelers returning to New Zealand during 2000-2005. The data consisted of travel patterns (from Statistics New Zealand) and the number of notified campylobacteriosis cases amongst travelers returning to New Zealand from several regions of the globe. A total of 58,061 cases were notified and 1,769 (3%) were travel associated; however, for more than half the cases (58%), short term travel status prior to notification was unknown. Therefore analysis to estimate the risk from traveling was restricted to the confirmed travel cases. We used all the cases to estimate the risk distribution in different Regional Councils (RC) of New Zealand in the five year period. At the outset, the expected baseline risk of campylobacteriosis was assumed to be the same for all RCs. A Bayesian Poisson gamma model which accounts for both correlated and uncorrelated heterogeneity was fitted to determine the smoothed estimate of relative risk for disease across travel destinations and RCs. The results of the analysis have shown a trend in the risk of travel associated campylobacteriosis for traveling to different regions, and a distinct distribution of risk in the different RCs of New Zealand. The spatial & temporal structures accounted in the model have broad applications to predicting future spatio-temporal distributions of other diseases in other regions of the world. This work is funded by the National Institutes of Health Ruth L. Kirschstein National Research Service Award Institutional Training Grant T32 RR023916 from the National Center for Research Resources.

Planning low pathogenicity avian influenza virus (LPAIV) surveillance in a live bird market: integrating the laboratory, field and computer

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Low pathogenicity avian influenza virus (LPAIV) may cause morbidity and mortality in domestic and wild birds and severe economic losses for commercial poultry operations. Live bird markets (LBMs) are settings where birds from several locations come into contact with other birds, poultry workers and the general public. Control of LPAIV is dependent on development of an efficient LPAIV surveillance program in LBMs, which may be assessed using simulation modeling. The development of a simulation model involves the integration of a variety of tools necessary to properly specify model parameters. In our situation, it was necessary to perform virus transmission trials generating data that were analysed with advanced statistical techniques, and then combine these findings with production and field data in order to parameterize a disease spread model. Only then, were we able to accurately assess alternative control strategies. In this study, we will report the results of simulated LBM-LPAIV transmission trials, the application of Bayesian statistics to quantify transmission coefficients of multiple virus transmission routes and infection state durations, combined with the specification of an LBM network in a computer simulation model. The approach used to simulate virus spread in the LBM network in a spreadsheet format will be illustrated. In addition, results of the simulation model will be presented to compare the efficiency of alternative surveillance strategies, including sample size and testing frequency calculations. Findings show the benefit of a multidisciplinary approach in solving disease control policy issues.

Non-inferiority clinical trials to evaluate the efficacy of teat disinfectants

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Protocols to evaluate the efficacy of teat disinfectants are based on those approved by Nat'l Mastitis Council. An experimental disinfectant is superior to an established one in studies planned as superiority trials. The aim could be just to show that an experimental product is not superior but equivalent to or not inferior to an established control. Collecting duplicate milk samples from all quarters at evenly spaced intervals is the basis of current protocols, but low SCC quarters are most likely to show negative results when cultured. Single quarter milk samples may be sufficient to define the bacteriological status of a quarter. Thus combining single quarter milk sampling and SCC thresholds to define eligibility for samples to be cultured might be adopted to test teat dips. Our objective was to describe the methodology to compare the efficacy of an experimental teat dip (ED) vs. a control (CD) based on proving non-inferiority. Trials have been designed as one-sided studies to demonstrate the ability to reduce naturally occurring new IMI. Two trials were conducted on commercial dairy herds to demonstrate that the difference in effect (risk of new IMI=ED-CD) should be no less than $-\Delta$. A new IMI rate of 0.03 was assumed for the CD, and a detectable difference between ED and CD $-\Delta=0.03$ (doubling of new IMI). The essence then was to identify whether the conclusion of no difference could be interpreted as a non-inferiority claim, also based on a proper power calculation of the performed trial. Logistic mixed models were used for analyses. Differences in new IMI were negligible, thus the ED were not inferior to CD. We conclude this with a power of 81%. For all practical purposes, this was as close as possible to concluding that the ED were equal in efficacy, providing evidence of a valid and field-tested methodology to evaluate the efficacy of teat dips under the assumption of non-inferiority.

A data mining approach to assessing EAD risk scenarios: an example of using cattle movement records to assess the effect of saleyard amalgamation

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Saleyards (or livestock markets) are critical points in the transmission of infectious exotic animal disease (EAD). Not only is there mixing of animals from different farms, but the stress of travel and intermingling can lead to increased shedding and /or susceptibility to infection. In addition, where saleyards receive and dispatch animals over long distances, the possibility for rapid spread over wide areas becomes possible. This was the case of the foot-and-mouth disease incursion in the UK in 2001, where sheep markets were a critical determinant in allowing the initial outbreak to become an epidemic. Traditionally in Australia, each rural town possessed a saleyard. However, in the past 10 years, the national saleyard network has become more regionalized with significant numbers of the smaller saleyards closing down. In order to assess the potential effect of this saleyard amalgamation on the management of an infectious exotic animal disease outbreak, we data-mined approximately 38 million records from Australia's cattle movement register, the National Livestock Identification System). Based on the presumption that one of the biggest challenges in managing an EAD event is tracing of potentially infected animals, we explored scenarios of a single infected animal entering a saleyard of five size categories. This nationwide analysis using all available data, was run for scenarios of spread of disease before detection of 1, 2 and 3 weeks. The estimated number of farms to be traced varied from a median of 5 from a small saleyard and 1 week of silent spread to median of 3,549 from a large saleyard with a three 3 week non-detection period, with a maximum number of 12,691 farms to be potentially traced. The results demonstrate the greater hazard posed by saleyard amalgamation, but this need not equate to greater risk, if these larger saleyards have in place better disease detection and/or tracing capability

Sample size optimization through a multimodel approach

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To assess disease transmission risk in developing countries, decision makers generally rely on livestock distribution estimates from survey records or projections of outdated enumeration results. Given the high cost of large-scale surveys, sample size is often restricted and the accuracy of estimates is low, especially on a high spatial resolution. Therefore, this study explores possibilities of improving livestock distribution map accuracy by applying spatial modelling procedures. Regression tree forest and multiple regression models were developed using subsets of the Uganda 2008 Livestock Census data and several covariates. The accuracy of the modelling techniques was evaluated by comparing the modeling results, aggregated at different administrative unit levels, with results from the complete census dataset. Because individual survey records, which are used to train the spatial models, hold important information about local livestock abundance, the accuracy of averaging spatial modelling results with locally aggregated survey records was also evaluated. Relative error analysis shows that spatial modelling results are more accurate than aggregated survey records when considering administrative units with low livestock numbers. High livestock numbers are often underestimated. When applying a weighted average to spatial model outputs and aggregated survey records, relative errors are significantly lower in each of the livestock abundance classes. The presented multimodel approach thus effectively increases livestock estimate accuracy without increasing sample size. Conversely, this implicates lower sample size requirements for similar accuracy levels leading to a more efficient use of financial resources. Main issues to consider when applying the described approach are the differential weighting of the aggregated model outcome depending on sample size, the weight of the spatial model and which administrative unit level to aggregate to.

Predicting the structural development in Danish livestock and how it affects control strategies against FMD

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The purpose of this study was to assess if the optimal control strategy against foot-and-mouth disease (FMD) spread is invariant to structural development in Danish livestock until 2030. The DTU-DADS model as presented by Halasa *et al.* uses demographic information of all farms including their location, size, and production type. The main challenge was to predict the demographic data. Based on data for all herds with animals susceptible to FMD in the Central Husbandry Registry from 1999 to 2010 and supplementary data for swine herds from Danish Agriculture & Food Council (2002 to 2009), all farms were classified by production type and size each year. A total of 88 classes were used. For each species group (cattle, swine, and sheep and goat) a transition probability matrix (TPM) was estimated based on the ten year to year transitions. It was hypothesized that there might be regional differences. This was assessed by dividing Denmark into 7 regions, counting all transitions per region, and comparing these counts to the country wide counts using a Chisq test. Due to the regionalization some of the less populated size categories were merged to reduce noise. All regions were found to have significantly different TPMs. These TPMs were used in a Markov chain to predict the distribution of farms in year 2030. However, the predictions were unrealistic as far too many farms opened – since all closed farms were allowed to reopen. It was decided to make the closed state a terminal state and make an independent prediction of how many farms should open each year. The best model was a log-linear model for each region. The combined result is a reduction from 51,031 herds in 2007 to 14,126 farms in 2030 with larger average size. From an economic point of view the best control strategy in 2030 will be depopulation whereas vaccination no longer is better than the basic EU control strategy.

How do we set the probability of introduction in a scenario tree model to demonstrate freedom from disease?

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As part of surveillance to demonstrate freedom from disease we may apply scenario tree models to estimate the probability that a population is free. Briefly a presentation of scenario tree models may be organized in five distinct categories: (1) definitions to present the objective (case definition (CD), population, design prevalence (DP), time period (TP)); (2) starting point; (3) inputs (probability of introduction (PrIntro), diagnostic test sensitivity); (4) data; and (5) outputs (system sensitivity, probability of freedom (PrFree)). With PrIntro we understand the probability that the disease is introduced to the population and it spreads among the units to the level of the DP in a TP. Therefore, PrIntro depends on the DP and TP. In addition, the TP should be defined to meet the underlying assumption of the model that the disease status of the units are independent from one time period to the next. Finally, the CD may affect how we determine the DP. We postulate that the impact of PrIntro and its relationships with DP, TP and CD may not be well understood. This is a problem in development of scenario tree models because a) the impact of PrIntro on the outcome PrFree may be substantial and b) PrIntro is very hard to determine empirically. A common way to determine PrIntro is to divide I by the number of TPs that the population has been free from the disease. We summarize how DP, TP and PrIntro were determined in published scenario tree models and then explore and describe the relationships in a simulation study.

A mathematical model to investigate the transmission of CTX-M genes between *E. coli* in the bovine gut

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Commensal *Escherichia coli* are bacteria commonly found in both livestock and people and they can also be involved in disease in both. As infection is generally asymptomatic, the bacteria can enter the food chain undetected and infect people. Extended spectrum beta lactamases are enzymes that break down 3rd and 4th generation cephalosporin antibiotics, which are commonly used as front line treatments in hospitals. CTX-M genes encoding for these enzymes are usually carried on plasmids and studying the molecular epidemiology of these genes is key to understanding their origin and spread and hence for designing control measures. We propose a model specifically designed to model the resultant transmission of CTX-M genes between donor and recipient bacteria in the bovine gut, via conjugation and transduction, due to invasion of 'foreign' donor bacteria. We parameterise the model based on the bacteria being strains of *E. coli* and use it to investigate the effect of cephalosporin use in cattle, which kill off and inhibit the growth of recipient bacteria. Based on comparing the model results with those of an experimental study, we extend the deterministic model to stochastically simulate the variability in the duration of infection and concentration of bacteria during the latter stages of infection, when levels shed in faeces are generally below the limit of detection (102 cfu/g), but sporadic 'spikes' in concentration of up to 104 cfu/g are observed. The model results suggest an association between antibiotic usage and high CTX-M levels. In the baseline model, initial concentrations of up to 107 cfu/g of CTX-M *E. coli* will decay exponentially, generally reducing to below 102 cfu/g within 10 days. However, when cephalosporins are used the bacteria persist for longer in higher concentrations. This could have consequences for farm level transmission, with high levels of bacteria being shed in the environment by infected animals for longer periods of time.

Modelling the within-herd transmission dynamics for bovine tuberculosis in British cattle

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Bovine Tuberculosis (bTB) in British cattle has been an increasing problem since at least the early 1970s. The control of bTB is mainly based on regular herd testing, slaughterhouse inspection and pre-movement testing in Great Britain. Each herd is regularly tested at intervals of 1-4 years and if an infection is found the infected animals are culled and the herd quarantined. We present a mathematical model of bTB transmission incorporating latent stages, a wildlife reservoir, animal ages and testing strategies. The model is run for bTB test data and a 'typical' herd areas using breakdown data from herds in 1 and 4 year testing areas. Several models including herd and individual super-spreaders are compared and assuming no knowledge of the parameters in the model, we determine those that maximise the likelihood of observed breakdown patterns. The transmission parameters obtained using this model broadly agree with accepted values but with low test sensitivities which are consistent across the areas modelled. The observed breakdown patterns are best explained by incorporating a small percentage of super-spreading individuals and herds into the model. From the parameters obtained from the model estimates of the time to detection of the disease within a typical herd show that 75-80% of the disease is captured by current testing strategies.

Modeling endemic foot-and-mouth disease virus transmission in Cameroon

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Foot-and-mouth disease is endemic in the Far North Region of Cameroon, where preliminary data show at least annual outbreaks. In this host-pathogen system, multiple serotypes infect migratory cattle. Mobile pastoralists in the region go on seasonal transhumance and share pastures with sedentary pastoralists and trade cattle from regional and international networks. To test competing hypotheses about sources of Foot-and-mouth disease endemicity, we use nested susceptible-exposed-infected-recovered (SEIR) models. First, we investigate seasonally dependent transmission driven by transhumance. Second, we probe seasonal changes in survivorship. Third, we test the effects of waning maternal and convalescent immunity. Third, we investigate the role of carrier animals, defined as those who have been persistently infected with foot-and-mouth disease virus for 28 days or longer. Lastly, we assessment host movement between herds, defined by local trade. Our work shows how mathematical models can be used within a hypothesis-testing framework and is important since identifying sources of long-term viral transmission can be helpful for optimal veterinary intervention of this harmful pathogen.

Bovine mortality predictive model: a new tool for veterinary-based syndromic surveillance

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Mortality monitoring contributes to early detect the introduction of diseases, guide risk-based surveillance programs and assess timely the impact of veterinary and public health threats, providing information for decision-making. The use of syndromic surveillance increased as new information systems making possible the exchange of data in near-real time are available. The objective of our study was to model unspecific mortality baseline in cattle in order to identify excess mortality and generate alert signals. This study covered a specific area of Spain. Data were obtained from the State Agency of Agricultural Insurance and the National Registry of Farms databases. Individual death records included information on date of carcass removal, animal ID, farm ID and production type. We analyzed cattle weekly mortality from 2005-2010. Specific mortality baseline was estimated for dairy cows, suckler cows and fattening calves. Data variability was stabilized by applying a Box-Cox transformation. A Serfling model, adjusted by Minimum least squares, was used to analyze trend and seasonality. We considered three thresholds (80%, 90%, 95% IC) to establish low, medium and high risk signals. A CuSum algorithm was used to quantify short term deviations from expected mortality. Models showed significant 6-months cycles, peaking in spring and autumn. In the study period 28 signals were detected: 14 low, 3 medium and 11 high risks. Four signals were observed in calves, 12 in dairy and 12 in suckler cows. This system considering different risk thresholds allows for easy classification of signals. We are working with veterinary authorities to verify signals generated, assess model performance with 2011 data and extend this model in other regions to strengthen the traditional surveillance systems in place.

Rift Valley fever in Kenyan pastoral livestock: simulation with an individual-based demographic model

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Rift Valley Fever (RVF) is a viral zoonosis and a mosquito-borne disease caused by a phlebovirus in the family Bunyaviridae. It affects livestock, humans and wildlife. Epidemic outbreaks of RVF in East Africa, which occur after heavy rainfalls in cycles of 5-15 years, have caused next to human morbidity and mortality considerable economic losses throughout the livestock production and market chain. Establishment of a pastoral livestock demographic model simulating alternating normal and drought periods (appropriate for the Sahel) and RVF epidemics. We have developed an individual-based model to simulate the following scenarios (1) the demographic dynamics of cattle, camels, sheep and goats in North Eastern-Province; (2) an RVF outbreak in livestock and the RVF immunity status afterwards; and (3) impacts of control measures (combinations of vaccination, sanitary measures, surveillance, vector control and awareness campaigns). The baseline and RVF-attributable mortalities can be simulated and show the losses due to RVF. Further, we can retrieve proportions of affected animals, grouped in species, age classes and sex, as well as the number of infected slaughtered and sold animals. Sheep and goats are most likely to spread the disease through livestock trade. Slaughtered infected sheep are an important risk factor to human RVF infection. Our results assist in the assessment of cost-benefit and cost-effectiveness of interventions which should improve future intersectoral livestock – public health contingency planning. The ratio of susceptible/immune hosts can further support the prediction system by consideration of the immunity levels years after a previous outbreak.

Space-time modelling of the spread of salmon lice within and between marine salmon farms*Aldrin, M. and Storvik, B., Norwegian Computing Center, Norway; magne.aldrin@nr.no*

Infectious diseases constitute a constant threat to the marine fish farming industry with major economic implications, in addition to being a problem for fish welfare and the environment. Sea lice are parasites that occur in both wild and farmed salmon. In the recent years, the incidence of sea lice in Norwegian marine salmon farms has increased significantly. Every month, the number of lice are counted on a small sample of fish (twenty, say) at each salmon farm in Norway, and the lice frequency, i.e. the average number of lice per fish, are reported to a central data base. We have developed a stochastic space-time model where the monthly lice frequency at all Norwegian salmon farms are modelled simultaneously. The set of salmon farms are regarded as a network where the degree of contact between each pair of farms depends on their seaway distance. The expected lice frequency at a each farm is modelled as a function of (1) the lice frequency previous month at the same farm; (2) the lice frequencies previous month at neighbouring farms; and (3) other, unspecified sources. In addition, the model includes explanatory variables such as sea temperature and fish abundance at each farm. The model can be seen as a complex vector autoregressive model, where the response variables are counts, the dimension is very high (about 1,400 farms) and the autoregressive coefficients are highly structured (depend on seaway distances, sea temperatures etc.). The model may be used to investigate the effect of various measures to reduce the incidence of sea lice. Of special interest could be simulations of various scenarios with regard to geographic location of fish farms. The work has been performed in close cooperation with the Norwegian Veterinary Institute and the Norwegian Institute for Nature Research.

A new tool for risk-based surveillance combining network analysis of animal trade and probability of disease introduction based on known animal movements and disease prevalence*Frössling, J.^{1,2}, Nöremark, M.² and Lindberg, A.², ¹Swedish University of Agricultural Sciences, Sweden, ²National Veterinary Institute, Sweden; jenny.frossling@sva.se*

In recent years, network analysis has become established in veterinary epidemiologic research. The different measures that are being used have usually been developed within other fields of research and therefore there is a need to evaluate their usefulness within the veterinary field, and also to develop new measures for specific disease control purposes. A new measure, the ingoing infection chain, has recently been proposed. It includes the direction and the temporal order of the contacts, and has been used to analyze contacts between cattle herds as regards live animal trade and potential introduction of disease. In this paper, this measure is developed further to include also the number of animals purchased. In addition, disease prevalence at different levels in the population is taken into account. For each trade contact, the probability of purchasing at least one infected animal is calculated considering the total number of animals purchased and the expected prevalence of disease within the herd of origin. In case there are known high-risk categories, different prevalences for different population strata are applied. The total probability of introducing disease through the purchase of animals is then calculated based on all purchases and the between-herd prevalence. The calculations are performed in a stepwise manner where the probability of disease at each step in the chain of contacts acts as a prior for the next. Examples are given for different diseases (bovine corona virus infection and bovine paratuberculosis) and a simple dataset of cattle trade to illustrate how this measure captures the characteristics of the specific diseases. The approach can be useful for classifying herds for disease control and surveillance purposes.

Between farm contacts in western Kenya: implications for disease transmission

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The transmission dynamics of infectious disease depends on the frequency and type of contacts between susceptible and infectious individuals or groups. Between-farm contact structures have been defined in several countries, and have been widely used to model disease spread. In this study, we describe the farm contact structure in an area of western Kenya where the frequency and range of between-farm contacts was previously unknown. We focus on the specific between-herd contacts that are thought to be risk factors for the transmission of *Brucella* spp.. Through door-step interviews, all cattle farmers within a single 30 km² administrative area, chosen as being representative of the diversity of cattle production systems present within the wider Western province of Kenya, were asked to report the identity and frequency of contacts with neighbouring herds, including co-grazing, the use of shared water points, and shared bulls. Moreover, the on and off-farm movement of cattle from within and outside the area under study, as well as a range of farm husbandry and production practices, were characterised. The between-farm contact network was investigated using social network analysis. To test for non-random interactions based on production type, we used multivariate statistical approaches to classify farms into distinct 'sub-groups' based on animal and farm management practices. This was followed by a set of 'mixing matrix' approaches in which herd assortativity based on sub-group membership was assessed. The contact network defined by this study will be used to inform disease transmission models for brucellosis in western Kenya. In particular, understanding the mixing patterns of different animal production systems in this mixed farming area will contribute to models describing animal reservoir dynamics for human brucellosis.

A within-herd state transmission model for MAP infection in farms co-grazing deer and sheep in New Zealand

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Pastoral farming in New Zealand (NZ) is characterized by all-year grazing and strong seasonality of production cycles. Sheep, beef and deer commonly co-graze on the same pasture concurrently or sequentially. *Mycobacterium avium* subspecies *paratuberculosis* (MAP) is the causative agent of Johne's disease (JD), occurring worldwide in farmed ruminants. JD is a chronic wasting disease limiting the production in intensive farming systems. MAP infection is endemic in all livestock species in NZ. This pathogen is sub-classified into type I (S, sheep) and type II (C, cattle) strains. In mixed species pastoral systems, both MAP types occur, are transmitted between species, and have been associated with different prevalence of infection and incidence of JD on New Zealand farms. Considering the interaction of C and S strains on inter-species MAP transmission dynamics allowed us to evaluate the beneficial impact of selected co-mingling strategies on prevalence of infection and incidence of JD in the two respective species. We developed a two-host two-strain state-transition model of MAP transmission dynamics among deer and sheep grazing the same pasture. The transmission was driven primarily by pasture contamination. Seasonal density changes and age-related grazing management influenced pasture contamination levels. MAP transmission was simulated with both type I and type II strains competing for hosts. The impact of two co-grazing interaction types between deer and sheep were studied (either concurrent or sequential). This model predicts the prevalence of MAP infection and incidence of JD in sheep and deer with two different strains of MAP, for different patterns of co-grazing. This contributes to identify optimal co-grazing strategies in multi-species farms regarding JD management.

A two-strain mathematical model of paratuberculosis in a sheep-beef pastoral farming system in New Zealand

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A deterministic model simulating the transmission dynamics of *Mycobacterium avium* subspecies *paratuberculosis* (MAP) and the effect of control measures on prevalence and clinical incidence was developed. The model considered the most common farming system for beef and lamb production characterised by whole year grazing both sheep and beef cattle jointly or in sequence with a strongly seasonal reproduction cycle. MAP was shed into the environment leading to indirect transmission. The model assumed closed breeding herd/flock, all-year co-grazing with random mixing of sheep and beef cattle, and a homogenous dispersion of MAP on pasture. All MAP transmission other than vertical/pseudo-vertical pathways was assumed to be due to indirect transmission through contaminated pasture. The model was calibrated based on field data on infection prevalence, clinical incidence, and associations between MAP-strains and host species. A recent survey indicates that MAP infection is widespread in sheep and beef cattle flocks/herds and suggested that most beef cattle herds were infected with MAP type I (S, sheep) strains commonly associated with sheep and assumed to be less pathogenic in cattle than MAP type II (C, cattle) strains. Most sheep flocks were infected with S strain. Our model assessed if beef cattle were able to sustain MAP type I infection after paratuberculosis was reduced in sheep, and vice versa, sheep were able to sustain MAP type II infection after paratuberculosis was reduced in beef cattle. Control measures included the variable use of pasture and the effect of management interventions such as test & cull or vaccination.

Network analysis of livestock movements in New Zealand pastoral farms in regard with disease transmission

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Social network analysis (SNA) provides valuable information to predict herd-level disease status. Livestock movement data for 2006 to 2010 were provided from Landcorp Ltd. (LC), a state-owned enterprise comprised of 127 farms throughout New Zealand (NZ). In total there were 3,531 movement events involving 1.15 million sheep, cattle and deer. In this paper we describe our analytical approach and its relevance to the transmission of infectious disease. Contacts were defined at the level of batches or valued with the number of animals (relevant for chronic disease transmission). Most movement events (97%) were within the same island (97%) rather than between the North and South islands. The network showed a high level of clustering of farms. There was a high variance in the number of individual contacts per farm and a positive correlation between the number of contacts in and out of farms. This could favour disease transmission through highly connected farms. Depending on the year, 82 to 95% of farms were directly or indirectly connected by animal movements, facilitating transmission of disease. Removing the 10% of farms linking the clusters contributed significantly to disconnecting the network, which fell apart into smaller, less interconnected clusters. Analysing the consistency of movements between years showed that the number and intensity of contacts were consistent across years. However, 80% of farms shifted their trading partners between years. Time (in)consistency of the pairs of farms is an appropriate measure to analyse farm-to-farm transmission of chronic diseases such as paratuberculosis. SNA identified central farms in the observed contact pattern. We show the potential impact of targeting these farms to efficiently decrease the connectedness of the network. The understanding of the pattern, intensity and consistency of contacts is a first step for evaluating associations between movements of livestock and infectious disease.

Quantifying and comparing input parameters based on GPS data of wild pigs in California, U.S.A.: implications for wildlife disease models

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Feral swine/wild pig populations are dramatically increasing in the U.S.A. and their distributions are becoming more widespread. Estimates of their numbers are over 5 million, with the majority of feral swine located in Florida, Texas and California. They pose serious risk for transmitting diseases in domestic and wildlife populations. Exotic transboundary diseases, such as foot and mouth disease and classical swine fever, introduced into this population could go undetected for prolonged periods of time, self-limit, or become endemic. Computer modeling is one tool that can be used to help understand a biologic system and predict the behavior and responses of disease spread to interventions when it is not possible to evaluate these on the real life system itself. However, high model confidence cannot be obtained without appropriate and sufficient empirical data as these data are needed to develop model input parameters. As such, we collected data from wild pigs fitted with GPS collars in various landscapes and ecoregions in California between 2010 and 2011. We used GIS and longitudinal analyses to quantify the spatial structure and movement behavior of wild pig populations across various landscapes. These input parameters were also compared by hog type, sex, age, time of day, and ecoregion. Quantification and distributions of these types of input parameters, and an understanding of their uncertainty, are needed in order for disease models to be developed and simulate infectious disease spread with confidence.

Effect of mixed livestock production types on foot and mouth disease outbreaks and interventions

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The central United States (U.S.) has a large livestock population including cattle, swine, sheep and goats. Simulation models were developed to assess the impact of livestock herd types and vaccination on Foot and Mouth Disease (FMD) outbreaks using the North American Animal Disease Spread Model (NAADSM), a spatially explicit, stochastic infectious disease model. Based on data from the U.S. Department of Agriculture National Agricultural Statistic Service, a simulated population of livestock operations was generated. The population included 151,620 herds defined by latitude and longitude, production type, and herd size. For the simulations, a single 17,000 head feedlot was selected as the initial latently infected herd in an otherwise susceptible population. Contact rates between herds were based on survey data of livestock producers in Kansas and Colorado or estimated from expert opinion. The livestock producer survey indicated a significant proportion of mixed beef-swine herds (approximately 8% of herds) not accounted for in previous models. As such, scenarios were simulated in two populations, one without beef-swine herds and one with beef-swine herds. Scenarios were simulated in each population with either no vaccination or a vaccination ring around each infected premise. The results of the scenarios were compared to assess the effect of mixed beef-swine herds on the impact of the outbreak and the effect of vaccination. Results demonstrated that the inclusion of mixed beef-swine herds had minimal impact on the median duration of disease, and the total number of herds and animals destroyed. While, inclusion of mixed production types could increase the contact rates between different livestock production types this did not seem influential for the modest proportion of mixed production types in these scenarios. Modeling of FMD outbreaks may be robust to small misspecification of production types.

Risk targeted surveillance for avian influenza in Cuba

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In order to increase the sensitivity of the active surveillance system for avian influenza (AI) a risk based model was developed to identify areas at higher risk of disease introduction, represented for Cuba by the migratory waterfowl transit in autumn and spring. A map with the risk of introduction of AI was constructed by Suitability Map with ArcGIS 9.3.1 de ESRI. This model considered distance from settlement of migratory waterfowl, densities of farms and poultry in a particular area combined by tool weighted overlay. The spatial model permitted to better focus the sampling activities, definitively improving the overall sensitivity of the AI surveillance system. The possible exposure of the population most at risk to be exposed to the infection, considering the consequences of such exposure, in terms of animal densities and the existence of the flocks with higher economical importance was also evaluated to better target the surveillance system.

Network analysis of cattle movements in relation to bovine tuberculosis transmission risk in Minnesota, US

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Bovine tuberculosis (BTb) was first diagnosed in cattle through slaughter surveillance in Minnesota (MN) in 2005. By the end of 2008, 12 cattle herds had found to be infected with BTb, and one of the causes for infection was determined to be the movement of infected animals between herds. USDA granted split-state status to MN in 2008, upgrading most of the state to modified-accredited advanced and only a smaller area of 6,915 km² in northwestern Minnesota as modified accredited (MA). The state has now been declared BTb free; however, since January 2008 all cattle movements within the MA were recorded. The objective of this study is to characterize cattle movements in a high risk area for BTb in MN and also identify which herds might have a higher risk to become infected and to infect other herds. The data used in this analysis includes the years 2008 through 2011. During this period, 3,762 movements were recorded with 57,460 cattle being moved, corresponding to permits issued to 682 premises, mostly representing private farms, sale yards, slaughter facilities and county fairs. Although, sale yards represented less than 2% of the nodes (premises), 60% of the movements were to or from a sale yard. Less than 2% of movements, both into and out of the MA zone involved locations outside MN (other states and Canada). Movements occurring between herds in the MA zone corresponded to 24% off the total number of movements. Preliminary network analysis was performed on 35% of the data (complete analysis will be presented at the conference). The network showed a density of 1%, a fragmentation of 88% and a clustering coefficient of 56%. The betweenness centralization index was 6.52%. The degree distribution showed that 25% of nodes performed 81% of movements. This analysis provides novel description about the contact structure of cattle movements in a high risk area for BTb, essential to support future surveillance decisions.

The impact of a delay in detection of a contagious disease on epidemic size in Western Australia

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Australia exports around one billion dollars worth of livestock every year. The impact of an outbreak of a disease that risked this trade could have a devastating effect on the economy if it were allowed to spread unchecked. The effect of a delay in detection in terms of the overall affected area was assessed using network analysis. Records of cattle movements in Western Australia were extracted from the National Livestock Identification System (NLIS) database for the period July 2005 to June 2008. The records were de-identified to ensure privacy. The origin and destination of each record was limited to the level of the local government area. The data were analysed for spatial and temporal patterns. Network analysis was used to identify important characteristics of the data related to disease spread. Nearly four million records were analysed. Significant seasonal variation in movement patterns existed, against a background of an increase in the number of movements recorded. A small number of shires are central to a large proportion of all cattle movements. A web-based query tool was developed to allow rapid analysis of a user defined subset of the data. Mandatory notification of cattle movements has created an opportunity for greater understanding of the movement of livestock in Australia. Every doubling of the time to detection could result in an additional 15 local government areas becoming infected. Restrictions on the use of the data are limiting the value of this resource for planning and protecting the livestock industry.

Epidemiological aspects of swine industry animal movements network in Minas Gerais, Brazil

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International trade requires accurate tracking of animal products by country members. Brazil stands as the fourth greatest producer of swine, producing more than three million tons per year. Minas Gerais is the fourth largest state in swine production and exhibits the classical swine fever free status. This article aims to describe a GIS-based epidemiological study for characterizing swine movement network in Minas Gerais. The swine industry involves the intensive animal movement, producing a complex network, interconnections which may represent risk of transmissible disease spread. Detailed description of transportation network may evidentiate the key disease risk pathways. Data provided by the Minas Gerais State Agriculture Institute involved 58,823 animal transportation authorizations issued in 2009 which were studied in three stages: descriptive, spatial and network flow dynamics analysis, involving 5,354,735 swine. After the descriptive, spatial analysis was performed by the software Terraview 4.0.0® and the flow analysis was carried out using the software Pajek 1.24®, both freeware. Network flow dynamics analysis revealed more intensive movement to slaughter house (79.95%) followed by finishing (10.64%) and reproduction purposes (9.38%). Transportation of swine in Minas Gerais is concentrated in five of its twelve regions, and all companies and compartments of the swine industry are connected. The network approach, based on graph theory, can be used more efficiently to the development of swine disease control programs and crisis management, because it considers the heterogeneity of the swine flow of Minas Gerais.

FAO EMPRES-i: a tool for early warning of animal diseases

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The increase in occurrence and emergence of Transboundary animal diseases (TADs) in countries around the world calls for timely and reliable disease information to enhance early warning and response. The web-based FAO EMPRES Global Animal Disease Information System (EMPRES-i), was designed to support country level veterinary services in this regard, facilitating access to regional and global disease information. The EMPRES-i system collects and processes animal disease outbreaks information to support analysis, risk assessment and early warning activities. New features being developed such as a module to collect information on animal disease surveillance activities implemented through FAO projects and joint projects with national, regional and international partners. In addition, a first genetic phylodynamics module is currently being designed to integrate genetic data from influenza virus sequences stored in open databases, such as Openflu for H5N1 HPAI viruses. IN the near future this module will be extended to include data from the FAO/OIE World Reference Laboratory Pirbright on sequences available for FMD virus. A mobile application prototype for smart phones is being developed, to be used for rapid reporting of disease information from the field will be available in 2012.s. Data sharing and interoperability is a key activity promoted by FAO EMPRES/GLEWS to enhance surveillance and early warning. FAO is further integrating databases with other information systems. Data sharing is also a key activity of the implementation of the Joint FAO/OIE/WHO Global Early Warning System (GLEWS). This paper describes the system with particular focus on new developments implemented and collaborations undertaken to better enhance early warning.

Introducing SERVAL: a new generic framework for the evaluation of animal health surveillance

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Animal health surveillance programmes tend to evolve but are rarely evaluated to ensure that they provide valuable information in an efficient manner. The evaluations that are conducted are often unstructured and therefore incomplete. To address this gap, we have developed SERVAL, a SuRveillance EVALuation framework, which is novel and generic and so suitable to evaluate any animal health surveillance system. SERVAL has been designed to assist in the comprehensive evaluation of single surveillance components (activities) or entire surveillance programmes. It is intended to be very flexible so it may be used to evaluate surveillance for any health condition in any species (or group of species). It is anticipated that its main use will be in the evaluation of existing surveillance systems but we believe that it will also prove useful in the design phase of new surveillance programmes. The SERVAL framework was developed following a technical workshop of international experts and a consultation process involving providers and user of surveillance and evaluation data. It has been applied in several case studies encompassing varying surveillance and evaluation objectives. Anyone familiar with epidemiological concepts and with a reasonable knowledge of a disease under surveillance should be able to use the SERVAL framework to conduct an evaluation. In this presentation, we will give an overview of the structure of the framework and illustrate how to use it. We will show its flexibility at facilitating comprehensive evaluations of animal health surveillance systems with a range of surveillance and evaluation objectives. Users' experiences of the framework will be discussed. This project is funded by Defra.

the effectiveness and enhancement of reporting of suspect exotic disease by private veterinarians

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The interaction between the private veterinary community and the farmer clients is an important means of passive surveillance for exotic disease in livestock. It is likely that the private veterinarian will be the first one to observe clinical signs relating to an incursion of a number of exotic, production limiting diseases in livestock. Hence, early reporting is essential to an efficient and effective response. A comparison was made between the reporting of suspect exotic disease by a veterinarian trained as an epidemiologist and skilled in exotic disease recognition and the wider veterinary community. This veterinarian was assumed to be the benchmark for the quality of reporting possible within an effective surveillance system. The frequency and validity of the reports made by the benchmark veterinarian was assessed by determining the number of reports made per unit time in relation to the number that resulted in a formal exotic disease investigation by government officials. The reports from the benchmark veterinarian were compared to the frequency and validity of reports made by other large animal veterinarians. On the basis of this assessment the potential level of under reporting was estimated. In conjunction to this analysis approximately 281 private veterinarians were surveyed in order to assess factors that might influence reporting. Factors examined in the survey included the country where veterinary training was received (local versus overseas); age, gender, experience of veterinarian; location of the veterinary practice. Different methods of publicising the process of reporting were examined as well as the timeliness of current reporting. The results from this survey are summarised.

Highly pathogenic avian influenza surveillance on the Gangetic Plains, a cost-benefit analysis

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Despite considerable efforts to control and eradicate Highly Pathogenic Avian Influenza (HPAI), subtype H5N1, the disease remains present in South Asia. HPAI causes great economic losses to the poultry industry and still has the potential to trigger a human influenza pandemic. This study compares the effectiveness and costs of different HPAI surveillance systems. From the countries, India, Bangladesh, Nepal and Bhutan, the HPAI situation, the economy of the poultry industry, the losses caused by HPAI, the costs of surveillance and response and the effectiveness of the national and regional control programs are recorded and compared. India conducts extensive and frequent sero-surveillance in all 35 states. Weekly over 1000 diagnostic specimens are tested at an annual cost of US\$ 10 million. Bangladesh employs over 1000 community animal health workers and 60 veterinarians to conduct active surveillance, at a cost of US\$ 2 million yearly. Bhutan and Nepal rely on passive surveillance; Farmers, village leaders and community animal health workers report to state veterinarians. Costs of US\$20,000 (Bhutan) and US\$250,000 (Nepal) arise from awareness training. Bangladesh has reported most HPAI outbreaks and suffered the biggest economical losses. Although considerable disease control efforts nationally and regionally, HPAI remains endemic in the Gangetic Plains. The expensive active sero-surveillance in India has not detected any HPAI, instead the disease outbreaks were reported through passive surveillance. In Bangladesh, only 40% of all HPAI outbreaks are detected by the active surveillance system. The current Surveillance systems have contributed to disease control but not sufficient. Our findings suggest that the costs of surveillance in India and Bangladesh are not justifiable and disease control efforts should be re-evaluated.

Relevance of the Indirect ELISA comparing to Real-Time PCR for Q fever diagnosis in sheep

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Q fever is a zoonosis widely reported in the world. The causative agent is *Coxiella burnetii*, an obligate intracellular bacterium. Clinically, the infection is asymptomatic in ruminants, but it can lead to reproduction disorders. In order to determinate the relevance of the Indirect ELISA comparing to Real-Time PCR for the diagnosis of Q fever in ewes at lambing or abortion period, a study was conducted with 56 sera and 61 vaginal swabs collected from the same females. The indirect ELISA was used to detect specific antibodies against *C. burnetii* and RT-PCR to detect bacterial DNA after shedding. Results indicate that 7 sera have a positive value in ELISA test and all the RT-PCR were negatives. Our findings can be only interpreted as an evidence of a previous infection or an ancient exposure to *C. burnetii* and Q fever has a relatively low role in abortion in the study area. We suggest that the indirect ELISA cannot be performed to detect a Q fever infection at an individual level, it becomes very useful for studies at population, especially when laboratories where Q fever can be diagnosed are limited.

Optimization of culture conditions for detecting *Mycobacterium avium* ssp. *paratuberculosis* in wood bison

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Wood bison (*Bison bison athabascae*) are a threatened species native to northern Canada and Alaska. One of the most critical actions for re-establishing viable free-ranging populations has been to translocate animals to begin new herds or to supplement existing ones. An inherent risk of moving individuals is the possibility of spreading infectious pathogens to new herds or geographic locations, for example *Mycobacterium avium* ssp. *paratuberculosis* (MAP), the causal agent of Johne's disease. MAP was previously detected in several wood bison herds using fecal polymerase chain reaction (PCR); however, attempts to culture those samples were unsuccessful. MAP strain(s) infecting wood bison have not been investigated in detail, and it is possible that a genetically distinct form with different culture requirements is present. Small variations in culture protocols can alter the sensitivity of a culture assay and culture requirements may differ depending on the strain of MAP. This study aims to optimize culture conditions for isolation of MAP from bison fecal and tissue samples by evaluating the sensitivity of a panel of different culture conditions (n=18) based on current methods used for MAP detection in domestic livestock. Variations will be made to the type of medium, the supplements added and the decontamination protocols. Fecal and tissue samples from bison that have tested positive by direct fecal PCR will be tested, and results will be presented on the success of the panel of conditions in culturing MAP from these samples. Establishing reliable culture techniques will assist in determining the distribution of MAP among wood bison herds and enable advanced molecular characterization of isolates for further epidemiological study of within and between-herd transmission. Understanding the distribution of MAP among wood bison herds will help facilitate informed conservation management of this threatened species.

A Bayesian model for herd prevalence estimate of Newcastle disease virus

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Newcastle disease virus (NDV) is the etiological agent of Newcastle disease (ND) and can infect domestic and wild birds. It can cause an acute and highly contagious viral disease. Infected birds can transport the virus over long distances and immune carriers can shed the virus indefinitely. Epidemiological data on NDV is scarce in Brazil. The aim of this study is to detect the presence of NDV in backyard flocks in the main wintering site for migratory birds in southern Brazil. The target population comprised all the domiciles raising poultry within 3.5 km around the main wetlands in the region (n=131). Sample size was designed to detect with 95% probability an infected flock with a herd-level prevalence (HP) of 5% (n1=48). Within each flock a fixed number of 9 (n2) birds were randomly selected. Considering an average test sensitivity (TSE=90%) and test specificity (TSP=93%) of a real-time reverse transcriptase PCR (RRT-PCR) applied in tracheal and cloacal swab and a within-herd prevalence of 30%, the average herd sensitivity (HSE) and herd specificity (HSP) were 96% and 76% respectively. A Bayesian model was developed to estimate herd-level prevalence using an uninformed prior with a HP likely to range from 0% to 25%. A binomial distribution was used as likelihood function considering the numbers domiciles infected, sampling size (n=48), HSE, HSP and HP. The posterior distribution for prevalence was normalized using a general function provided in @risk. Ten thousand iterations were used. A total of 411 birds were sampled from 48 domiciles. All swabs were negative in RRT-PCR. The mean HP estimated by the model was 2.1%; the cumulative distribution showed that there is approximately 95% probability that the HP is less than 6.1%. Results suggest that if the NDV is present the prevalence is probably low.

Prevalence of bovine viral diarrhoea virus in bulk tank milk in southern of Brazil

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Bovine viral diarrhoea virus (BVDV) has worldwide distribution and tends to be endemic in most cattle populations, reaching herd prevalence of 60-80%. Economic losses occur mainly due to reduce milk production, respiratory and reproductive disorders and even death among animals that acquire acute infection. For these reasons it is necessary to study the herd prevalence of the disease for the purpose of detection and monitoring infected herds. The purpose of this study was to estimate the prevalence of BVDV antibodies in bulk milk tank samples of dairy herds in an important dairy production region in the state of Rio Grande do Sul, Brazil. The target population was composed by 1,604 dairy herds from which 314 were randomly sampled. Sample size was calculated considering an absolute precision of 5%, expected prevalence of 43%, and 95% confidence level. Samples of bulk milk tank were collected from those herds to determine antibody levels against BVDV by a commercial ELISA test. The results of ELISA were interpreted according to the Swedish BVDV control scheme, which classifies the herds into four different classes (0, 1, 2, 3) based on corrected optical density (COD). About 96.5% of herds were distributed in class 0 or 1 (absence of antibodies or very low prevalence), 2.5% in class 2 and only 1% in class 3 of antibodies to BVDV. The true prevalence of BVDV was 24.3% (IC 95%: 20.1-29.3%). This low percentage of herds with high levels of antibodies may be due to the current biosecurity and sanitary condition of the farms as well as the low numbers of animals per herd. The epidemiological situation of BVDV infection in this population represents conditions favourable to launching a control program; it also demonstrates the studied population's high susceptibility to the introduction of new infections.

Prevalence survey and spatial analysis of bovine herpesvirus

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Bovine herpesvirus (BoHV) is an important pathogen of cattle that has worldwide distribution. Infection can cause substantial economic losses due reproductive failures and increased calf mortality. The identification of infected herds is commonly based on the detection of BoHV-specific antibodies in sera or milk samples. The aim of this study was to estimate the herd prevalence of BoHV in dairy herds and to evaluate the viral dissemination with spatial scan statistic. The target population was composed by 1,656 semi-intensive dairy herds in southern Brazil from which 300 were randomly sampled. Sample size was calculated considering an absolute precision of 5%, expected herd prevalence of 58%, and 95% confidence level. Samples of bulk milk tank were collected from those herds to determine antibody levels against BoHV by a commercial ELISA test. SaTScan 9.1 software with Bernoulli model was used to detect areas of significantly high rates of BoHV infection. The software has a circular window, variable in size and position in a given study region, and each circle is a possible candidate cluster. This window was set in maximum radius of 10 km and an upper limit of 50% of the population at risk. From the 300 samples, 12 were excluded due to inconclusive results. The prevalence of BoHV antibodies in bulk milk tank was 27.1% (CI 95%: 22.5%-33.3%). There were observed one most likely cluster ($P=0.099$) and five secondary clusters ($P\geq 0.675$). The most likely cluster had 8.91 km radius window with all 5 herds positive, when only 1.38 positive herds were expected. The moderate prevalence of BoHV and the presence of clusters of positive herds suggest the relation between cases and possible viral dissemination among them due to proximity. Disease clusters may occur either because herds share common risk factors or via transmission between herds through the movement of infected animals.

Matched case control study of bovine viral diarrhea virus (BVDV) in a dairy cattle population in the State of Rio Grande do Sul, Brazil

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Bovine viral diarrhea virus (BVDV) is one of the most important diseases of cattle in terms of economic cost and welfare, being widespread in dairy cattle population. The aim of this study was to identify risk factors for the presence of antibody against BVDV in bulk milk tank in dairy herds. The target population was based on a companion study done for the estimation of the prevalence of BVDV in bulk milk tank samples. BVDV antibody-positive herds presenting corrected optical density (COD) ≥ 0.25 ($n=21$) were classified as cases and matched ($n=63$) by the milk production level with herds with COD <0.25 (case-control ratio of 1:3). A questionnaire was applied to get information about possible risk factors. The outcome variable of interest was whether the herd had high levels of BVDV antibody (i.e. COD ≥ 0.25) or not. Univariate conditional logistic regression was performed in order to select potential risk factors variables (PROC PHREG, SAS). Only variables with a $P<0.15$ were offered to the multivariable model. The model was built using forward selection starting with the variables with the lowest AIC values from the univariate analysis and backward elimination. Three variables were significantly associated with the presence of BVDV antibodies in the dairies ($P\leq 0.05$), which were included in the final multivariable model: area for isolation of sick animals (OR=0.14, CI 95%: 0.02-0.90) and farms that uses age as a criterion to cull cows (OR=0.10; CI 95%: 0.01-0.80) which were protective factors and farms that had already provided milk to others industries (OR=4.10; CI 95%: 1.00-15.63). It is important to generate hypothesis about risks of diseases in order to understand the mechanisms of disease transmission and spread.

Beta lactam antibiotics residues in cow's milk: comparison of efficacy of three commercial screening tests used in Bosnia and Herzegovina

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Beta (β) lactam antibiotics are widely used as therapy for bacterial infections in cattle, especially for mastitis. Monitoring of antibiotic residues in cow's milk in Bosnia and Herzegovina (BiH) is in accordance with the European Union standards. All commercial dairies use antimicrobial residue tests, and 95% of the testing is for β lactams. The aim of this presentation is to show the results from a study conducted to evaluate and compare the efficacy of three most widely used screening tests for β lactam residues in cow's milk in BiH. Following tests were used in the study: SNAP β Lactam test (Idexx), Rosa Charm β Lactam test (Charm Sciences) and Inhibition MRL test (A&M), applied by testing procedures as prescribed by their manufacturers. Study samples included: 10 each of the six standardized concentrations of penicillin (0, 2, 3, 4, 5 and 6 ppb) and 120 milk samples from four study animal groups. The groups included: 30 animals treated with β lactams for diseases other than mastitis, 30 animals treated with β lactams for mastitis, 30 animals treated with β lactams but sampled after withholding period and 30 animals not receiving any antibiotic therapy during current and prior lactation. Analytic sensitivity was determined for each test using standard penicillin concentrations. Agreement of the tests results was assessed in each study animal group using Kappa coefficients with correspondent 95% confidence interval calculated for each test pair. Even though rapid tests for β lactam residues have many advantages, positive results for concentrations of residues under prescribed maximum residue limit (MRL) result in unnecessary losses of milk and cost related to its disposal.

Use of a lung scoring method for pigs at slaughter to identify farms with high mean lung scores in the Philippines

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The main objective of this study was estimate the prevalence of high lung scores farms based on lung scores of individual animals in the Philippines. The study was conducted between 1st October 2011 and 31st January 2012 in Region III. Multistage stratified random sampling was used to select calendar days and slaughterhouses. Systematic random sampling was used to select pigs for lung scoring. The lungs were palpated and visually appraised to detect lesions of pneumonia by one experienced veterinarian. Mean lung scores of slaughtered batches originating from the same farms were compared using a Kruskal-Wallis test. The prevalence of high lung score farms (HLS) and confidence intervals was estimated using a logistic regression model. Total number of lungs scored was 1,255 originating from 305 farms. Mean batch lung scores were different among backyard and commercial farms ($\chi^2_{119,36,df1}$, $P < 0.001$). The prevalence of HLS farms was high (30%, 95% CI 25-35%). This is in agreement with the literature and shows the feasibility of adopting a quantitative lung scoring method to monitor lung lesions in slaughtered pigs in this region. The results also suggest that some pigs can be infected late in the cycle developing lesions close to slaughter. Compared with backyard farms, commercial farms were three times more likely to have mean lung scores values higher than the mean of all farms (OR 3.14 95% CI 1.91-5.21; $P < 0.001$). This demonstrates the effect of production system on respiratory disease dynamics in the study farms. The overall mean lung score for farms in Region III was high and the production system was associated with high mean lung scores at the farm level. It is recommended that potential risk factors associated with respiratory disease are identified and further investigated in an attempt to reduce mean lung scores on Region III pig farms.

Accuracy of visual inspection of cause of death of dairy cows at incineration plants

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Dead cows are routinely brought to incineration plants and monitoring the influx may be useful for early detection of emerging (infectious) diseases. A prerequisite is that it can be determined if the cow was euthanized or died unassisted, because a sudden increase in the latter may be indicative of an outbreak. The objective of this study was to evaluate the accuracy of visual inspection at the incineration plant as a means to distinguish between the two types of deaths. The two main incineration plants in Sweden were visited 3 times, 3 days each, in spring, summer and autumn during 2011. The identity, and whether the cow was shot in the forehead or not, was recorded for all dairy cows entering the incineration plants during these days. We phoned the owner of the cow within 3 weeks after the cow was examined and asked whether the cow died unassisted or was euthanized. A total of 468 cows examined, also had information from the farmers. The comparison demonstrated that there were discrepancies between the observations. According to the farmers (gold standard) the proportion of cows that died unassisted was 30%, while the visual inspection (test) found that the proportion was 40%. Three cows were euthanized by an overdose of an anesthetic, which explained some of the discrepancy. The sensitivity and the specificity of the visual examination were 93% and 83%, respectively. The positive predictive value was 70% and the negative predicted value was 97%. This study showed that visual inspection of dairy cows at incineration plants overestimate the proportion of cows that died unassisted. The accuracy of the method is however judged to be sufficient to monitor the proportion of unassisted death.

Use of a national Johnes serum survey to help design a least cost surveillance programme in a low prevalence environment

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A serum prevalence survey was carried out in Ireland in 2009 on 1,654 herds picked randomly from all the herds in the country, which were subject to an annual brucellosis test. All 78,123 females and breeding bulls over 24 months-of-age in these herds were tested using a ID vet ELISA test. There were 286 positive herds and 91 herds had two or more positives. The overall prevalence of infected herds, based on the presence of at least one ELISA-positive animal, was 17.41%. The herd prevalence level amongst dairy herds (27.76%) was higher than among beef herds (12.7%). The animal level prevalence for all breeds was 0.60% but some breeds had a higher prevalence than this. Only 5.5% of all herds had more than one ELISA-positive infected animal. The herd corrected seroprevalence excluding herds with only one positive result was 5.50%, dairy herds were 9.7% and beef herds 3.6%. The data was analysed to investigate the possibility of screening herds for Johnes's disease using a sub sample of the total herd. Using data from the present survey it was determined that if a sub sample of eight of the oldest animals in the herd were selected 64.58% of the positive herds would have been missed.

Agreement of diagnostic assay results within and between laboratories

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Rapid expansion in the inventory of laboratory assays available for detecting animal disease has stimulated interest in finding better ways of describing their performance. Guidelines for validation of assays now emphasise the need to assess agreement within laboratories (repeatability) and between laboratories (reproducibility). However, methodology suited to providing robust inferences on agreement is poorly defined. For these reasons we aimed to assess repeatability and reproducibility for an ELISA used to detect antibody against bovine herpes virus 1. One thousand assays were performed on 20 sera in five laboratories in 10 weekly batches. Ten of the sera were negative for antibody by virus neutralisation test (VNT) and ten were VNT positive. Agreement of S/P ratio results was assessed graphically, using the coefficient of variation statistic and intraclass correlation coefficients (ICC) derived from variance components. Simulations evaluated the impact of sero prevalence on the estimates of reproducibility of S/P. Graphically, the S/P of VNT -ve sera had low repeatability due to low signal to noise ratio confirmed by the low values of ICC across all laboratories (range 0.01 to 0.27). S/P for VNT +ve sera showed a high signal to noise ratio, greater variation due to sera and higher estimates of repeatability (ICC range 0.63 to 0.92). Lab to lab variation caused the reproducibility of S/P ratio (agreement between laboratories) for VNT +ve sera (ICC 0.52) to be lower than repeatability estimates. Coefficients of variation were high for VNT -ve sera and unexpectedly low for VNT +ve sera. While measures of agreement do not replace measures of diagnostic accuracy, they are informative in many practical circumstances provided their limitations are acknowledged. Epidemiologists could encourage wider adoption of the measures illustrated here and so improve the development and validation of laboratory assays for animal disease.

Sensitivity of mortality reporting by the French oyster farmers

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As diseased shellfish show only very seldom symptoms, any mortality event can be a disease suspicion. In theory, monitoring of mortality events in shellfish can thus provide a tool for early detection of infectious diseases in order to implement effective control measures. This consists in passive mortality event reporting by shellfish farmers to the local competent authority. Sensitivity of the detection of mortality events is a key quality indicator for this type of surveillance. Since 2008, increased mortality outbreaks occur in Pacific oysters *Crassostrea gigas* in France, leading to economic losses. It is important to evaluate how much the outbreaks have altered the quality indicators of the reporting system and if this modification is long-standing, to achieve an effective early detection tool. The yearly evolution of sensitivity of the passive farmer reporting was estimated during 2007-2010 in the main oyster production area in France, using a capture-recapture analysis and accounting for unequal catchability. Information on mortality events were obtained from existing annual databases of mandatory mortality reporting (capture) and from a questionnaire-based cross-sectional survey conducted in 2010 as part of larger study of oyster mortalities (recapture). Sensitivity significantly varied according to the year, from 0.25 (CI_{95%} 0.18-0.39) to 0.79 (CI_{95%} 0.67-0.96), 0.52 (CI_{95%} 0.42-0.70) and 0.75 (CI_{95%} 0.62-0.96) in 2007, 2008, 2009 and 2010, respectively. Important under-reporting was observed in 2007. Sensitivity increased concurrently with outbreaks occurrence and with implementation of financial incentive for mortality reporting. The achieved completeness was satisfactory. However, bottlenecks for reporting or solutions to facilitate reporting have to be identified to improve sensitivity of the reporting system on a long term period, whatever the epidemiological situation is.

Bovine tuberculosis slaughter surveillance in the United States and the ability to trace detected cases back to a herd of origin 2001-2010

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The detection of gross bovine tuberculosis (bovine TB) lesions in cattle at slaughter and the successful trace-back to the herd of origin is critical to the detection of infected herds and for the progress of the national bovine TB eradication program in the United States (U.S.). The aim of this study was to determine the ability to trace infected cattle identified through the current bovine TB slaughter surveillance system back to their herd of origin in the U.S. and to evaluate factors associated with a successful trace back. Data obtained for the period 2001-2010, in which 386 granulomatous lesions were confirmed as bovine TB in the U.S., were used for this study. Descriptive statistics and multivariable logistic regression were used to analyze the data. The majority of the confirmed bovine TB lesions (69%) disclosed at slaughter were in imported cattle, and 31% (n=119) were found in cattle with a potential herd of origin in the U.S. Overall, from these 119 bovine TB cases, 33% were successfully trace back to a herd of origin in the U.S. Adult bovine TB cases were significantly more likely (82%) to be successfully traced back than young (<2 years of age) bovine TB cases (10%) (adjusted OR=15.5, P<0.001). Animals with an 'official' animal identifier were also more likely (86%) to be successfully traced back than those cases without 'official' identification (16%) (adjusted OR=7.1, P<0.001). Overall, 69% of the epidemiological investigations that found a herd of origin in the U.S. identified additional bovine TB infected animals, resulting in the detection of a TB-affected herd. The results of this study provide an important tool to aid U.S. officials in their decision-making with respect to the evaluation and implementation of strategies for the national bovine TB eradication and traceability programs.

Implementation of the French platform for epidemiological surveillance in animal health

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One key initiative of the national consultation on the animal health sector held from January to April 2010 in France was 'Creating an epidemiological surveillance platform for animal health surveillance' (the Platform). The platform aims at improving coordination, fostering and capacity building in epidemiological surveillance activities in animal health. It comprises a National committee for epidemiological animal health surveillance and an operational body. The platform joins together various entities, including the Directorate General for Food of the Ministry of agriculture (DGAL), the independent assessment body (Anses), producers organisations (GDS France, Coop de France), veterinary association (SNGTV), laboratories (ADILVA) and will progressively include technical and scientific organisations (INRA, CIRAD, ONCFS, etc.). The platform assists the production of epidemiological data needed to provide risk evaluation and to enable risk management and control. Its mission is to ensure the smooth running of epidemiological surveillance systems at a national level including their capacity for quick response. The activities implemented by the platform include: (1) contributing to the collection, standardisation and consolidation of health data and to the production of epidemiological reports; (2) development of performance indicators; (3) information feedback; Several subjects are handled as top priorities by the Platform, including the surveillance of bovine tuberculosis, bluetongue, abortions in ruminants, avian influenza, influenza in swine, honeybee diseases, molluscs mortality.

Epidemiological models for controlling porcine respiratory and reproductive syndrome in the United States

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Porcine Respiratory and Reproductive Syndrome (PRSS) is a viral disease of swine that causes annual losses for US\$ 664 million in the United States. Here, we present features of a new surveillance system for PRSS developed in partnership with the United States swine industry. The objective of the surveillance system is to support disease control at a regional scale. Data are collected and organized using a web-based system referred to as Disease BioPortal. Phylogenetic analysis is used to identify in-contact farms and companies. The web-based system is used to map, display, and analyze the data, using models for epidemiological display and analysis. Techniques and methods for identification of disease clusters and anomaly detection were developed and incorporated into the web-based system. Rule- and model-based anomaly detection models are used to identify unusual or unexpected changes in the data, based on results of one or more of the cluster tests (model based detection; e.g. a high risk of cases in a given area and time) or to recognize a situation previously unrecorded in a given region (rule based detection; e.g. the first case in a given county). Contact-rates are computed for pig farms and companies, to determine clusters (compartments, zones) at similar risk for the disease. Systematic sequencing and phylogenetic analysis of PRSS samples is conducted in near-real time in a regional basis to identify compartments or zones in which virus transmission exist, which is prerequisite for the implementation of a regionalization strategy for controlling the disease.

Assessment of bovine tuberculosis surveillance in France

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Since the 1950s, the prevalence of bovine tuberculosis (BT) in France has regularly decreased towards an official free status reached in 2000. The number of BT infected herds increases since 2005. The sensitivity of the BT surveillance system was questioned. Therefore, the French Ministry of agriculture asked Anses to carry out the assessment of the national surveillance system based on the OASIS qualitative method. An in-depth assessment was implemented from June 2011 to February 2012 by a team of epidemiologists from Anses and the Ministry of agriculture. All stakeholders and actors of surveillance have been involved through interviews performed in three different regions and at the central level. As a control procedure, a flash assessment was performed by a second team of two BT national experts who scored the OASIS assessment criteria during a one day working session. The OASIS outputs suggested as a main feature the lack of specificity of the system. The assessment identified pitfalls in the fieldwork as well as in the overall organisation and provided detailed recommendations for the improvement of the surveillance. The recommendations focused on the setting of a steering committee, the improvement of the information system as well as field operators training. The lack of specificity, the complexity and length of the laboratory diagnosis and the administrative consequences of suspicions impaired the efficacy and acceptability of the surveillance system. The flash assessment had similar OASIS outputs but did not provide as many detailed comments on how to improve the system. Whereas the flash assessment was sufficient to characterize the surveillance system through OASIS outputs, only the in depth assessment was able to provide the risk manager with relevant and practical recommendations.

Avian influenza virus in Belgian professional poultry holdings: identifying risk farms, a step towards risk based surveillance

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Circulation of notifiable low pathogenic avian influenza H5 and H7 (NLP AI) remains a constant threat for commercial poultry holdings, as it might mutate into highly pathogenic AI (HPAI) and cause serious outbreaks with devastating consequences as seen in past H7HP outbreaks in Europe in 2003, 2004. International standards as well as EU legislation encourage countries to implement risk based surveillance programs to detect NLP AI. The aim of the present study was to determine if some holdings could have an increased risk of being infected. Data set of all holdings tested within the routine AI monitoring program from 2009 till 2011 in Belgium and the results of the biosecurity check list of all active professional poultry holdings were merged together. A generalized linear mixed model was developed to model the probability of having AI NP ELISA positive results given a set of biosecurity characteristics, using 2009-2011 AI monitoring program results. Models at holding and animal level were compared. In parallel a spatial temporal analysis was carried out to determine if any significant spatial or temporal clusters were present. Results showed that the risk of being infected was higher for holdings present in some locations but these risk areas were not specially related with migratory bird flyways. Higher probability of being positive was found in holdings with outdoor access and with different poultry species on the farm (mainly geese and ducks). The results of this study revealed interesting features regarding the epidemiology of LP AI and key elements for setting up a risk based surveillance program, such as required by the international standards and EU legislation.

Risk-based surveillance of chicken diseases using poultry trader networks in Oromia Regional State, Ethiopia

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Highly pathogenic avian diseases such as Newcastle disease and avian influenza have serious social and economic impact in developing countries, including Ethiopia. Live bird markets and poultry traders are known risk factors for the spread of these diseases. In Ethiopia, Oromia regional state is an active chicken breeding region and the live bird markets are located on the main poultry trade road to the capital city Addis Ababa. The networks of chicken movements between 29 shared markets in Oromia regional state were built for festive and non-festive seasons, using a 'trader questionnaire' survey. Five centrality indices, in-degree, out-degree, in-closeness, out-closeness and random-walk betweenness, were calculated and the markets were ordered according to these indices. The festive seasons did not appear to impact the network structure, implying no necessary change of surveillance and control policies during these periods, merely a strengthening due to an increased volume of traded chicken. Three markets emerged as central in the network, with different epidemiological roles. Our findings indicate that these three poultry markets would ideally be chosen in a risk-based type of surveillance system and in targeted control policies.

Bayesian latent class analysis to estimate sensitivity and specificity of faecal culture and Paralisa to detect *Mycobacterium avium* subsp. *paratuberculosis* infection in young deer

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This study aimed to estimate the sensitivity and specificity of individual faecal culture (IFC) and an IgG1 serum enzyme-linked immunosorbent assay, the Paralisa™, to identify young (12-24 month old) deer subclinically infected with *Mycobacterium avium* subsp. *paratuberculosis*. The test purpose was 'freedom from infection' sampling for use in a herd classification programme. Individual faecal and serum samples were collected from 20 individual yearling deer from each of 20 herds in the South Island and 18 herds in the North Island of New Zealand, and the candidate tests were applied. The differing infection prevalence between the two islands enabled a two-test two-population Bayesian latent class model to be developed. A zero-inflated random effect logistic model was incorporated to allow zero-infection herd status, as well as capturing variation in within-herd prevalence. Modelling was carried out in WinBUGS, using informative priors sourced from published literature and expert opinion. The estimate of IFC sensitivity was 77% (95% CI: 61-92%) with specificity 99% (95% CI: 98-99.7%), while the Paralisa™ sensitivity estimate was 19% (95% CI: 10-30%), with specificity 94% (95% CI: 93-96%). Estimates were robust to variation of priors and assumptions tested in a sensitivity analysis.

A transition plan to transfer surveillance related trainings by donors to recipient governments

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A skilled workforce is paramount for the effective working of a country's veterinary services. Under the Biological Threat Reduction Program (BTRP) of the Defense Threat Reduction Agency (DTRA, US Dept of Defense), 440 veterinary officials have received training on especially dangerous pathogen (EDP) surveillance since 2006 in Uzbekistan. After six years of sustained efforts, DTRA is preparing to transfer the training program to the Government of Uzbekistan. To support this action, a resource and transition plan is in preparation. The plan details the required stakeholders and splits the training effort into discrete areas fully described by logic models. These models allow the identification of indicators to measure training impact on the delivery of surveillance. For example, subject matter-specific standards of knowledge, e.g. on epidemiology, are required for all officials. These standards, which are reviewed regularly, allow the identification of subject matter-specific gaps. They also facilitate the quantification of additional training requirements, given current structures and processes, to support an efficient EDP surveillance program in country. Logic models also identify the inputs required to support the training efforts: a sustainable supply chain, regulatory requirements, evaluation approaches, etc. The inputs to the training component are themselves separate components of the overall BTRP transition plan. The identification of dependencies between the multiple logic models supports prioritization of components. Prioritization will be formally assessed with a panel of Uzbek officials in a facilitated session and following multi attribute utility theory. Assumptions to reach this resource model and scenarios as to how different assumptions would affect an effective EDP surveillance will be presented. In an effort to standardize evaluation metrics and facilitate compliance with other international programs, components within the logic models closely follow the criteria of the OIE PVS tool.

Fagan's nomogram: finally completed after 37 years!

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In 1975, Fagan published a nomogram to help practitioners determine, without the use of a calculator or computer, the probability of a patient truly having a condition of interest given a particular test result. This is necessary for the interpretation of a test result as no test is perfect. Nomograms are very useful for speedy interpretations, and Fagan's has been adopted by several reference textbooks specializing in evidence-based medicine and clinically applied epidemiology, both in the human and veterinary context. However, the practicality of Fagan's nomogram is limited by its use of the likelihood ratio (LR), a parameter not usually reported in evaluation studies of diagnostic tests with a dichotomised outcome. The LR reflects the strength of evidence provided by a test result and can be computed from the conventional diagnostic sensitivity (DSe) and specificity (DSp) of the test. This initial computation is absent in Fagan's nomogram, making it impractical for routine use. We have improved Fagan's nomogram by seamlessly integrating an initial step to compute the likelihood ratio. The resulting two-step nomogram allows the user, be it a clinician or researcher, to quickly interpret the outcome of a test without using any in silico support. With the addition of the DSe and DSp, the nomogram, for the purposes of interpreting a dichotomous test result, is now complete. Overall, this tool is more accessible and flexible than the original, which will facilitate its use in routine practice of evidence-based medicine.

To cut, or not to cut: that is the 'real-time' question

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Diagnostic laboratories frequently select a subjective cutoff value for real-time amplification assays, above which a threshold cycle (Ct) value is deemed false. Commonly, higher and isolated Ct values are assumed to be amplification or fluorescence artifacts, or cross contaminations. The selection of this Ct cutoff should be based on evidence. This presentation reviews evidence-based strategies to select Ct cutoffs grouped in analytical and epidemiologic approaches. Analytical strategies use criteria gathered during the assay development and include fluorescence threshold, reaction end-cycle, limit of detection, and artifact investigation. Variability in amplification efficacy across test runs may induce some instability in an intended Ct cutoff and requires some standardization or normalization procedures. Epidemiologic strategies use criteria based on either the probability or the cost of a false test result associated with a specified cutoff. Cutoffs, depending on the intended purpose of the test, can be selected graphically to minimize the probability of either false-positive or false-negative results by using two-graph receiver operating characteristics curves. The assay's diagnostic sensitivity and specificity may vary with the tested population, thus, the estimated two-graph receiver operating characteristics curve is population dependent and should be established for the targeted population. Although the selection of a cutoff based on misclassification cost depends on infection prevalence, the selection based on predictive values does not. To optimize the test average diagnostic performance, the Ct cutoff should be selected when the diagnostic odds ratio is maximal.

Development and validation of a qPCR for the detection and quantification of *Actinobacillus pleuropneumoniae* DNA in pigs

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Actinobacillus pleuropneumoniae is a common pathogen of pigs, causing respiratory disease and economic losses. Detection of *A. pleuropneumoniae* antigen in live pigs is difficult and improvement of the current diagnostic procedures could contribute to better disease control. A common test for quantitative *A. pleuropneumoniae* detection in samples from live pigs is selective bacterial examination (SBE) using tonsillar or nasal swab samples, but differentiation between *A. pleuropneumoniae* and other members of the Pasteurellaceae family in the oropharyngeal flora is difficult. Therefore a quantitative real-time PCR (qPCR) protocol for detection of the apxIVA gene was developed based on primers apxIVANEST1-F and apxIVANEST1-R and a fluorescent probe. Validation studies were performed using pure cultures of *A. pleuropneumoniae*, as well as samples from both experimentally inoculated Caesarean-derived, colostrum-deprived (CDCD) piglets and conventional pigs. The analytical sensitivity was 5 colony forming units/reaction. Diagnostic sensitivity was estimated at 0.98 in inoculated piglets, compared to SBE. Specificity was estimated at 1.0 in samples from 77 *A. pleuropneumoniae* free CDCD pigs and from 70 pigs from three SPF farms, free of *A. pleuropneumoniae*. A small-scale cohort study on two infected farms showed consistent results in repeatedly sampled pigs. No difference in *A. pleuropneumoniae* quantities between points in time or between farms was found, except at 24 weeks of age when incidence, as well as *A. pleuropneumoniae* quantities were significantly raised in one farm. Tonsillar brush samples and additional apxIVA qPCR analysis could therefore be a valuable additional tool in monitoring and epidemiological studies on *A. pleuropneumoniae*.

Educating surveillance stakeholders: a novel e-tool to improve engagement and decision making across different sectors

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Biosecurity surveillance activities protect New Zealand's economy, environment and people from the risks and consequences of the introduction and presence of risk organisms, including important livestock pathogens such as Food and Mouth Disease Virus. Stakeholders in biosecurity surveillance are diverse and include livestock industries, aquaculture, horticulture, conservation organisations, as well as Maori. In this context the aims of animal health surveillance have to be integrated with those from other sectors to ensure a consistent approach to biosecurity surveillance across all sectors and to build a basis for collaboration on surveillance tasks. This provides several challenges as surveillance awareness, expertise and needs vary considerably between different stakeholder groups. For example freedom-of-disease surveillance programs are common in the forestry and animal sector to meet trade requirements, but are less familiar to the marine or environmental stakeholder groups. There is however a desire for consistent tools or standards to aid or guide the development of surveillance programs to prevent miscommunication, duplication of effort and inefficient use of resources. In response to this need an e-tool is being explored as a mechanism to provide surveillance stakeholders within and outside the regulatory environment with high-level content to support their choice of surveillance methodology and increase their ability to actively engage in surveillance and meet their surveillance needs independently. In this paper we present the development of this tool from stakeholder interviews, instructional design to usability testing. We show some of its interactive components and discuss further applications of media education to work better with stakeholders to improve the efficiency and effectiveness of surveillance activities.

Assessing surveillance: identifying areas of greatest likelihood of disease introduction and establishment
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Australia is a major exporter of livestock and livestock products; a trade assisted by a favourable animal health status. However, increasing international travel and trade, land use changes and climatic change have resulted in greater risks of exotic and emerging diseases. At the same time, public sector resources for managing these risks are static or declining. Veterinary authorities have identified the need to develop a consistent national approach to surveillance that allocates resources according to risk. This study maps the risk of occurrence of eight significant diseases within 12 livestock production regions of Australia. The likelihood of disease occurrence was divided into likelihoods of introduction (LI) and establishment and spread (LES). Pathways for both I and E/S were identified and data layers representing the factors contributing to each pathway produced as raster maps. The Multi-Criteria Analysis Shell (MCAS) was used to combine data layers into pathways and pathways into likelihood maps using weightings that reflect the relative importance of each layer and pathway. The likelihood maps for introduction and for establishment and spread were then combined to generate national likelihood maps for each disease. The eight diseases were subsequently grouped (foot and mouth disease, zoonotic diseases and other diseases) and combined using weightings to reflect their relative consequences. The result was a map of relative risk of occurrence of any significant disease. Current surveillance activity was assessed by combining data layers for government disease investigations, proximity to vets and wildlife disease investigations. Comparison of the overall risk and current surveillance maps showed that the distribution of current effort was well matched to the distribution of risk.

regional vulnerability to an outbreak of foot and mouth disease in Australia

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Australia is a significant exporter of livestock and livestock products. This trade is assisted by a favourable animal health status. Increases in international travel and trade, together with other factors, mean greater risks of exotic and emerging diseases, and at the same time public sector resources available for managing these risks are static or declining. General, passive surveillance (GS) is the principal means for early detection of incursions of exotic animal diseases. Accompanying papers describe spatial variation in: (1) the likelihood of disease introduction, establishment and spread; (2) the sensitivity of current GS activities; and (3) the speed and extent of spread of a foot and mouth disease (FMD) incursion, in each of 12 livestock production regions. In this paper we utilise results from each of these analyses to estimate the size of an outbreak of a FMD at the time of detection, and compare the relative vulnerability of each region to outbreaks of this disease. The time to detection for a single farm determined in the assessment of current surveillance sensitivity was used within the FMD spread model to determine the likely number of infected farms at the likely time of detection. Outbreaks varied in size between 1 (range 1-8) in central and northern Australia to 21 (range 1-163) on the temperate south-east coast of Australia. The relative vulnerability of each region to outbreaks of FMD was determined by combining the results from the suite of analyses. A simple linear additive model was developed that required a 'score' for each of the above criteria in each region. The coastal regions of south-east Australia were identified as the regions most vulnerable to outbreaks of FMD, whereas hotter, more arid areas with lower stocking densities were less vulnerable.

Descriptive results of a prospective cohort study of avian influenza in poultry in the Mekong region of Viet Nam

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A prospective cohort study was carried out to identify the frequency of avian influenza viruses in duck and in-contact species (chickens, Muscovies, geese) populations. One hundred and fifty seven poultry flocks from eight villages in two provinces (Can Tho and Bac Lieu) in the Mekong region of Viet Nam took part between December 2008 and April 2010. The RRT-PCR was used to detect the matrix (M) gene of influenza Type A viruses, followed by the H5 Multiplex assay for H5 viruses in swab samples. The HI test was used to detect antibody against H5 viruses in serum samples. A total of 17,968 swab and 14,878 blood samples were collected throughout the follow-up period. Eleven percent (95% CI 10-12%) of birds and 58% (95% CI 50-66%) of flocks were M gene positive. The prevalence of H5 viruses was 1% (95% CI 1-2%) and 15% (95% CI 10-22%) at the bird and flock level, respectively. Broiler ducks had the highest M gene and H5 positive proportions at 31% (95% CI 28-34%) and 3% (95% CI 2-5%), respectively. Seven out of eight villages and 0.26% (95% CI 0.15-0.41%) of vaccinated birds were positive for H5 viruses. Forty six percent (95% CI 45-47%) of unvaccinated birds were H5 seropositive compared with 59% (95% CI 58-60%) of vaccinated birds. The proportion of layer ducks that were H5 seropositive was 77% (95% CI 76-78%) compared with 27% (95% CI 21-30%) for broiler ducks and 32% (95% CI 31-34%) for in-contact species. Our results suggest that interventions to control HPAI H5N1 need to be implemented throughout the year and focus on broiler duck flocks. We hypothesise that the co-circulation of H5 and non-H5 viruses in highly dynamic, vaccinated poultry populations poses a high risk for virus reassortment.

A model for evaluating and planning avian influenza surveillance in New Zealand

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Surveillance for notifiable avian influenza (NAI) in New Zealand (NZ) consists of periodic targeted surveys and the general surveillance (disease reporting and investigation) system (GDS). Assurance that the country is free of NAI is important for both trading partners and the general public. We developed a stochastic spreadsheet tool to facilitate evaluation and planning of surveillance activities. The tool's outputs, for each surveillance time period, include the individual and combined sensitivities of the surveillance components, the resulting level of accumulated confidence in the population being free of NAI, and the cost of conducting the surveillance. Outputs are reported for the whole NZ poultry population and for relevant subpopulations, eg all commercial poultry farms. The tool allows risk-based targeting of active surveillance effort and exploration of the gains in sensitivity/confidence in freedom for different survey expenditures; any one of up to ten survey plans may be specified and applied to each future time period. The tool has highlighted the relative value of the GDS over intermittent targeted surveys, particularly for confidence in freedom from highly pathogenic AI in all NZ poultry. Past comprehensive surveys of commercial poultry have provided value primarily for the commercial poultry population. Around 95% of NZ poultry flocks are 'backyard' flocks, and development of this tool has also highlighted the importance of surveillance in these flocks. Plans for future surveillance can incorporate the appropriate balance to deliver the necessary confidence in national freedom from both high and low pathogenicity NAI at the required cost.

Model-based surveillance of CSF in backyard pigs: an example from Bulgaria

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Based on official data of backyard pigs and backyard pig holdings at the municipality level in Bulgaria, a simulation model for surveillance of these holdings with respect to Classical Swine Fever (CSF) occurrence was developed. In the context of this paper, backyards are small-scale holdings with limited numbers of pigs and few trade contacts. In the first scenario of a suspicion or an outbreak of CSF within a limited area, the authorities have to enforce CSF control measures according to the Council Directives 2001/89/EC and 2002/106/EC. These measures were designed for and have been derived from domestic pigs kept in larger, non-backyard holdings, therefore, the implementation of these preventive or control measures in backyard holdings is more difficult to achieve. Our analysis led to the detection of short-comings that occur only in backyard holdings. In some simulation runs, for example, a considerable number of infected farms remained undetected depending on the used test systems (including a new DIVA-ELISA). A second surveillance scenario deals with the detection of the disease and the certification of freedom from disease, respectively. For the surveillance at municipality level, it is difficult to detect very low levels of herd prevalences due to the herd size distribution. Enlarging the surveillance units from municipality to province level, an approach that may be attractive as it could save resources, leads to a high number of undetected outbreaks, even if high herd prevalences are tested. All simulated scenarios show the importance of the problem of missing registration of backyard pigs, farms and holders.

Assessing general surveillance: estimation of detection sensitivity and time to detection for exotic disease incursions

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Australia is a significant exporter of livestock and livestock products. This trade is assisted by a favourable animal health status. Increases in international travel and trade, and other factors, mean greater risks of exotic and emerging diseases, and at the same time public sector resources available for managing these risks are static or declining. General, passive surveillance (GS) is the principal means for early detection of incursions of exotic animal diseases. In considering options for boosting GS efficacy where needed, veterinary authorities require a means of assessing the efficacy of the GS process with or without 'enhancements'. An assessment tool (GSAT) was developed for estimation of both single farm sensitivity of GS and time to detection, in each of 12 livestock production regions of Australia. The tool was trialed for foot and mouth disease (FMD). The GSAT is a stochastic spreadsheet model of the GS process in Australia, which is divided into three stages; syndrome recognition and notification, clinical investigation, and laboratory investigation. The endpoint is the chief veterinary officer being notified. Three 'players' can be exposed to clinical signs (the producer; saleyard inspector; abattoir inspector) and initiate the detection process. Probabilities of observation, recognition, notification, veterinary investigation, sample dispatch, laboratory testing and diagnosis are estimated for each susceptible species and farm-type in each region. Probabilities are averaged across a region by weighting farm-type probabilities by their within-region proportions. Mean estimated single farm sensitivity for FMD varied among regions from 28% to 56%, while mean time from introduction of FMD to the farm to CVO notification ranged from 22 to 38 days.

Characterizing pig fattening farms by combination of farm and lab data

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Reg. (EC) No. 854/2004, more precisely Reg. (EC) No. 1244/2007, opened the possibility of risk based meat inspection for pigs raised under controlled conditions. But type of information and required tests for such a condition are still under discussion. In this study, we investigated the information value of farming systems ('controlled conditions'). Data from 296 farms of 2 farming associations and elements of their management system (yes/no answers) including 11 *post mortem* results regarding the hygiene were gathered for 2005 to 2009. In addition, 3.346 meat juice samples (a maximum of 10 samples for each farm) for ELISA tests for *Trichinella*, *Salmonella* and *Yersinia* were brought together. All samples were negative for *Trichinella*, three farms were negative for *Salmonella*, *Yersinia* and *Trichinella*. Most of the farms (193) were positive for *Salmonella* and *Yersinia*. Using management parameters of these positive and negative farms, no significant differences were found between and in both associations. In consequence, the cut off levels for *Salmonella* and *Yersinia* were raised. 22 farms had high levels for *Salmonella* and *Yersinia*. Comparison of management parameters of these farms with negative farms did not show any significant difference, too. In a next step, p. m. findings with potential hygiene background were used from these 22 farms. 3 farms showed suspicious results, their management parameters were compared again. This time management parameters were identified, which could be associated with high antibody titres and frequent p. m. findings. It was concluded that a stepwise approach may identify conditions which had not been noted before. It was concluded, too, that 'controlled conditions' serving as an opener for risk based meat inspection may be farm specific.

Diagnostic accuracy of a commercial antibody ELISA for detection of bovine tuberculosis: a Bayesian approach

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The first 2 authors contributed equally. Belgium obtained the bovine tuberculosis (bTB) 'officially free' status in 2003 (EC Decision 2003/467/EC). However, sporadic outbreaks do still occur (FASFC, 2010). This study aims to investigate the diagnostic accuracy of a commercial bTB-specific antibody ELISA kit, i.e. the IDEXX® *M. bovis* Ab Test, and its potential for bTB surveillance in Belgium. Well-defined individual plasma/serum samples (n=1500) were selected and assigned to Positive/Suspect and Negative populations, based on previously obtained test results with other reference assays (intradermal skin test [ID], bTB bacterial culture [CUL] and interferon gamma tests [IFN]), and on the herd status. The IDEXX® *M. bovis* Ab Test was compared to the other assays using a Bayesian approach in order to assess the diagnostic test characteristics. A 'two dependent tests in one population' Bayesian model was adapted for this purpose and 6 prior scenarios were simulated per comparison. An apparent diagnostic sensitivity (DSe) of 12.22-16.19% and an apparent diagnostic sensitivity (DSp) of 93.68-98.08% were observed, resulting in a low positive predictive value (PPV) and a high negative predictive value (NPV) when applied to the Belgian cattle population. These results indicate that the IDEXX® *M. bovis* Ab Test may be less suitable for large scale screening of the Belgian cattle population at slaughter or during the yearly cross-sectional winter survey, mainly due to expectation of a high absolute number of false positives. In contrast, the test might be used efficiently in a targeted approach, to detect bTB in cattle subpopulations with higher expected prevalences, such as imported or purchased cattle. Additionally, the test may be useful as an ancillary, parallel, targeted test in suspected bTB outbreak herds, to detect additional infected animals missed by ID, IFN or CUL.

Serological prevalence of Torque teno sus virus 2 infection in pigs and epitope mapping of capsid protein

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Torque teno sus viruses (TTSV) are small non-enveloped viruses with circular, single-stranded DNA genome. TT viruses belong to the family Anelloviridae and may infect humans and different animal species. Two different virus species have been identified to date in pigs, Torque teno sus virus 1 (TTSV1) and Torque teno virus sus 2 (TTSV2), which belong to the genus Iotatorquevirus. TTSV are widely prevalent in the pig population but TTSV infection is not directly responsible for any disease. The genome of porcine TT virus contains three open reading frames. ORF1 is coding for nucleocapsid protein which potentially induces immune response of infected animals. The goal of this work was to identify immunodominant peptides in the structure of ORF1 protein of TTSV2 which could be used as serological markers to detect TTSV2 antibodies following natural infection in the pig population. ORF1 gene of TTSV2 strains was analyzed for prediction of linear epitopes from protein sequence. Peptides were synthesized and used as the antigens in indirect ELISA test. Selected and synthesized peptides covered more than 40% of the length of ORF1 protein. The total of 307 pig serum samples was collected from 16 herds and different age categories of animals were chosen. TTSV2 specific IgG antibodies were detectable in piglets at age 4 weeks. After vanishing of these maternally derived antibodies post-infection antibody titers started to increase significantly at week 16 and peaked at week 20. Relatively high antibody titer persisted till the adulthood. This work was supported by the Grant agency of Ministry of youth and education project no. ME08108 and Coopelia project no. CZ.1.07/2.4.00/17.0045 and IGA VFU Brno project no. IG121241.

Evaluation of the surveillance system for highly pathogenic avian influenza subtype H5N1 in Thailand using scenario tree modelling

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This study aimed to evaluate the surveillance system for highly pathogenic avian influenza virus (HPAIV) subtype H5N1 implemented in Thailand since 2004 in order to improve its efficiency. The current system consists of 6 surveillance system components (SSC); passive surveillance based on disease reporting; and active surveillance comprising pre-movement/pre-slaughter testing, laboratory surveillance for breeder and layer farms, testing of fighting cocks, nationwide intensive disease search surveillance (so-called 'X-ray surveillance'), and a compartmentalisation scheme. A scenario tree model was developed for each SSC and simulated with 10,000 iterations to estimate the sensitivity (Se) of the SSCs, i.e. the probability of detecting at least one infected poultry farm at different levels of HPAIV H5N1 prevalence (0.5%, 0.1% and 0.05%). The model found a high Se for all active SSCs at different design prevalences, mainly due to the large number of pooled samples processed and the high sensitivity of virus isolation used in active SSCs. Any of the active SSC on its own would achieve an acceptable Se level (>95%) if a total of >100,000 pooled samples is processed. For the disease reporting system had a medium Se (36.7%) in high risk areas of the country, and a high Se (91.3%, 100%) in medium and low risk areas of the country, respectively, at a 0.5% of HPAIV H5N1 prevalence, assuming a low willingness to report (WTR) level. WTR was the most influential factor on the Se of passive surveillance. A better understanding of farmers' behavior and their biosecurity practices related to HPAI risk in each production type are required to assist the Thai government in designing HPAI education and awareness campaigns to improve WTR.

Cost-benefit evaluation of risk-based meat inspection for bovine cysticercosis in a Danish cattle abattoir

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The aim of this study was to incorporate knowledge about food chain information consisting of known risk factors into a stochastic scenario tree simulation model for analysis of future risk-based meat inspection systems for the zoonotic infection bovine cysticercosis (BC) in Danish cattle. We estimated surveillance system component sensitivity (SSCSe), specificity and potential monetary benefits compared to the current system, which has an estimated SSCSe of 15%. The population of cattle slaughtered in a large Danish abattoir during a 1-year period was divided into high-risk and low-risk groups according to the following risk factors: gender, grazing and access to risky water sources. All animals in the low-risk groups would be subjected to visual inspection only. It was assumed that the abattoir would be able to reorganise the work at the slaughterline to save money by introducing visual inspection and gain on the price of sold uncut beef from the masseter muscles from visually inspected cattle. Under these assumptions, gender and grazing were preferable due to their only slightly lower SSCSe than seen in the current system, and highest cost-effectiveness ratios. However, these two factors had a lower net gain than the scenario using access to risky water sources to differentiate low and high-risk groups. Using gender to differentiate high and low-risk groups is preferable over grazing due to feasibility, because this food chain information is readily available at the slaughterline. The potential national net gain depends on how many abattoirs would be able to reorganise the work at the slaughterline to save money on inspection of the head of carcasses. Overall, the SSCSe was low in all scenarios. Therefore, improving the meat inspection sensitivity would be beneficial.

Evaluation of the Zagreb mastitis test as a screening method to detect subclinical mastitis in dairy cattle

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Mastitis is the most prevalent production disease in dairy herds world-wide and is responsible for serious economic losses due to decreasing milk production and lower quality of milk. Therefore, screening of subclinical mastitis under field conditions is of great importance in dairy farming. The aim of present study was to estimate prevalence of bacterial mastitis in dairy cattle in the northern part of Croatia as well as to evaluate Zagreb mastitis test as a screening test for diagnosis of subclinical mastitis in dairy cattle. In the period 2005-2008, 1549 quarter milk samples from 389 Simmental dairy cows were subjected to Zagreb mastitis test (ZMT) and bacteriological examination and in 760 (49.06%) quarter milk samples microorganisms were found. The most isolated microorganisms *St. aureus*, *Streptococcus D*, and *P. aeruginosa* were found in 388 (51.05%), 84 (11.05%), 62 (8.16%) positive quarter samples, respectively. Using a cut-off of ZMT by scores at ≥ 1 as positive, 63.20% (CI 95% 60.80-65.60%) quarter samples were estimated as being positive for subclinical mastitis. This cut-off had quite high sensitivity (96.84%, CI 95% 95.60-98.06%) and predictive negative value (95.79%, CI 95% 94.14-97.44%), however specificity (69.20%, CI 95% 65.98-72.42%) and predictive positive value (75.17%, CI 95% 72.47-77.86%) were low. Using a ZMT cut-off of ≥ 2 as positive, 48.16% of quarters were positive. Sensitivity (82.76%, CI 95% 80.08-85.45%) and specificity (85.17%, CI 95% 82.69-87.65%) as well as predictive values were similar. Likelihood ratio by cut-off of ≥ 1 and cut-off of ≥ 2 was 3.14 and 5.58, respectively.

Assessment of the sensitivity and specificity of gamma-interferon test for the diagnosis of bovine tuberculosis and evaluation of its use in screening schemes in France

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Bovine tuberculosis (bTB) is a bacterial disease mainly due to *Mycobacterium bovis*. It is characterized by a chronic evolution, polymorphic lesions and rare clinical signs. In France, in 1955, about 20% to 50% farms were infected. France was reported as 'officially bTB free' in 2001 by the European Commission, but few herd breakdowns are still being reported and complete eradication of bTB is uneasy to reach. In some French areas, disease re-emerged after a phase of apparent absence (Dordogne, Côte d'Or, Pyrénées Atlantiques, Seine-Maritime, Eure), or has never disappeared (Camargue). Furthermore, wild animals (deer, wild boar, badger) can be a source of infection for cattle. The principal screening test (i.e. the tuberculin test), is imperfect. The single tuberculin skin-test lacks specificity but is more sensitive than comparative tuberculin skin-test. This lack of specificity raises an issue over its diagnostic value as tuberculosis prevalence is low in most areas. In the last few years, new screening tests (gamma interferon, PCR) have been used in addition to conventional methods, in order to improve the quality of bTB diagnosis. These tests are already used in some French areas (Côte d'Or, Dordogne, Camargue) but they have not been fully evaluated yet. The aim of this study was to assess the diagnostic sensitivity and specificity of the gamma interferon test in different contexts and to evaluate the efficacy of its use in various screening schemes.

The Canadian swine health intelligence network

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Livestock surveillance is commonly conducted by governments to estimate the risk of diseases that impact trade in livestock and livestock products. Few are aimed directly at enabling veterinarians and producers to deal more effectively with diseases that do not directly impact trade and access to markets. The Canadian Swine Health Board (CSHB), an organization aimed at providing leadership, coordination and support in the management of the health of the Canadian swine herd, is leading the implementation of a Canadian Swine Health Intelligence Network (CSHIN). The purpose of the network is to support, and enable Canadian veterinarians and swine producers to better manage infectious diseases. The intelligence network will be based upon a novel approach to surveillance that uses web based veterinary practice surveillance to generate near real-time swine health intelligence that is distributed through a formal web-enabled social network of veterinarians, academics, diagnosticians, producers and other stakeholders. The social network will be composed of a single national network and a small number of regional networks where stakeholders evaluate the intelligence produced by the veterinary practice surveillance system in terms of its validity and relevance to the management of swine disease. Representatives of the regional networks will participate in scheduled and adhoc meetings of the national social network. Governance of the CSHIN will be defined in a national meeting of swine industry and veterinary stakeholders and coordinated by the CSHB. The CSHIN will be an important addition to Canada's animal health surveillance arsenal by providing information that will help to document the health of Canadian swine and demonstrate the effectiveness of Canada's swine veterinary service.

A nomogram to calculate output estimates from surveillance models used to confirm freedom from infection

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A nomogram is a graphical representation of mathematical relationships that calculates outcomes derived from one or several parameters by using a simple ruler. Surveillance models, used to confirm freedom from disease, apply Bayes' theorem and rules of probabilities to incorporate historical surveillance data. These complicated equations make it difficult for policy-makers to understand the relationship and the impact of the surveillance system sensitivity and the risk of introduction on the confidence of being free. A nomogram that graphically captures these equations and includes the information, in the form of parameters, needed for the model, allows policy-makers to easily explore the relationships and understand the impact of model parameters on the outcome. The objective of this nomogram is to serve as a pedagogical tool to facilitate the understanding of surveillance models by those not actively involved in analytical modeling. The nomogram is designed as a series of vertical scales starting with the prior probability of infection (far left). A line is drawn through the surveillance system sensitivity for the first time period, the intercept indicating the negative predictive value. The line is then extended until it crosses through the probability of introduction during the first time period and indicates the posterior probability of freedom after that time period. The posterior probability of freedom becomes the starting value for the second time period [1-Prior Pr(Infection)], and the process is repeated for subsequent time periods. We hope this nomogram will serve as a visual link between analysts and those making decisions based on surveillance models.

Sensitivity of dairy cow disease recordings in the Nordic countries

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The conditions for milk production in the Nordic countries Denmark (DK), Finland (FI), Norway (NO) and Sweden (SE) are different with respect to average herd size, housing and feeding. Previous research, based on treatment recordings from national databases, showed that there were large differences in the incidence of important diseases such as mastitis, ketosis, milk fever and retained placenta in 1997. However, disease recordings from national databases may not be a valid measure of the 'true' disease incidence. If the farmer does not see a sick cow or if he/she decides not to treat the cow, no disease treatment is recorded in the database. Additionally, even if the cow is treated, the treatment may not be recorded correctly in the database. Therefore, in order to estimate possible differences in the 'true' incidence of a number of dairy cow diseases, the 'apparent' incidence needs to be adjusted based on knowledge about the sensitivity of disease recordings. Such sensitivities have recently been estimated in a common Nordic project (DAHREVA). In the present study, information about all recorded disease treatments for mastitis, retained placenta, ketosis and milk fever in dairy herds in DK, FI, NO and SE for the year 2007 was collected from the national cattle databases. Incidences will be calculated with and without adjustment for country and disease specific sensitivities. Possible differences in disease incidences between countries – as well as trends in incidences between 1997 and 2007 – will be presented and discussed.

Evaluation of a rapid serological test for the diagnosis of *Leptospira* spp infection in domestic dogs

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The aim of this study was to evaluate the performance of a rapid test (rELISA) for the detection of specific IgM antibodies of pathogenic serovars of *Leptospira* in serum samples of domestic dogs. For that, a cross-sectional study was conducted using 92 serum samples from dogs of different breeds, sex and age from regions of Los Ríos and Los Lagos, Chile. As reference test, it was used Microscopic Agglutination Test (MAT) with a panel of 6 serovars. The rapid test was developed by KIT and performed according to designers instructions noting the presence or not of staining in the test line in the output window of the device to categorize the result as positive or negative. It was evaluated the agreement and the diagnostic performance of the rELISA against MAT. Forty four of the samples were positive for MAT (serogroups Sejroe, Pomona, Canicola, Icterohaemorrhagiae, Ballum and Autumnalis with antibody titers between 1:100 and 1:1600) and 48 samples were negative. Out of MAT positive animals, 12 were patients with recent vaccination against leptospirosis and 2 samples were from dogs with clinical signs: depression, anorexia, jaundice and/or alterations to the biochemical profile indicative of kidney disease. The agreement between tests was low (Kappa=30,3%) and rELISA sensitivity was 25,0% (95% CI=13,2; 40,3), specificity was 97,9% (95% CI=88,9; 99,9%). The positive predictive value was 91,7% (95% CI=61,5; 99,8) and the negative predictive value was 58,8% (95% CI=41,2; 69,7). The rELISA could be useful for the detection of clinical cases of leptospirosis in veterinary clinics to be used as an 'in house test', to provide preliminary information about the serological status of suspected dogs, but this data should be confirmed with a more accurate diagnostic test.

Development of a rapid, user-friendly, diagnostic test for *Taenia solium* cysticercosis

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In this presentation we would like to introduce a novel diagnostic tool for *Taenia solium* cysticercosis in the porcine host. This tool is a rapid, user-friendly lateral flow format assay utilising the HP10 monoclonal antibody. We will describe the production of this assay, its performance as judged using a Bayesian no-gold-standard analysis and discuss the utility of such a test in the field. Neurocysticercosis, the development of the larval stage of this parasite within the central nervous system of man, is a leading cause of acquired epilepsy in the developing world. The parasite is sustained in a population by factors intrinsically linked with poverty: low-input free-range pig husbandry, poor latrine provision, lack of formal pig slaughter and meat inspection and low levels of education or awareness of hygienic meat preparation techniques. In order to assist the affected communities, who are by definition often those with scarce resources, it is imperative that cost-effective and easy-to-use diagnostic assays are made available. Although checking the tongue of a pig for cysts has been recommended as a low-cost screening method for *T. solium*, the sensitivity of this test is notoriously poor. Several antibody and antigen ELISA assays have been developed, but the time, equipment and skills required to perform them makes them unsuitable for many of the situations where diagnostics are required. To rectify this situation work has been ongoing to develop a rapid, user-friendly, antigen detection test for use in the field. We believe that such an assay has a real utility both as a tool for epidemiological studies and within intervention strategies as we work towards control of this important parasitic disease.

Differences between Nordic veterinarians in their threshold for starting treatment for mild clinical mastitis and possible effects on disease registers

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The aim of this study was to investigate if Nordic dairy veterinarians have different behavioural intention to start medical treatment the same day as diagnosing a mild clinical mastitis (MCM) in a lactating dairy cow, as this is one step in the process leading to a disease event being recorded to the national cattle database. Previous studies have shown differences between the Nordic countries with regards to the completeness of disease data. This project aimed at investigating if this may partly be due to differences in thresholds for a veterinarian to start treatment. In a previous study, the attitudes of Nordic farmers towards contacting the veterinarian due to MCM have been studied. A questionnaire-based survey was carried out in the Nordic countries Denmark, Finland, Norway and Sweden. The questionnaire followed the Theory of Planned Behaviour from the field of social psychology. In brief, the theory assumes that behavioural intention is strongly correlated to the actual performance of the behaviour. After qualitative face-to-face semi-structured elicitation interviews with, in total, 25 dairy veterinarians, a set of statements about treatment of MCM was identified. These were grouped into behavioural, normative and control beliefs. The most frequently mentioned beliefs were rephrased to questions. The questionnaire was pilot-tested, translated to the four Nordic languages, back translated and distributed to all veterinarians mainly in dairy practice. The response rate was a bit over 50% in all four countries (545 participating veterinarians). Descriptive statistics will be given.

Assessing diel flight activity and biting behavior of *Culicoides* in the Netherlands

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The emergence and massive spread of bluetongue virus serotype 8 in north-western Europe confirmed the importance of Palaearctic *Culicoides* species in disease transmission. Surveillance of *Culicoides* in European countries is currently carried out using standardized suction light-trap protocols that sample adult midge populations. However, it is not clear whether light-trap catches accurately reflect the *Culicoides* biting population. The aims of our study were threefold: (1) to investigate the *Culicoides* diel flight activity using different collecting methods; (2) to estimate the species-specific hourly attack and biting rates on cattle; and (3) to compare *Culicoides* abundances in light-trap (as traditionally measured) to midge population levels in the field. Field experiments were carried out fortnightly from May to September 2010 on a cattle farm in the Netherlands. Collections were made over 24 hours using direct (mechanical aspiration, pootering and sweeping) and indirect (suction light-trap) methods both inside a stable and outside in a pasture. Meteorological data were logged continuously by a weather station at the site. For each collection sample *Culicoides* were identified to species level and age graded. *Culicoides* maximum diel activity periods in relation to meteorological conditions and relative species composition, as obtained using different collecting methods, are discussed. Finally, the relative attack and biting rates experienced by cattle under field conditions are compared to the number of midges caught by light trap.

A study on prevalence, risk factors and economic impact of sheep pox in North and South Kordofan States of the Sudan

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The current study is an attempt to better understand the epidemiology of sheep pox in the Kordofan region in the western part of the Sudan, which is one of the largest production sites for sheep. The study was designed as a cross-sectional survey in the Kordofan region, with collection of specimen from the target population of sheep from March to September 2011; a concurrent questionnaire was done. The current study revealed that the estimated overall sero-prevalence of SPP in Kordofan region was 20.1% and that SPP prevails both in SKS and in NKS. Also, a number of risk factors like locality, herd size, insect bites and rain fall/year and traditional treatment were found to be significantly associated with SPP occurrence in the Kordofan region. The average cost of SPP was estimated at 20.5% of sheep flock production costs. The Indirect ELISA test to detect antibodies to capripox viruses was evaluated to have a diagnostic sensitivity of 33.33% and a diagnostic specificity of 60%.

A spatial zero-inflated modelling approach for assessing the H5N1 surveillance system in Thailand

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In Thailand, the major epidemic lasted from July 2004 to May 2005. The H5N1 surveillance system has often been assumed to be very efficient during this epidemic. However, no quantitative assessment of the Thai H5N1 surveillance program has been so far undertaken. Here, we propose to use zero-inflated (ZI) models to analyze unilist capture-recapture surveillance data collected during the 2004 epidemic at subdistrict level, to identify the factors driving the presence/absence of the disease and those influencing the detection process. ZI models use the number of detections of infection in the different sites for estimating the total number of infected sites, including those where infection was never detected. We considered each subdistrict of the country as the epidemiological unit (site), and that each H5N1 outbreak notified during the 2004 epidemic constituted a detection of the disease in the site. Therefore, our count dataset focused on the number of detected outbreaks in each subdistrict. To derive the real number of infected sub-districts, we fitted a ZI Poisson model (ZIP) and a ZI negative binomial model (ZINB) to our dataset. We tested the residuals for spatial autocorrelation, proved it was significant and thus added a spatial autocorrelation term in the model. As expected, the spatial ZINB fitted the data better than the spatial ZIP, suggesting the presence of overdispersion in the counts of detections. Derived from the spatial ZINB model, we were able to estimate the real number of infected subdistricts during the epidemic and the sensitivity of detection at sub-district level. We also identified the most important factors that determine the presence/absence of the disease in subdistricts (density of human population and density of free grazing ducks), and influence the detection process (density of free grazing ducks and density of native chicken).

Evaluation of four enzyme-linked immunosorbent assays for the serological survey of avian influenza in wild bird species

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Concerns about the threat H5N1 High Pathogenic Avian Influenza Virus poses on animal and human health has risen since it broke out in Hong Kong in 1997. Since then, Avian Influenza surveillance of aquatic birds has increased. More and more commercial Enzyme Linked Immunoassay (ELISA) tests are available for serologic surveillance but these tests are often developed and validated for use with domestic poultry. However, for a correct interpretation of ELISA test results from wild bird sera, more information is needed. In present study, four ELISA assays (ID-Vet IDScreen®, IDEXX FlockChek™ AI MultiS-Screen Ab Test Kit, Synbiotics FluDETECT™BE and BioChek AIMSp) were compared for the serological analysis of 172 sera from wild duck, mute swan and Canada goose. Samples were selected based on ID-Vet IDScreen-results to obtain an approximate 0,5 prevalence rate. A total of 92 sera from experimentally infected Specific Pathogen Free (SPF) chickens and Peking ducks were included in the tests as well. Cohen's kappa statistics and Pearson correlation coefficients were calculated for each combination of 2 tests and for each bird species. Test agreement for wild duck sera varied from no until moderate agreement while test results for Canada geese and swan sera agreed fairly until almost perfectly. Tests agreed the most for sera from experimentally infected SPF chickens and Peking ducks. This study shows not every commercial ELISA can be used for the testing of sera from every wild bird species and that more reliable validation studies should be considered for the use of these tests in serologic surveillance of wild bird species.

Assessing the use of an electronic telephone log to enhance early warning surveillance in England and Wales

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Detection of new or re-emerging threats (NRT) relies on effective surveillance coverage of the target population. Telephone discussion of clinical cases between AHVLA Veterinary Investigation Officers (VIOs) and practitioners is recognised as an important method for the early detection of NRT. This extends the traditional pyramid of surveillance, which relies on the formal collation of laboratory data. A telephone log was introduced for *post mortem* submissions to AHVLA laboratories in January 2011. A review of the content of this log over a six month period was undertaken. The aim was to evaluate its use and how it may be developed to enhance early warning surveillance by collating data provided by all telephone communication with veterinary practitioners. During the period, 1076 telephone discussions were recorded, the findings of which will be discussed. This represented 24% of AHVLA carcass submissions within the time period. Telehealth systems are used successfully for surveillance in other European countries. The current system in AHVLA laboratories provides telephone support to practitioners using over 50 VIOs. Telephone consultations are varied including discussion of differential diagnoses in aid of a diagnosis. There is no formal method to capture data which does not result in a submission and yet 22% of NRTs are initiated through the phone discussions with practitioners. Systematic collation of information between the practitioner and VIOs is likely to reduce the time for detection of a threat and reduce the window of opportunity for silent spread. Managing this communication stream effectively is therefore likely to be beneficial to animal health and disease control.

Comparing four non-random farm selection methods applied in the Canadian notifiable avian influenza surveillance system

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Analysis of surveillance data to demonstrate freedom from a disease may include estimation of probability of being free from the disease (PrFree) and a descriptive analysis of the geographical representation as well as a relevant description of species and production types. To be efficient the surveillance should be designed to yield a high PrFree while representing the area, species and production types therefore non-random sampling may be more efficient than random sampling. In addition, random sampling from a registry of farms may not be feasible in all countries. We use data from the Canadian Notifiable Avian Influenza Surveillance system (CanNAISS) to compare four non-random farm selection methods. Specifically we compare the distribution of poultry types, age of poultry and geographical representation. The farm selection methods were: M1 was based on slaughter schedules and monthly target sample sizes. Breeders and layers had high priority, turkeys and roasters (chicken >3.7 kg) lower priority; M2 was based on hatchery supply flock lists. All farms with a flock coming to the end of lay were selected; M3 was based on registered poultry producers in British Columbia. Priority was given to multi species farms and farms with more than one production type; and M4 was a combination of M1, M2 but included a list of table egg layer farms. The geographical representation was ensured by setting target sample sizes for each of the 10 provinces and by no re-test of a farm within 6 months. Method 1 yielded a good geographical representation, about 50% turkey farms and a lower age of the tested poultry than methods 2, 3 and 4. Table egg layers were only well represented by method 3 and 4. We conclude that a combination of the four methods may be the most efficient farm selection method.

Detection of hyperketonemia in dairy cows using FTIR and test day information

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The objective of this study was to assess the quality of a diagnostic model for the detection of hyperketonemia in early lactation dairy cows at test days, using FTIR spectroscopy analysis of milk ketone bodies and available test day information. Blood samples of 1,678 cows from 118 randomly selected farms were collected on the test day and analyzed. The prevalence of hyperketonemia was 11.2% in this study but observed herd prevalences varied largely between farms. The value of FTIR predictions of milk acetone and milk BHBA concentrations as single tests for hyperketonemia were found limited given the relatively large number of false positive test day results. A multivariate logistic regression model with a random herd effect was constructed, using test day information and FTIR predictions of milk acetone and milk BHBA as predictive variables. The obtained diagnostic model had a sensitivity and a specificity of more than 80% for the detection of hyperketonemia at test days. Confirmation of test-positive samples with wet chemistry analysis of milk acetone or milk BHBA concentrations (serial testing) improved the diagnostic performance of the test procedure. The presented model was considered not suitable for individual detection of cows with ketosis due to the length of the test day interval and the low positive predictive values of the investigated test procedures. The diagnostic model is in our opinion valuable for herd level monitoring of hyperketonemia, especially when the model is combined with wet chemistry analysis of milk acetone or milk BHBA concentrations.

Impact on sensitivity of a commercial iELISA test for brucellosis, when serological samples are pooled
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Uruguay has an eradication program for *Brucella abortus*. The susceptible population is approximately 6 million cattle and 25% of it is tested annually with a high cost for farmers and government alike. With a farm prevalence of 1% and a cattle prevalence of 0.26%, an increase in surveillance is needed to eradicate the disease and maintain the cost at a reasonable level. The objective of this study was to assess the dilution effect in test sensitivity when using pool samples, in order to determine the viability of this type of sampling. 18 serum samples were selected from animals with positive diagnosis to *B. abortus* and 100 serum samples from animals in farms without a history of Brucellosis. Previously, all samples were tested with Bengal Rose, FPA, and ELISA to corroborate their status. Each positive serum was diluted to half 10 times and tested with a commercial iELISA. Each dilution was classified by iELISA as positive or negative to develop a probit model with a base 2 logarithm of the dilution. The model was significant with a constant value of 2.275 (EE=0.292) and the coefficient $\log(\text{dilution})$ -0.300 (EE=0.043). The test sensitivity (Se) for each dilution was estimated with the probit model. The dilution are: 1, 2, 4, 8, 16, 32, 64, 128, 256, 512, 1024, and the respective sensitivities (Se) are: 99%, 98%, 95%, 92%, 86%, 78%, 68%, 57%, 45%, 33%, 23%. With this information, in a hypothetical case of positive farms with a herd prevalence of 10% and a random sample of 32 cows, the herd sensitivity changes from 96% with individual samples to 93% if we process all the samples in one pool. In conclusion, it is possible to increase the surveillance and keep costs at reasonable level.

Evaluation of the specificity of two ELISA tests for detection of *Salmonella* antibodies in bulk milk
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Sweden has a documented low prevalence of *Salmonella* in animals. After years of successful control, based on bacteriology, the need for more cost-effective diagnostic tools as a complement to bacteriology has become apparent. Serological tests for detection of antibodies against *Salmonella Dublin* and *S. Typhimurium* has been developed for cattle. As test performance may vary in different populations it was important to evaluate the specificity of these serological tests in Swedish dairy herds before considering use within the control program. The sensitivity was not evaluated in this study. From a national biannual bulk milk sampling in 2007, every sixth sample was selected, resulting in 1,067 samples. The samples were analysed with PrioCheck® *Salmonella* Ab bovine Dublin ELISA and PrioCheck® *Salmonella* Ab bovine ELISA. Specificity was calculated assuming disease free status of the Swedish dairy population. As the specificity depends on the chosen cut-off value, the results will be presented as a graph with specificity as a function of PP-value (PP = percent positivity). It was concluded that the specificities of these ELISA tests are high enough to be used as a complementary test in the Swedish control program, also with a lower cut-off value than recommended by the producer. Consequences of different cut-off values, when used on Swedish dairy cattle, will be discussed.

Cost effectiveness analysis of participatory disease surveillance in Kenya

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Effective surveillance for infectious diseases is an essential and resource-consuming activity for mitigating unwanted consequences for animal and public health. Allocation of scarce resources for surveillance must be considered against alternative prevention and control measures and regularly reviewed. Few studies estimate cost-effectiveness and benefits of different animal disease surveillance approaches and systems. In this study, we considered the benefits and resource costs of participatory epidemiology (PE) surveys and participatory disease surveillance (PDS) compared with routine passive surveillance. Focusing on a 6-month interval in a primarily pastoralist district in Kenya, basic performance indicators for surveillance measured were (1) number of outbreaks; (2) number of samples generated from suspected outbreaks; (3) number of positive laboratory confirmations. Costs of passive surveillance and interventions mounted were determined for the 6-month interval. In the same district, PE surveys were conducted in randomly selected communities to determine the number of outbreaks of notifiable cattle diseases in the same 6-month interval. Additional information was collected on the scale of morbidity and mortality for historical outbreaks (numbers and duration), the value of individual animals and the number of active outbreaks. Costs associated with mounting PE visits were ascertained and extrapolated to district level. One month after completion of PE visits, district level stakeholders were interviewed to determine the response, if any, to outbreaks detected during the visits. The study provides cost effectiveness estimates at a district level for the 6-month interval, including losses which occurred from outbreaks missed by passive surveillance and costs if PE were applied at regular intervals. In addition, the findings consider available prevention and control responses and provide decision-makers with evidence to inform future application of participatory approaches in animal disease surveillance.

Comparison of alternative systems for the detection of emerging diseases by surveillance of fallen stock

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For diseases that may cause increased mortality or specific post-mortal changes, surveillance activities targeting fallen stock could improve the overall ability to detect disease. The aim of this study was to compare the sensitivity and the cost-effectiveness of different alternatives for such surveillance activity. Different scenarios for sampling fallen stock were designed: (1) sampling of fallen stock at the farm which could be performed by a veterinarian, a carcass collector or by the farmer; (2) selection of fallen stock at the rendering plant for necropsy and sampling of macroscopic findings, or alternatively routine sampling of selected organs; (3) sampling of fallen stock at *post mortem* facilities when referred for necropsy with sampling of macroscopic findings or alternatively by routine sampling (present system). The sensitivity of each surveillance alternative was estimated using scenario-tree modelling and based on actual numbers of fallen stock, and numbers of animals and herds in different risk categories. Bovine tuberculosis in cattle (bTb) and classical swine fever (CSF) were chosen as model diseases. The sensitivity to detect these diseases was calculated for each scenario with several hypothetical levels of sampling intensity. In addition, the costs for each surveillance activity were roughly estimated. The results show that the present system for sampling of fallen stock has a very low sensitivity for bTb and CSF, because very few animals are sent for necropsy. However, with a different system the sensitivity can be increased considerably. The most efficient alternative for both diseases were selection of carcasses at the rendering plant with transfer to *post-mortem* facilities for necropsy and routine sampling of selected organs.

Comparison of traditional laboratory parameters with acute phase proteins in visually identified diseased feedlot calves

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Changes in blood parameters such as white blood cell count (WBC), total plasma protein (TP) and fibrinogen (Fb) have been used to support clinical infectious disease diagnosis. Recently, laboratory tests for acute phase proteins (APP) have been described and used as biomarkers of inflammation. The objective of this study was to create a reference interval and compare test results of APPs in a field setting to clinical evaluation of bovine respiratory disease (BRD) in feedlot cattle by the staff. This study included 429 auction-derived mixed breed calves at two southern Alberta commercial feedlots identified as BRD cases in the first 5 weeks after arrival. Sick calves were immediately bled and treated according to feedlot protocols. Treatment records and rectal temperature were collected. Blood samples were used to quantify TP, Fb and WBC. Commercial ELISA tests (Tridelta Ltd, Maynooth, Ireland) for haptoglobin (Hp) and serum amyloid A (SAA) were performed on serum samples, stored at -20 °C. A reference interval was created with 72 healthy feedlot cattle 10 days before slaughter. Test results from sick animals were compared to this reference interval. The rate of detection was compared to feedlot staff evaluation. Preliminary results showed sensitivity estimations of 82.6% (78.2-86.4) and 51.5% (46.2-56.9) for Hp and SAA respectively, while sensitivities of 29%, 16.6% and 41.7% were determined for WBC, TP and Fb. Specificity estimations based on the healthy individuals was estimated 88.5 (79.2-94.6) for Hp and 73.1 (61.8-82.5) for SAA. Feedlot staff identifies sick calves based on experience and knowledge of cattle behavior. However, due to cattle's stoic nature, visual appraisal might not be accurate. Our results suggest, that Hp is a strong tool to assess disease in feedlot animals, while SAA, WBC, TP and Fb showed low sensitivity when compared to visual appraisal.

Performance indicators of the active surveillance system for avian influenza in Cuba

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The sensitivity of the active surveillance system for avian influenza was assessed by a stochastic model quantifying the probability of revealing by the system at least one infected animal within a farm. The diagnostic sensitivity of the haemoagglutination inhibition assay and different levels of within flock prevalence (5%, 10% and 30%) were considered, under five different samples size scenarios: testing 20, 30, 40, 50 or 60 animals in each flock. Similarly the probability of revealing at least one infected farm at a between flock prevalence of 5% were assessed, as well the timing right investigations according to risk period constitutes by waterfowl migrations. The results of the simulation model demonstrated that 30 tested birds for each flock can likely detect the infection when the within prevalence of infection is around 30%. In this case, in fact, the probability of having at least one positive result is more than 99%. When lower levels of within flock prevalence are considered, the probability of failing to detect the infection with 30 tested birds raises up to 7.5% and 19.8% with, respectively, 10% and 5.7% within flock prevalence.

The role of carry over in test day samples in dairy herds with different milking systems

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Test day samples are analyzed for fat, protein, somatic cell counts and in some cases bacteria by real-time PCR. The variation between cows within a herd is normally limited with regard to fat and protein, but for SCC and bacteria counts in the milk the variation between cows might be very big. The methods for sampling the cows depends on the milking system and studies in Danish dairy herds have shown carry over between cows from 2 to 15%. The carry over might result in misclassification of cows as infected or healthy based on SCC or PCR analysis and result in unnecessary costs for treatment, culling or repeated sampling of cows. The presentation will present results for carry over and the effect on the classification of cows based on both SCC and PCR in herds with parlor milking and different automatic milking systems. Furthermore the effect of the carry over on different sampling strategies and the possibilities for correction of the measurements based on information about the milking order depending on the prevalence of the bacteria of interest will be presented based on data from 30 Danish dairy herds.

The use and management of an online spreadsheet as database for epidemiological surveillance

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For several years, the Costa Rican Veterinary Services (SENASA) employed self-developed software for animal surveillance, but its use was finally discontinued due to little flexibility and other problems. There was an urgent need for a quick replacement of the former system, which would be able to register disease events investigated in the frame of passive epidemiological surveillance by official veterinarians. A digital database was created, using a spreadsheet in 'google docs', which is a free application in 'Gmail', an open email service provided by 'Google'. This spreadsheet, which we called BOEE (Bulletin Of Epidemiological Events) was shared with field veterinarians, animal health program coordinators, the laboratory and a few others, who were given access to edit or view the data. The spreadsheet contains information on the date of notification, the veterinarian attending the event, location, farm code, disease syndromes, measures taken, number of samples sent to the lab, a unique consecutive case number, some other variables and the final result. Disease events and outcome of the lab analysis must be registered within 48 hours. The data can easily be downloaded in Excel, PDF or other formats. Once a month, the data is saved into an Excel file, in which all data throughout the year are accumulated, the online data base is left empty in order to make reporting easier. Data analysis, which used to be a weary process, is now done in little time by using filters in an Excel file. All data are available in one central data base. Although BOEE is a simple online spreadsheet, and not a very robust informatics system, it has helped SENASA maintain a good and timely register of disease events, which is easily accessible to all official veterinarians in need of this data, and may serve as an early warning system. This spreadsheet could be used by developing countries as a potential solution to establish an easy, cheap and flexible reporting system.

Post-vaccination technical monitoring of *Brucella melitensis* in Albania

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The aim of monitoring the efficiency of REV1 vaccination campaign against *Brucella melitensis* in small animals is to determine if the current policy is still valid and guide the decision to change the strategic approach. The currently applied strategic plan, started in 2004 and aims to vaccinate all replacement stock each year. Such population fraction represents 25% of the total small ruminant population and by 2008-2009 the whole population would have been immunized. The primary objective of the technical monitoring programme was to determine efficiency of the vaccination strategy by identifying the proportion of animals in the target population with significant titres of *Brucella* specific antibodies. This in turn is determined by the proportion of animals which have been vaccinated, and by the rate of sero-conversion in vaccinated animals. In 2007 a multistage fashion survey has been carried out in ten southern districts of Albania on three separate fractions of small ruminant population. According to the sampling protocol have been blood sampled, (1) 1,335 animals of 3-6 months old replacement females in order to assess the proportion of the target population which has been effectively vaccinated; (2) 359 unvaccinated adult breeding males to estimate the prevalence of *B. melitensis* infection; and (3) 450 breeding females with a history of abortion in order to estimate any association between abortion and previous vaccination history. The results of vaccinated animals based on Rose Bengal Plate Test, indicates that an overall sero-conversion rate of around 48% has been achieved, considering the wide variation between districts ranging from 13% to 78%. From the unvaccinated male animals the sero-prevalence resulted 23% and that *Brucella* antibodies were detected in 24% of aborted females. Such results suggests that there is a need to change the strategic approach toward a policy of mass vaccination of all small ruminant population in selected areas of Albania, or even nationwide.

Cost minimization analysis for low pathogenic avian influenza surveillance systems based on blood or egg samples

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As low pathogenic avian influenza viruses can mutate into high pathogenic viruses the Dutch poultry sector implemented a surveillance system for low pathogenic avian influenza (LPAI) based on blood samples. From a cost reduction point of view it has been suggested that egg yolk samples could be sampled instead of blood samples on egg layer farms. To support future decision making about AI surveillance economic criteria are important. Therefore a cost analysis for the Netherlands is performed on systems that use either blood or eggs as sampled material. The effectiveness of surveillance using egg or blood samples was evaluated using scenario tree models. Then an economic model was developed that calculates total cost considering cost for sampling, sample preparation, sample transport, testing, communication of test results and for the confirmation test on positive results. The surveillance systems varied in sampled material (eggs or blood), sampling location (layer farm or packing station) and location of sample preparation (laboratory or packing station). It is shown that a hypothetical system in which eggs are sampled at the packing station and samples prepared in a laboratory had the lowest total cost (i.e. € 273,393) a year for the Netherlands. The hypothetical system in which eggs are sampled at the farm and the currently implemented system in which blood is sampled at the farm have 6% and 39% higher cost respectively. This study shows that surveillance for avian influenza on egg yolk samples can be done at lower cost than surveillance based on blood samples. The model can be used in future comparison of surveillance systems for different pathogens and hazards.

Bovine TB interferon- γ assay at slaughter: a novel strategy for targeted surveillance

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Screening for bovine tuberculosis (bTB) at points-of-concentration (POC) of cattle would aid in the global efforts to eradicate bTB. Three separate studies evaluated the application of the interferon-gamma (IFN- γ) assay for use at slaughter facilities, a POC of cattle. Study one tested blood obtained at commencement of exsanguination (COE) of cattle experimentally sensitized with inactivated *M. bovis* for retention of a positive result in the IFN- γ assay. Results indicated that most sensitized cattle would retain a positive IFN- γ assay result at COE, despite a decline in IFN- γ production. In study two, at the time of blood collection, and total lymphocyte counts were evaluated as potential factors affecting measurable IFN- γ production at COE. Results indicated that blood obtained from sensitized cattle at COE was more likely to remain positive than blood collected at successive time points post exsanguination; hence time of blood collection is crucial to obtaining valid bTB IFN- γ assay result at slaughter. Lymphocyte counts progressively declined following exsanguination, which might contribute to the reduction in IFN- γ production. To compensate for the reduction in IFN- γ production, a different set of positive cut-off values might be needed for blood collected at COE. Study three tested cattle under field conditions. The cattle originated from herds designated as one of three risk categories: known infected, potentially exposed, and non-exposed. Cattle with or without bTB-like gross lesions were identified as IFN- γ assay positive using blood collected at COE. One of those cattle was confirmed bTB positive by bacterial culture. All the IFN- γ assay positive cattle originated from either known infected or potentially exposed herds. Therefore, blood collected at COE could be used to identify bTB exposed herds or to monitor a bTB-free area, providing an additional tool for the control and eradication of bTB.

An effective sero-surveillance program for detection of low pathogenic avian influenza outbreaks in layer chickens

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Low pathogenic avian influenza virus (LPAIV) of the H5 and H7 subtypes can mutate to a highly pathogenic virus when infecting poultry. Hence early detection of LPAIV outbreaks will reduce the probability of pathogenicity mutations and large epidemics. The objective of this study was to develop a model for the design and evaluation of an effective and efficient serological surveillance programme for LPAIV infections in layer chicken flocks. We aimed at early detection and culling of an infected flock before it infects more than one other flock (between flock reproduction ratio $R_f < 1$), hence a large epidemic cannot occur. We used a mathematical model that explores the effect of sample size and sampling frequency on timely detection. The model takes into account the LPAIV within- and between-flock infection dynamics as well as the diagnostic performance of the test used for surveillance. Since layer flocks are the target population, we explored the value of using eggs as an alternative to sera as sample commodity. The model was subsequently applied to refine the Dutch serological-surveillance programme. Using a transmission kernel, the R_f for each flock was estimated and a transmission-risk map was constructed. The latter was used to target a risk-based surveillance strategy. Most flocks (79%) had an $R_f < 1$ and an early detection programme in areas where these flocks are located would not be required. Early detection could be implemented in areas with flocks with an expected $R_f > 1$. For example, in areas/flocks where $R_f = 2.2$, sampling ten sera samples/flock every month would ensure early detection. If eggs are sampled, 90 samples every month would be required. In conclusion, we present a model that can be used to explore different sampling strategies and can aid implementation of effective surveillance programmes for low pathogenic avian influenza.

Re-introduction drives the within-herd persistence of bovine tuberculosis in Great Britain

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The number of cattle herds placed under restrictions in Great Britain (GB) due to the suspected presence of bovine tuberculosis (bTB) has progressively increased over the past 25 years despite a costly test-and-slaughter control program. Recent research has focused on the contribution of cattle-movements and wildlife reservoirs on incidence as measured by the number of so-called 'breakdown' herds. However, around 38% of herds that clear restrictions experience a recurrent breakdown within 24 months suggesting that infection may be persisting within herds. Persistence is likely to be facilitated by the imperfect sensitivity and specificity of the tuberculin skin test. The contribution of missed infection cannot be directly quantified, as the sensitivity of the tuberculin test is dependent on the time from infection and thus the frequency of testing and the history of transmission within the herd. In this study we develop a systematic framework to infer the efficiency of the GB surveillance regime using dynamic within-herd models. We use statistical measures of persistence, which describe the balance between local persistence and the rate of re-introduction of infection, as a probe for inference. Stochastic persistence has been extensively studied for endemic childhood diseases, but has not previously been used as a basis for inference for managed infections such as bTB. We introduce a systematic, and general, framework for model-based inference based upon measures of stochastic persistence using Approximate Bayesian Computation (ABC). Using routinely collected epidemiological data we estimate that 8.4% (3.7-16; 95% credible interval) of British breakdowns have infected animals remaining after a herd has been declared 'bTB free', leaving a median of 1 (1-3; 95% CI) infectious animals within these herds. Our analyses suggest that it is extrinsic transmission into herds, rather than this infectious burden, that drives recurrence.

Predicting cow-calf producers' intent to report suspect cases of FMD in Texas

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Livestock producers serve as an important line of defense for early detection of an introduction of foot-and-mouth disease (FMD). However, due to the complexity of moral, social, and economic issues surrounding the control of highly contagious diseases, producer participation in disease reporting may not be assured. Two questionnaires were developed and distributed to 2,018 and 2,022 Texas cow-calf producers, respectively, in order to determine the factors which best predict producers' intentions to report cattle with clinical signs consistent with FMD either in the absence of or during a hypothetical outbreak of FMD. Factor analysis, followed by multivariable, ordinal logistic regression was used to predict producers' intentions. Reporting of cattle with clinical signs of FMD in the absence of an outbreak was related to producers' beliefs about the consequences of reporting, beliefs about what other producers would do, trust in agricultural agencies, and their perception of the risk posed by FMD. During a hypothetical outbreak, intentions to report were determined by producers' beliefs about the consequences of reporting, perception of the risk posed by FMD, prior experience with federal disease control programs, and age. Recommendations for improving reporting include targeting specific beliefs related to the consequences of reporting, increasing transparency in the post-reporting process, planning for and communicating plans for maintaining business continuity in order to better inform risk perception, and partnering with organizations to ensure sustained and meaningful communication that supports trust between producers within the affected agricultural community.

Heartwater surveillance network in Guadeloupe: a model for the Caribbean

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Heartwater, a tick-borne disease of ruminants transmitted by *Amblyomma* ticks is present in 3 Caribbean islands: Guadeloupe, Marie-Galante and Antigua, representing a threat for neighboring islands and North America. Despite the availability of efficient acaricides, no significant improvement has been seen in vector and disease control. The Ticks and tick borne disease working group of the Caribbean animal health network (CaribVET) recommended Guadeloupe the conduct of (1) a sociologic study to understand farmers' reluctance to adopt efficient treatment; and (2) heartwater surveillance. A passive surveillance network monitoring ruminant neurological syndromes, RESPANG, was set up in July 2010. RESPANG objectives are to assess the burden of heartwater and sensitize farmers. Private veterinarians collect blood and ticks after farmer reporting of clinical suspicion. Diagnostic for heartwater, babesiosis and anaplasmosis is performed at CIRAD. An online database displays results on interactive maps allowing the identification of areas where communication campaigns by farmer association can be focused. Leaflets and key messages were developed, based on the recommendations of the sociological survey. Out of 238 suspicions, 30.5% were positive for heartwater all along the year. Analysis of the factors associated with heartwater is currently ongoing. RESPANG shows excellent partner involvement and interaction. Surveillance performance indicators will improve network operation and coordination. Long-term data set will enable to assess the impact of communication campaign and possibly to detect introduction of diseases with similar clinical signs. In parallel, pathogen and vector genetic characterization is being developed using RESPANG samples. This shows the tight link between surveillance network and research activities. CaribVET supports the establishment of similar networks for other diseases in other Caribbean islands.

Enhancing laboratory capacities in the Caribbean for better animal health regional surveillance

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The Caribbean Animal Health Network (CaribVET) is a collaboration network of veterinary services, laboratories, research institutes and regional/international organizations in the Caribbean. Its goal is to improve animal and veterinary public health in the 32 Caribbean countries and territories. In the past, CaribVET had evaluated 34 CARICOM diagnostic laboratories and organized several workshops on IATA regulations and on diagnostic techniques. CaribVET coordinated simulation exercises on Avian Influenza samples' shipment and inter-laboratory assays on Classical Swine Fever diagnostic. The 'Laboratory Quality Assurance and Diagnosis Working Group' (WG), created in 2011, gathers main actors involved in diagnostic and laboratory activities and meets every 3-4 months physically or virtually. The WG (1) regularly updates diagnostic capabilities and capacities in the region; (2) identifies training needs, promotes and strengthens links with reference labs; (3) provides guidance for the development of a regional network of laboratories while promoting the exchange of data, protocols, materials, and human resources; (4) promotes the implementation of quality assurance in veterinary diagnostic laboratories; and (5) supports the logistics of inter-laboratory assays. Recent achievements include (1) the development of an online database of laboratories in the Americas (CaribVET, CIRAD Guadeloupe, OIE collaboration); (2) signature of a letter of understanding between OIE and CaribVET to develop joint activities in accordance to both structures' recommendations; and (3) organization of a workshop on diagnostics of swine influenza and quality assurance in Guadeloupe within the FAO technical cooperation project on swine influenza surveillance. These coordinated activities reinforce diagnostic capacities and capabilities in the Caribbean which are essential for efficient surveillance of animal health.

Surveillance of equine influenza viruses in the United Kingdom, 2009-2011

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Equine H3N8 influenza A virus (EIV) causes clinically severe respiratory disease in horses. Antigenic variation (drift) of the surface haemagglutinin protein, the major immune target of EIV, leads to reduced vaccine efficacy. As antigenic drift is continuous, ongoing virus characterisation is necessary to inform periodic vaccine updates. Viruses isolated around the world are submitted to the Animal Health Trust, UK for antigenic and genetic analysis so that antigenically distinct viruses can be assessed for their spread in the equine population. Antigenic and genetic characterisation was carried out on EIV isolated in the UK between 2009 and 2011. In the 3 years, 37 viruses were isolated from 53 swabs testing positive by antigen ELISA. All EIV were characterised as being of either one of two clades now recognised of the Florida sublineage (clades 1 and 2), with a distinct temporal clustering of each clade. With the exception of one clade 1 isolate (Lincolnshire/1/07), only clade 2 Florida sublineage EIV were isolated in the UK to mid-2009. However, for the latter part of 2009 only clade 1 EIV were isolated (7 isolates from England, Scotland and Wales) and were shown genetically to be closely related to clade 1 EIV isolated in USA in 2009. Although it was assumed this would confirm a change in predominance from clade 2 to clade 1 in the UK as seen previously with the emergence of American lineage and Florida sublineage viruses, only clade 2 EIVs were isolated in the UK throughout 2010 and 2011 with no evidence of continued circulation of clade 1 EIV. Clade 2 viruses were also active in this period elsewhere in Europe and in India, Mongolia and China. Although cases of EI in the UK have mainly been recognised in non vaccinated animals, suggesting continued vaccine effectiveness, recommendations for strains included in vaccines were updated in 2011 to include representatives of both clade 1 and clade 2 EIV, thereby optimising global relevance.

Surveillance for *Trichinella spiralis* Canadian swine: proposed standards for reporting of surveillance information in freedom from disease modeling

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The Atlantic Veterinary College, the Canadian Food Inspection Agency, and the Canadian Swine Health Board are collaborating to confirm the absence of infection with *Trichinella spiralis*, a zoonotic parasitic roundworm, in Canadian commercial swine. We use scenario tree models that combine historical and current *T. spiralis* surveillance data from different sources to estimate the probability of freedom from disease. Scenario tree modelling has become an established methodology and is well described in the literature; however, standards for organizing and reporting the surveillance information incorporated into such models are less developed. Based on our work on *T. spiralis*, we propose that information in surveillance models be organized in distinct categories, each with specific parameters and values that are thoroughly described and justified. The proposed categories are: (1) definitions for objectives; (2) starting point; (3) inputs; (4) data; and (5) outputs. Data from the project will be used to illustrate the proposed method for reporting surveillance studies. A standardized manner of reporting such studies will facilitate their validation and expedite their evaluation by experts in the field. Our scenario tree modelling reflects that current international guidelines by the World Organisation for Animal Health (OIE) require reporting of presence or absence of infection with *T. spiralis* in two distinct populations: sows and hogs. We discuss the implications hereof for scenario tree modelling and compare results from analysis in a combined population with a common design prevalence to those of analyses in two distinct populations with different design prevalences. For the latter analysis we also describe how to arrive at a single probability of freedom at the country level.

Assessing agreement between diagnostic methods: an example of coccidia oocysts counting techniques in broiler flocks*Veldhuis, A., Peek, H. and Swart, W., GD Animal Health Service, Netherlands; a.veldhuis@gddeventer.com*

To be able to decide whether an alternative diagnostic test can replace an existing one, a reliable measure of agreement between test results is needed, in particular when no reference is present. In this study, results obtained of an oocyst counting technique (a modification of the standard McMaster technique) and of a recently developed qPCR are compared. The purpose was to assess whether agreement between both tests is sufficient to replace the conventional method by the new. Both methods are applied on faecal samples to measure the level of parasitic infection pressure in broiler flocks, expressed on a continuous scale (oocysts/gram faeces). Pooled faecal samples of 10 flocks, from 4 farms, were repeatedly collected and tested with both tests between d7 and d40 of the production cycle. It is generally accepted that Pearson's correlation coefficient is not suitable to quantify agreement between continuous results of diagnostic methods, as it ignores systematic error (bias). Various alternative methods exist, such as Cohen's kappa for ordered categories and the intraclass correlation coefficient. It was decided to apply the concordance coefficient of correlation (CCC). This method takes into account both precision and bias of test results, by measuring the variation of their linear relationship from the line of perfect agreement through the origin. This resulted in a CCC of 0.751 (95% CI 0.719-0.783), based on Pearson's r of 0.755 (precision parameter) and a bias correction factor of 0.994 (accuracy parameter). Although this outcome seems fairly low at first sight, interpretation of the CCC greatly depends on the purpose of comparison and the desired agreement. For example, a high level of agreement is needed in particular when false results have large consequences. In this study, the new test is developed for routine monitoring purposes and the CCC could be considered sufficiently high. The considerations to use the CCC in relation to the characteristics of the data will be discussed.

Participatory disease surveillance evaluation: findings from Africa (HPAI) & Pakistan (rinderpest)*Hannah, H.¹, Pali, P.¹, Rware, H.¹, Bett, B.¹, Randolph, T.¹, Grace, D.¹, Njuki, J.¹, Pissang, C.² and Hisrich, E.³, ¹International Livestock Research Institute, Kenya, ²VSF, Belgium, ³CSU, USA; vetepi@gmail.com*

Participatory disease surveillance (PDS) has been promoted in developing countries to complement conventional surveillance, particularly for rinderpest eradication and Highly Pathogenic Avian Influenza (HPAI) control. We conducted an evaluation participatory epidemiology (PE) and PDS capacity building outcomes by examining PDS as a surveillance tool for national animal disease surveillance. The evaluation framework pillars (relevance, effectiveness, efficiency, sustainability and impact) were developed from over 30 indicators adapted from established animal and public health surveillance criteria together with additional measures of sustainability and participation. Data were collected from 120 individuals by workshops, questionnaires and semi-structured interviews in Benin, Nigeria, Pakistan, Tanzania, Togo and Uganda. PDS results were consistent with other data for absence of disease but the absence of detected cases and a dearth of epidemiological and surveillance data prevented quantification of some indicators. In contexts of limited epidemiological capacity, PDS was considered a useful epidemiological tool, most appropriate for small-scale farmers and applied in complement to conventional surveillance. PDS generated large amounts of unanalyzed data which were incompatible with conventional databases. The approach did not alter the one-way information flow characteristic of surveillance systems. PE skills continued to be used by some individual practitioners but PDS sustainability was compromised by dependence on external funding, the lack of legal frameworks and failure to integrate into national surveillance systems. In extracting surveillance information from communities, PDS was inconsistent with empowerment and ownership espoused by participatory learning and action approaches. Stakeholders had a positive attitude towards PDS despite the limited evidence for impact or cost effectiveness.

The influence of uncertain knowledge about the true classification of evaluation samples on the characterization of imperfect diagnostic tests

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Epidemiological parameters are often determined by stochastic models, whereby it is assumed, that the measured values used in the model correspond exactly to the true situation. In practice, this assumption is not always fulfilled, especially, if complex diagnostic methods are used for producing large numbers of measured values. Uncertainties and errors in results of diagnostic techniques must be quantified and have to be considered in the above-mentioned models. To this end, it is necessary to characterize the diagnostic test methods in respect to their corresponding error rates. Sensitivity and specificity are established parameters that allow as probability values the required theoretical characterization of diagnostic tests. In principle, both parameters do not depend on each other, as they are defined for non-infected and disjoint infected sub-populations. However, the practical determination of sensitivity and specificity of diagnostic tests is often associated with the following problem: The required prior knowledge of the elements membership in evaluation samples used for test evaluation in non-infected or infected is uncertain for certain diseases. As a consequence of the diagnostic results obtained by evaluation samples implies, that the estimation of both sensitivity and specificity is not independent. General Task: to find a solution for estimating sensitivity and specificity in a situation where samples used for diagnostic test evaluation cannot unambiguously be attributed to non-infected or infected populations. The correlation between the two characterizing parameters is shown in an example which investigates the impact of the uncertainty in the classification of evaluation samples on estimating the test parameters sensitivity and specificity.

Use of dna sequencing and phylogenetic analysis to investigate a bovine rabies outbreak in Minas Gerais Brazil

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Bovine rabies in Brazil is transmitted by hematofagous bat (*Desmodus rotundus*). Since the first report, in 1900, many aspects about rabies epidemiology have been elucidated by DNA sequencing, genetic and phylogenetic analysis. Most recent epizootics affecting livestock took place in Sao Paulo state between years 1997-2002 with possible expansion to neighbor areas of Minas Gerais. There is scarce information about genetic diversity of rabies virus isolates in this state. Considering background, present work is intended to analyze potential epidemiological connections among 22 bovine rabies cases in 12 municipalities of Minas Gerais (during 2000 to 2009) and Sao Paulo's epidemics to contribute to current surveillance rabies program. RNA extraction, reverse transcription, PCR and sequencing reaction were performed according to Sato *et al.* 2004. For genetic analysis a phylogenetic tree was constructed based on of rabies virus glycoprotein segment of 540 nucleotides using Neighbor-joining method with software – MEGA, fixing Kimura 2 parameters evolution model with a bootstrap level of 1000 replications. Results suggest that the same viral sublineage is involved in Sao Paulo epizootics and Minas Gerais cases. Although genetic distance is subtle among Brazilians isolates it is possible to observe that bovine rabies virus in the border region of the aforementioned states are distinguishable from the rest of the country. Vaccination is recommended for livestock concomitantly with mapping of bat shelters and reinforcement of control *D. rotundus* population.

DNA fingerprinting of ten different dermatophyte species using short single primer

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Dermatophytes are a group of closely related keratinophilic fungi that can invade keratinized human and animal tissues such as skin, hair and nail causing dermatophytosis. Superficial mycoses due to dermatophyte fungi had been among the most common communicable diseases in the population so it became crucial to identify these fungi to enable appropriate diagnosis and treatment. Conventional methods used to identify dermatophytes are often lengthy and may be inconclusive because of atypical microscopic or colonial morphology. One step PCR-based approach employing the simple repetitive oligonucleotide (CAGA)₄ was used in this study as a single primer for identification of dermatophyte species. This primer managed to produce species specific profile to ten different dermatophyte species.

***Mycobacterium bovis* in slaughtered swine: the public health implication for Mubende district of Uganda**

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Tuberculosis caused by *Mycobacterium bovis* is a persistent but evolving complex problem whose eradication has eluded some of the least and most developed countries in the world. In most developing countries, animal TB is endemic but with little available information on the relationship between *M. bovis* infection in animals and the disease in humans. Given that the transmission route or pattern from swine to human is unclear, this is a cause for concern in predominantly pork eating populations especially those infected with HIV/AIDS. Mubende is a district in central Uganda with an HIV/AIDS prevalence of 18% and home one of the highest free range reared pig populations. Therefore this study was aimed at establishing the prevalence of *M. bovis* among slaughtered pigs in this district, furthermore, to establish the potential risk to the human population. Out of the one hundred and fifty pigs sampled from the slaughtered population, Only three (2%) were found to have *M. bovis* in mesenteric lymph nodes after mycobacteriology. Further molecular analysis revealed that the isolates belonged to spoligotype SBX and lineage Y. The parallel survey conducted at Mubende hospital on suspected TB patients to establish the potential risk revealed that 213/344 (62%) of the interviewed patients consumed pork, furthermore, 72% and 75% of pork consumers were young and HIV positive while. 45% of the interviewed reared pigs as livestock and 21% of these used pig fecal material as garden manure. *M. bovis* was isolated for the first time from slaughtered pigs in Uganda. This is of public health concern in this predominantly pork eating populations especially among the HIV/AIDS infected individuals.

Adult infection of dairy cattle with *Mycobacterium avium* subspecies *paratuberculosis*

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Mycobacterium avium subspecies *paratuberculosis* (MAP), which causes chronic granulomatous enteritis in ruminants, conventionally is believed to infect predominantly young cattle. However, the assumption that adult cattle are resistant to either infection or progression to detectable shedding has not previously been challenged due to insufficient animal exposure data. In this study, we evaluate the relationship between tissue-infection and fecal shedding of specific MAP strains as adults with exposure to high shedding animals in the adult herd. As part of the Regional Dairy Quality Management Alliance study, all adult animals on a farm were tested for MAP via fecal culture semiannually and a subset were tested via tissue culture. Positive samples were strain typed using a short-sequence repeat method. For low-shedding animals, probability of fecal shedding or being tissue positive at slaughter was evaluated with respect to time spent in the same pen as current same-strain high-shedders via logistic regression. For the dominant on-farm MAP strain, time exposed to a high shedder as an adult increased risk of becoming tissue positive or becoming a fecal shedder. Time spent unexposed and total lifespan were not associated with probability of being tissue positive or fecal shedding at any sampling point. For other strains which had supershedders present, there was no association between exposure and tissue or fecal-culture status. Some but not all MAP strains appear to cause not only infection but shedding among adult animals which are exposed. On this farm, the dominant strain seemed capable of causing infection which could lead to infectious adult animals, thus creating a second potentially important transmission cycle that is not managed by standard control programs.

Molecular diversity of non-structural protein coding genes of infectious bronchitis virus Brazilian strains

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In Brazil, despite of the wide use of vaccines, infectious bronchitis virus (IBV) is endemic, due to continuous emergence and spread of new viral types. Molecular studies on the structural proteins S (spike) and N (nucleoprotein) have been used for monitoring emergent IBV strains. However, most of the IBV genome codes for non-structural proteins, and hitherto these targets have been poorly explored regarding the diversity of IBV lineages. Thus the aim of this study was to investigate the diversity of papain-like protease (PLpro) and non-structural protein 2 (nsp2) coding genes of Brazilian IBV strains. Thereunto, a RT-PCR targeting PLpro (470 bp) and nsp2 genes (750 bp) were performed in 12 IBV strains isolated in embryonated eggs. Obtained amplicons were sequenced and submitted to distance analysis, with homologous sequences, from GeneBank. One of the studied strains (sample C) showed a concordant segregation pattern for both targets, grouping with other worldwide IBV strains and with another one Brazilian strain, regarding Plpro gene. The remaining isolates showed a Brazilian-specific cluster for both PLpro and nsp2. Interestingly, S gene analysis previously performed showed that sample C fits to Brazilian genotype/serotype IBV lineage, what may indicate a recombination phenomenon. Found results help to understand IBV evolution patterns and contribute to unveil IBV molecular epidemiology based on poorly explored genome regions.

Phylogenetic analysis of rabies virus glycoprotein of herbivorous isolated from north Brazil

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Rabies is an acute viral encephalitis that can infect all warm-blooded animals. This disease has a worldwide distribution and causes important economic losses to livestock. Analysis of the gene G may improve the understanding of the epidemiology and prevention measures of rabies in South America. The aim of this study was to characterize genetically isolated samples from North Brazil based on glycoprotein gene. Rabies virus from cattle (5), equine (3) and buffalo (1), obtained between 2006 and 2008, from Para (4), Rondonia (2) and Tocantins (3) States were investigated. A RT-PCR targeting a glycoprotein-coding gene (914 nucleotides) were performed. Obtained amplicons were sequenced for genetic analysis. Phylogenetic analysis suggests presence of five main subclusters. Subcluster I, composed of one samples from Tocantins which are related to isolates of *Desmodus rotundus* and *Diphilla ecaudata* from São Miguel Tapuio Piauí. Subcluster II, the samples from Tocantins which are related to isolates of *D. rotundus* from Goiás State. Subcluster III, composed for one isolate from southeastern region of Pará related to one isolated from Colina (Tocantins). Subcluster IV composed of isolated from Rondonia and one sample from Ipora (Goiania). Subcluster V, grouping samples from Northeast Pará related to human rabies cases occurred in Maranhão, showing circulation of rabies virus among hematophagous bats, livestock and humans in this region. Evidence of genetic proximity of isolates from different geographic areas should be interpreted taking in consideration livestock migration attending to food availability and consequent bat migration to more favorable conditions. Chiropterans have high mobility, hematophagous bats visit neighbor colonies, promoting rabies dissemination among livestock, humans and other bat species.

Molecular epidemiology: a tool for source attribution investigation of *Escherichia coli* O157:H7 infections in New Zealand

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Since the first case of *Escherichia coli* O157:H7 was detected in New Zealand (NZ) in 1993, the number of Shiga toxin-producing *E. coli* (STEC) notifications per year has increased steadily. Cattle are considered as a source of infection for both environmental and foodborne outbreaks of STEC in humans. As part of a source attribution investigation, *E. coli* O157:H7 isolates were obtained from the national Enteric Reference Laboratory and compared to bovine *E. coli* O157:H7 isolates from faecal samples collected from very young calves and adult cattle at four slaughter plants. A total of 28 bovine and 209 human isolates, originating from the North and South Islands of NZ, were screened for the presence of virulence genes characteristic of STEC, and genotyped using pulsed-field gel electrophoresis (PFGE), stx-encoding bacteriophage insertion (SBI) and single nucleotide polymorphisms (SNP) typing. The genotypic analysis of bovine isolates revealed three distinct PFGE profiles, each represented by a specific SBI type (1, 3, and 5). A distinct between-Island prevalence distribution of SBI types was observed among bovine and human isolates (P=0.001). SBI type 5 (SNP IVa) accounted for 21% of the studied human isolates. Internationally, this genotype has been reported only rarely in association with STEC infections in humans and is therefore of particular interest. Findings of this molecular study provide evidence for historical introduction of O157 strains into NZ and localised transmission between cattle and humans. A prospective case-control study is underway currently to investigate source attribution risks and possible exposure pathways for human cases of STEC in NZ.

Identifying co-infections of *Mycobacterium avium* subspecies *paratuberculosis*

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Mycobacterium avium paratuberculosis (MAP) causes chronic wasting of domestic and wild ruminants. Animals are assumed to acquire infection once, despite high lifelong infection pressure. The aim of this study was to evaluate the utility of single genome analysis (SGA) for the detection of multiple strains that coexist in clinical samples and thereby in animals. The methodology of SGA was standardized using MAP isolates from bovine fecal samples previously considered to include at least two different strains evidenced as overlaps in short sequence repeat loci used for strain typing. Control isolates were selected from animals that had consistent lifelong MLSSR profiles. DNA was extracted, diluted and used as template for PCR amplification using specific primers for each of 5 short sequence repeat of interest. Dilutions were titrated to allow an average of one genomic template copy per amplicon generated. Amplicons were purified, sequenced and analyzed with the SeqMan software. The isolates identified as mixed by short sequence repeat typing each two distinct strains (15-50% of replicates representing the minor bacterial strain). SGA also detected low prevalence point mutations which had not been detected by bulk typing methods. SGA allows the detection and molecular characterization of the different strains that coexist in some MAP isolates evidenced by different repeat profiles and point mutations, even if these are present as minor strain types in a host. With the predominance of liquid culture techniques and the poor growth of many MAP strains on solid media, SGA allows determination of whether animals carry multiple concurrent infections. Given the highly contaminated environment around dairy animals and the methods available to identify MAP strains, models of transmission dynamics need to consider the effect of co-infections on dynamics.

Molecular epidemiology to study paratuberculosis transmission at the bighorn sheep-cattle interface

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Introduction: The role that wildlife may play in the transmission of *Mycobacterium avium* subspecies *paratuberculosis* (MAP) in the ecosystem, and the potential consequences of infection in these wildlife populations are being given increasing consideration. Southwestern Alberta has a high density of cow-calf ranches where cows often share the pastures with various wildlife. In this area, an emaciated yearling Rocky Mountain bighorn sheep was found in 2009. Clinical signs, as well as histological findings consistent with described cases of Johne's disease were found. Tissue and fecal samples were proven to be MAP culture positive. In a follow-up herd level survey, three of 44 (7%) fecal samples from individual bighorn sheep from the same region as the index case tested positive by culture and polymerase chain reaction (PCR) and were identified as Type II MAP strains by MAP1506 gene sequencing. Twenty-five samples collected from a geographically distinct population were all negative. From 3 sheep, we identified MAP strains with 7 repeats at G1, and 4 at GGT. The fourth strain showed 10 repeats at locus G1 whereas all strains differed for number of repeats on locus G2. **Conclusion:** Strain typing through sequencing of three discriminatory short sequence repeat (SSR) regions has proven its potential as 4 different genotypes in the bighorn sheep population were identified. **Discussion:** We will present an additional study design to gain understanding of pathogen transmission in the ecosystem shared by bighorn sheep and cattle, using social network analysis through behavioral observations and GPS location and molecular epidemiology. With a better understanding of potential spread of disease, these results will aid in decision-making for both cattle and wildlife management actions for disease control strategies.

An investigation of possible sources of human campylobacteriosis in Lithuania

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Poultry products are well recognized sources of human campylobacteriosis, however there is increasing evidence that wild birds and environmental water may contribute to the burden of illness as well. The occurrence of *Campylobacter* spp. in raw broiler meat is regularly monitored in Lithuania, however an incidence of this bacterium in other sources was not yet reported. To obtain more knowledge on possible sources of human campylobacteriosis the occurrence of *Campylobacter* spp. in environmental water samples, wild birds, pets, pork, beef, milk and broiler meat was investigated. Samples were collected twice a month from October of 2011 till January of 2012. Unexpectedly campylobacters were isolated from water samples from swimming places more often (64%) in comparison to broiler meat samples (52%). Interestingly, broiler marinated products were also frequently (35%) contaminated with these bacteria. We also showed that wild crows and pigeons may serve as important reservoir of *Campylobacter* spp. (35% positive samples) as fresh feces were collected in the parks and other public places in town. Samples of raw milk and pet feces were contaminated much rare, 13.6% and 6.5% of samples respectively. No campylobacters were found in fresh pork and beef meat samples including marinated products. Based on results we speculate that as well as broilers, environmental water and feces of wild birds may pose high risk for human infection with campylobacters in Lithuania as well. In progress MLST typing of selected *Campylobacter* spp. strains from various sources including humans will enable us to quantify the number of human cases attributable to each of the source examined.

On the molecular analysis of *Giardia duodenalis* Brazilian isolates

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Giardia duodenalis (syn: *G. intestinalis*; *G. lamblia*) is an enteric protozoan that causes giardiasis in humans and in a wide range of domestic and wild animals. Studies based on genetic analyses have been showing that *G. duodenalis* can be assigned in eight different Assemblages (A to H) in which only the Assemblages A and B have been considered potentially zoonotic. In the present study thirty stool samples from human origin were amplified using two genes, glutamate dehydrogenase (gdh) and beta-giardin (bg), and then characterized by sequencing. Assemblages A and B was detected in twelve and thirteen samples respectively by both locus. Five samples had different identities, three isolated belonged to Assemblage A by gdh analysis were characterized as Assemblage B after using bg gene. The inverse situation was observed in the other two isolates. Heterogeneous sequences, characterized by presence of double nucleotides peaks in specific position in chromatogram, was observed in seven samples belonged to Assemblage A and in eight samples classified as Assemblage B, by gdh gene analysis. This situation was not found in none of the thirty samples analyzed by bg gene. The found results can be explained by true mixed infection or genetic recombination, highlighting the importance of careful analysis of *G. duodenalis* obtained chromatograms and analysis multilocus. Moreover the present findings bring out the importance of developing new methodologies to discern recombination events from co infection.

Molecular epidemiology of coronavirus in quails raised near to laying hens

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Although coronavirus has already been detected in quails in Brazil and other countries, knowledge on molecular characterization and epidemiology of this virus in the referred host is poorly known. In Brazil, quails flocks are frequently raised in laying hens properties. Thus, the aim of the present study was to detect coronavirus occurrence in quails raised in laying hens properties, and perform molecular characterization of the detected virus. To this end, pools of lungs, trachea, female reproductive tracts, kidneys and enteric contents were collected from quails flocks co-housed with laying hens, showing IB-like symptoms. Samples were screened for IBV with a RT-PCR to the 3'UTR and positive samples were also submitted to a RT-PCR targeting RNA-dependent RNA-polymerase (RdRp) and a typing-multiplex one. Amplicons of 3'UTR and RdRp genes were sequenced and submitted to distance analysis, with homologous sequences obtained from GeneBank. All avian coronavirus found were classified as variants by multiplex RT-PCR. Based on the DNA sequences for RdRp and 3'UTR regions its possible to conclude that avian coronavirus detected in quails are closely related to avian infectious bronchitis virus. Therefore, it is possible to speculate that quails co-housed with laying hens may be important in avian coronaviruses epidemiology and might interfere on gammacoronaviruses evolution.

Approaches for attributing human cases of brucellosis to animal sources in Kenya

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This poster outlines the design and initial results of a collaborative molecular epidemiological study currently underway in western Kenya. The study is investigating the importance of a range animal production systems as reservoirs of human brucellosis in an endemic area. We are employing recently developed multi-locus VNTR molecular techniques, as well as a range of epidemiological tools, to perform source attribution for this neglected zoonotic disease. Data collection involves parallel surveys in animals and people. A range of livestock species, including cattle, goats, and pigs, are sampled from a random selection of farms and tested for brucellosis using a series of serological tests. Additional surveillance for brucellosis is achieved through central point sampling, milk screening and slaughterhouse sampling. At the same time, and in the same geographic area, patients presenting to the outpatients clinic of a selection of hospitals and health centres with symptoms suggestive of brucellosis are screened for the disease. Biological material from seropositive animals and people is subjected to PCR, culture and molecular typing of any *Brucella* spp. isolated. We explore clustering of *Brucella* strain types within livestock species, production systems and geographic areas. Source attribution is explored through the use of genetic assignment and risk-based models, which integrate molecular and epidemiological data collected from brucellosis cases. Through the identification of the most important livestock reservoirs for zoonotic brucellosis, this study provides novel information for the design and implementation of targeted control strategies for the disease in western Kenya.

The molecular epidemiology of *Blastocystis* spp. in members of the indigenous Tapirapé tribe, Mato Grosso state, Brazil: an possibility potencial zoonotic

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Blastocystis is the most common eukaryotic organism reported in human and wildlife and domestic animals fecal samples and numerous epidemiological surveys carried out in different countries. However, *Blastocystis* was identified in stool samples during a survey of the intestinal parasites of members of the Tapirapé tribe, who live in the Mato Grosso State in the Brazilian Amazon region. Faecal samples were preserved in ethanol and characterized using *Blastocystis*-specific primers targeting the SSU rRNA gene. The prevalence of this parasite in 378 stools was 21%. Three subtypes were identified (subtype 1, subtype 2 and subtype 3). ST1 was the commonest subtype and was found in 27 individuals (41%), followed by subtype ST2 found in 21 individuals (32%) and ST3 in 11 individuals (17%). Five mixed infection of ST1 and ST2 was identified (7%), one single mixed infection of ST1 and ST3 and another mixed infection of ST2 and ST3. The relative proportion of the different subtypes is different from that seen in Europe and North America where ST3 is the commonest subtype. The ST1, ST2 and ST3 are common in both animals and human. Also ST4 which occurs in the above mentioned regions was not found. Our studies are the first molecular characterizations of *Blastocystis* spp. in Brazil and in Indian communities from Latin American and showed zoonotic potential important to the parasite. (Financial Support: CNPq, DECIT, FAPEMAT, FUNASA).

Zoonotic *Giardia intestinalis* assemblages detected in indigenous Tapirapé tribe from Brazilian Amazon

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The indigenous Tapirapé community, located in Brazilian Amazon, has a history of gastrointestinal problems associated with diarrhea. Data on the occurrence of intestinal parasites in indigenous populations are scarce, however, the present study aimed to determine the participation of *Giardia duodenalis* in role of acute and chronic gastroenteritis in the present population. *G. duodenalis* has been considered potentially zoonotic (Assemblages A and B) and is a significant cause of diarrhea in human and in a wide range of domestic and wild animals. A total of 737 stool samples were obtained and in 102 was possible to identified *G. intestinalis* by conventional flotation method. DNA was amplified targeting glutamate dehydrogenase (gdh) and beta-giardin (bg) coding genes. Amplicons were sequenced and submitted to distance analysis. A total of 47 isolates were sequenced of which 11 isolates clustered in Assemblage A and 36 were classified as Assemblage B. On gdh gene, obtained sequences showed similarity to findings observed in fecal samples from cats in Brazil, whereas Assemblage B classified Indian samples were similar to those found in dog feces from Canada. Assemblages A and B has already been characterized as zoonotic genotypes of *G. intestinalis*, thus, the found results may lead to consider a zoonotic chain of transmission for this protozoan in Tapirapé tribe, Brazilian Amazon.

PFGE characterization of *Salmonella enterica* isolates from pigs at slaughter in Italy

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In 2005-2008, 1,152 samples (451 faecal samples, 451 carcass swabs and 250 tonsils) were collected from 451 finishing pigs at slaughter in Northern Italy. *S. enterica* was isolated from 21.5% of faecal samples, 10.9% of the carcasses and 10.4% of the tonsils. Seventeen different serotypes were identified among 155 *S. enterica* isolates genotyped by PFGE (Pulsed-field gel-electrophoresis) method. The prevalent serotypes were *Derby* (42), *Rissen* (12.3%), *S. enterica* 4,[5],12:1:- (10.3%), *Typhimurium* (7.1%), *London* (4.5%) and *Give* (3.9%). The aim of this study was to investigate the genetic variability among prevalent serotypes of *S. enterica* genotyped by XbaI-PFGE according to standard protocols. Among serotypes *Derby* and *Typhimurium* we observed the highest variability with 6 main profiles per serotype. *S. Derby* was the predominant serotype in faecal samples, carcasses and tonsils, followed by *S. Rissen* on carcasses and in tonsils. PFGE typing was also useful to investigate self-contamination and cross-contamination of pig carcasses. *Salmonella*-positive carcasses were evaluated for positivity in tonsils and intestine. Only in few cases pharyngeal carriers had the same *Salmonella* serotype on their carcasses showing identical PFGE profiles. Similar results were obtained for positive carcasses of intestinal carriers. In addition our data indicated that serotypes and PFGE profiles were diverse within a single slaughtering day with some exceptions that suggest the likely occurrence of cross-contaminations.

Molecular epidemiology of rabies virus in Bhutan

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The objective of this study was to understand the rabies virus strains circulating in domestic dog population in southern Bhutan. Twenty-three rabies virus isolates originating from dogs and other domestic animals were characterized by sequencing the partial nucleoprotein (N) gene (395 bp). Phylogenetic analysis was conducted and the Bhutanese isolates were compared with rabies viruses originating from other parts of the world. Bhutanese rabies virus isolates were found to be highly similar and did not form any distinct sub-groups, suggesting this viral group originated from a common ancestor. Phylogenetic study indicate that Bhutanese rabies strains were closely related to Indian strains and the Arctic-like-1 lineage circulating in South Asia and could be grouped together as a large cluster of South Asian Arctic-like-1 lineage. The translocation or trans-border movement of dogs along the border may have facilitated the spread of this rabies virus variant between the two countries.

An African swine fever virus genotype present in both the resistant bushpig (*Potamochoerus larvatus*) and adjacent domestic pig populations does not induce detectable clinical ASF symptoms

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The role of the bushpig in the transmission of the African swine fever virus (ASFV) to domestic pigs remains little understood. We describe a study conducted in Homabay district in Western Kenya in which free range-low input pig management system was characterized in relation to potential risk of ASFV infection posed by bushpigs. A questionnaire was used to collect information from 81 randomly selected pig-rearing households. Blood was collected from 179 domestic pigs. Also, 8 Bushpigs were sampled from Ruma National Park that neighbour the same study area, 8 for blood and 1 for tissues. The samples were analyzed using OIE serological and nucleic acid-based prescribed diagnostic techniques. The household survey showed all farms practiced free range/tethering feed management. The animals exhibited inapparent African swine fever and farmers had not observed the disease. The PCR assay of blood based on the p72 gene primers demonstrated 22% positivity to ASFV, but no animals were sero-positive by the OIE indirect ELISA. One of the 8 bushpigs sampled was PCR positive in Kidney tissue. Dendrograms based on the sequence of the C-terminal end of the p72 gene and the full-length p54-gene of domestic pig and bushpig ASFV viruses indicated that the domestic and bushpig viruses clustered together genetically. Similarly, the predicted amino acid sequence of the tetrameric repeats that constitute the central variable region of the B602L gene also exhibited a high degree of identity. These results suggest a common source of infection or viral transmission between the two pig species.

Global animal diseases surveillance initiative

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During the rinderpest eradication period, FAO and partners supported the implementation of disease management campaigns, the establishment of epidemio-surveillance and laboratory networks as well as the collection of sera from rinderpest susceptible species that lead to the eradication. It elimination significantly contributed to improving the livelihoods and food security of almost a billion people. During the 37th FAO Conference (2011), the resolution declaring global freedom from rinderpest was endorsed by all 192 members countries. One of the recommendations of this resolution 'encourages FAO to take full advantage of the rinderpest eradication achievement and apply the lessons learned to prevent and control other diseases impacting food security, public health, the sustainability of agriculture systems and rural development'. In line with this recommendation, the overall objective of the global animal diseases surveillance initiative is to contribute to the global animal health security through strengthen epidemio-surveillance systems and establishing sera/tissue banks, using the findings of the tested samples to formulate, monitor and evaluate disease management schemes. Lacking information on disease prevalence and impact remains a major impediment to improve incomes and livelihoods that accrue to livestock raisers through livestock trade. The initiative aimed to: (1) Promote the development/implementation of methods including quality assurance procedures for the design and implementation of the epidemio-surveillance system; (2) Establish a global sera bank and up-date it regularly; (3) Test these sera to examine the role of potential new pathogens and finding to be used for the formulation of diseases management strategies; (4) Improve research in epidemio-surveillance system and response preparedness for better disease management; and (5) Implement diseases management schemes to sustain livestock trade.

Building capacities in animal health in the Caribbean: the veterinary epidemiology/para-epidemiology project (VEP)

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Disease surveillance and control within the Caribbean has historically been difficult. The region is made up of over 31 countries, territories, and protectorates, with concomitant differences in language, culture, and historical experiences. Given the diversity of challenges the region faces in terms of disease introduction and spread, there is a need for longer-term, sustainable training in epidemiology, surveillance, and emergency response. The Veterinary Epidemiology/Para-epidemiology Project (VEP) was a four-year, capacity-building project conducted in 9 countries in the Caribbean region: Antigua and Barbuda, Barbados, Dominica, Dominican Republic, Grenada, Haiti, St. Lucia, St. Kitts and Nevis, and St. Vincent and the Grenadines. Project participants (10) received training in 7 key domains: epidemiologic methods, disease surveillance, diagnostic tests and sample handling, emergency preparedness and response, data management, communication and coordination, and management and leadership. Both didactic and hands-on trainings were emphasized, and all participants were required to complete an epidemiologic study in their respective countries. Project participants were mentored by experienced epidemiologists in the design and implementation of their studies. Lessons learned were identified which contributed to the success of the project overall. Coordination of the technical component of the project through the regional network for animal health, CaribVET, ensured that the project had both national and regional relevancy. Although costly, the VEP brought the participants together frequently and provided opportunities to build relationships, which strengthened cross-border communication and collaboration in the region overall.

Improving cost-effectiveness of cross-border routine veterinary measures

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Cross-border trade in livestock is subject to additional, costly routine veterinary measures (RVM) compared to domestic trade, such as veterinary checks of live and slaughter animals, and export certificates. A short-distance transport just across the border requires many additional measures compared to a long-distance domestic animal transport, and the necessity of these additional measures is often questioned. In that respect, the key objective for veterinary policy makers is to improve the cost-effectiveness of these RVM, without compromising both the economic advantages of cross-border trade and veterinary risks. The aim of this study was to examine possibilities to lower the financial-economic impact of RVM, i.e. to improve their cost-effectiveness. RVM were analysed for the cross-border region of the Netherlands (NL) and Germany (GER) for cross-border trade in the pig, poultry and dairy sectors for the year 2010. Costs were calculated per region and stakeholder, and the impact on risk of contagious livestock diseases was considered. Total costs of RVM for the joint region NL-GER were €37.8 million/year; the additional cross-border measures contributed for 70% (€26.5 million/year). Of this €26.5 million, 40% resulted from trade in slaughter animals, i.e. mainly broilers (GER) and fattening pigs (NL). Costs for trade in live animals mainly resulted from trade in veal calves, laying hens (GER) and piglets (NL). Main costs were veterinary checks of animals (twice in case of slaughter animals), animal health tests and documentary controls. Although for different animal species, both NL and GER have several possibilities to improve the cost-effectiveness of RVM. Especially slaughter animals (dead-end hosts) encounter RVM that might be overdone in preventing contagious livestock diseases, e.g. veterinary checks on both sides of the border. It is therefore concluded that various possibilities exist to improve the cost-effectiveness of RVM which is beneficial for both countries.

Brucellosis in West and East Timor

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Eastern Indonesia has grasslands ideal for breeding beef cattle for meat or breeding stock, helping to address food security and rural poverty in both Indonesia and East Timor. However this opportunity is constrained by endemic bovine brucellosis on Timor island. Brucellosis impacts profoundly on smallholder livelihoods due to severe reduction in reproductive efficiency of affected cows. Export of breeding cattle from Timor to other parts of Indonesia is banned due to brucellosis, lowering prices of Timorese cattle. Control attempts since the early 1990s have been hampered by disrupted veterinary services in East Timor, and variable budgets and policies due to regional autonomy in West (Indonesian) Timor. Eradication of the disease remains a distant aim. Results of a scoping study in East and West Timor from January to June 2012 will be reported. The study team will visit the central governments of Indonesia and East Timor, the provincial government of East Nusa Tenggara, five West Timor district governments and some of East Timor's thirteen districts. With information on brucellosis prevalence and impacts and cattle production systems and market supply chains, prospects for improved brucellosis control will be assessed, and a plan for a three country (Indonesia, East Timor and Australia) integrated whole-of-Timor control program developed. Major issues will include integrated government policy and implementation at central, provincial and district levels, and improved cattle identification and movement control, diagnostics, and veterinary services capacity.

The effectiveness of inactivated vaccine against foot and mouth disease

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Inactivated foot and mouth disease (FMD) vaccines are used in many endemic and non-endemic countries either to prevent or to control outbreaks. In non-endemic countries, high potency vaccines are used for reactive vaccination (called frequently 'emergency vaccination') during outbreaks in order to prevent virus spread, while in endemic countries low potency vaccines are used for routine vaccination. Despite their wide use there are hardly any data on the field effectiveness of inactivated FMD vaccines. Epidemics of FMD occur frequently in Israel and are mostly caused by viruses of serotype O. Therefore, cattle, sheep and pigs vaccination is mandatory in Israel. A high potency ($\geq 6PD_{50}$) vaccine is routinely used for both reactive and routine vaccination. During 2011 a large outbreak of FMD, caused by a virus of serotype O, occurred in Israel and affected many herds of cattle and sheep. R-value for this virus with the vaccine strain (O/Manisa) was between 0.28 and 0.45. We investigated one of these outbreaks, which took place in a feedlot and an adjacent dairy herd. Comparison of morbidity and antibodies to NSP enabled the assessment of the effectiveness of various vaccine regimes and reactive vaccination. We have found that 96% of the calves that received two doses of vaccine at least three months prior to the outbreak were infected and more than 50% showed clinical signs compatible with FMD. Heifer calves vaccinated 3-5 times, 7 months prior to the outbreak showed 100% infection and 18% showed clinical signs. As opposed to these groups, animals vaccinated as low as only once but up to two weeks before the outbreak, were almost 100% protected from clinical disease and to a lesser extent, protected from FMD virus infection. We conclude that reactive vaccination was highly effective for prevention of clinical and sub-clinical infection. Routine vaccination with the same vaccine provided only limited protection due to poor longevity of the immune response.

Mexico and United States binational collaboration in the prevention of transboundary animal diseases
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Mexico – U.S. Exotic Animal Disease Commission (EADC) was created as a binational institution that would help both countries control any occurrence of FMD or any other transboundary animal disease in Mexico. Cattle from Mexico cross the shared border between both countries. One BSL-3 laboratory in Mexico City, 20 other regional laboratories support the regional operations in the field. Personnel from the laboratory network are in constant communications with USDA animal health laboratories. In 2011, a collaboration effort took place in the State of Guanajuato to conduct animal disease investigations. Personnel from the USDA and SAGARPA worked hand by hand to visit two swine operations to collect samples, process them in a mobile laboratory for shipment, and then processed them in the BSL-3 laboratory in Mexico city. This activity helped the USDA understand better how Mexico operates in the field, and laboratory. Both countries have also worked together in investigations on the border, where inspection pens are located in both countries, but the strong relationship between both partners have made this operations go smoothly with great results. The USDA and SAGARPA have demonstrated that technical collaboration, direct communications, and trust go a long way to improve animal health systems between countries. Models like the EADC should be explored when initiating international collaboration efforts between border sharing countries, and countries that share trade routes for animals and animal products. On the high level decision making, authorities have an agreement that allows them to discuss possibilities to improve existing programs and to extend the reach of the programs over the border by having a direct safeguarding partner. The continuity and expansion of bilateral agreements like the EADC are vital for countries that share borders, have an active animal trading relationship, and share common animal health threats.

Tracking progress along the joint FAO/OIE progressive control pathway for foot and mouth disease
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The Joint FAO/OIE Progressive Control Pathway for FMD Control (PCP-FMD) was developed by FAO, EuFMD and OIE as a tool to assist FMD endemic countries to develop risk-based, sustainable and feasible strategies to progressively reduce the impact of FMD and circulation of FMD virus. The PCP-FMD consists of 5 Stages, and as it becomes more widely used there is a need for a procedure to identify the appropriate Stage for each participating country. The primary objective of the assessment is to track progress along the PCP-FMD globally; important secondary objectives are to provide useful feedback to the country, to enhance understanding about the PCP-FMD and to identify priority areas to target technical and/or financial support. The assessment procedure balances a number of criteria: to be consistent across diverse regions and situations yet acknowledge that outcomes may be achieved through a variety of means; to be evidence-based yet user-friendly and not too arduous; and to be transparent yet respect confidentiality. A checklist has been developed consisting of yes-no questions that can be easily answered by one or more people familiar with livestock husbandry and the FMD situation in a particular country. Each Stage is defined by a series of Outcomes, and the assessment gauges the level of achievement for each Outcome. There are required and recommended achievements; in order to complete a Stage a country must fulfill all required elements while the recommended achievements indicate how to improve the quality or thoroughness of the work. This checklist will be completed in early 2012 by African and Eurasian countries in anticipation of a Regional Roadmap meeting, during which countries will share information in order to improve and coordinate FMD control and review regional progress along the PCP-FMD. In this annual meeting, each country will present evidence to substantiate their achievements, and results of the PCP-FMD assessments will be presented and discussed.

Incident response information system (IRIS) for disease investigation and control

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This software manages information concerning disease surveillance and control in people and animals. It is a completely generic system, which treats any group of activities or tasks with a common purpose as a project. Within a project, all data can be subdivided into events, categories, relationships and filters. Spatial data can be associated with each of these data types through the built-in GIS. The user defines the nature of each variable, so the system can evolve to meet changing needs, since the database structure is defined through a dynamic object model, not a fixed set of data tables. The user manipulates and analyses data using an expandable set of tools, available through the dashboard-style interface. As well as generic analytical capabilities, individual tools can be built by the user to meet particular needs. The software security allows each user to have individual access rights. IRIS can operate in any language, and has been developed initially for Mongolia, operating in Mongolian and English. The language is user-selectable on the fly. Spatial data can be drawn from any spatial database or satellite image, and data can be displayed against these. People can be easily trained to enter data and produce routine reports, while advanced users can manipulate the data in more sophisticated ways. IRIS operates over the web, and is therefore available to everyone who has internet access. Off-line data entry will be added to allow users without broadband access to enter data and upload it to the national system. The software can be linked to other tools, such as spatial disease models. The basic system can be made available without charge to any collaborating country, and developer support can then be obtained to adapt it to meet local requirements.

Estimating the R₀ of African swine fever

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African Swine Fever (ASF) is a highly transmissible, lethal, viral disease of swine. Controlling an ASF outbreak requires culling of infected herds and quarantining of affected areas, since no vaccine is available. The basic reproductive ratio (R_0) is an indication of disease spread, providing useful information for the design of control strategies. To determine the R_0 , transmission experiments were done with two isolates (Malta'78 and Netherlands'86), with five inoculated pigs and five contact exposed pigs. The Malta'78 isolate was used in two groups, in two doses. The Netherlands'86 isolate was used in one group. The transmission rate was estimated using a Generalized Linear Model (binomial distribution, complementary loglog link) with the number of new contact infections as outcome variable, the number of susceptible as explanatory variable and $\ln(\text{number of infectious animals} \times \text{time interval} / \text{total number of animals})$ as offset variable. Pigs with positive results on oropharyngeal swabs were assumed to be infectious. The infectious period was calculated based on two criteria. The transmission rate and infectious period were used to estimate the R_0 in all groups. For the group Malta'78 (high dose), the R_0 was 13.2 [3.71; 46.63] using the conservative criterion and 62.80 [8.08; 482.99] using the upper bound criterion. For the group Malta'78 (low dose), the R_0 was 24.17 [8.99; 64.91] using the conservative criterion and 66.02 [7.10; 620.17] using the upper bound criterion. For the group Netherlands'86, the R_0 was 4.92 [0.82; 29.34] using the conservative criterion and 9.78 [0.76; 125.21] using the upper bound criterion. Although the R_0 values are not significantly different, the Malta'78 isolate seems more transmissible than the Netherlands'86 isolate.

FMDV infection in vaccinated and non-vaccinated sheep: transmission to contact animals and diagnostic aspects

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As FMDV infections might go unnoticed in both non-vaccinated and vaccinated sheep, knowledge about transmission of FMDV and good strategies for detection of infection in this species are very important. Using a study-design optimized to quantify transmission, we examined transmission of FMDV strain Asia-1 in groups of vaccinated and non-vaccinated sheep. Also, the results of different laboratory tests were compared to select the best possible strategy to identify infected individuals. After infection, in both vaccinated and non-vaccinated sheep, limited or no clinical signs were observed. Viraemia was detected, for a short period only, in some of the infected non-vaccinated and in none of the infected vaccinated sheep. However, FMD virus could be isolated from OPF swab samples, from the majority of the infected animals, for the whole duration of the study (21 days) and virus excretion was estimated to be as long as 52 days for the non-vaccinated and 32 days in the vaccinated sheep. Despite this long duration of virus excretion, the transmission ratio R remained relatively low, being 1.14 in the non-vaccinated and 0 in the vaccinated sheep. In the non-vaccinated population, transmission to contact sheep occurred mainly in the first week after infection, coinciding with the period in which the largest amount of virus was excreted in the environment. In the infected vaccinated sheep, the viral shedding in the first week post infection was reduced significantly as compared to the non-vaccinated sheep, which might especially be of importance to reduce the risk of FMDV being transmitted from sheep to other animals species. Finally, we recommend that the use of OPF-swabs as an alternative for vesicle material / plasma samples for diagnostic use should be evaluated further.

***Cryptosporidium parvum*: determination of ID50 & description of the dose-response relationship in experimentally challenged dairy calves**

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Cryptosporidium parvum causes diarrhea in neonatal dairy calves, contributing to calf morbidity and mortality, and is an important zoonosis. The objectives of this study were to determine the median infective dose (ID₅₀) of *C. parvum*, describe the dose-response relationship, and associated clinical illness in experimentally challenged neonatal dairy calves. Within 24 hours of birth, 27 calves were experimentally challenged with *C. parvum* oocysts at 1 of 8 possible doses (25, 50, 100, 500, 1×10³, 1×10⁴, 1×10⁵, and 1×10⁶ oocysts), and 3 control calves were sham dosed. Fecal shedding occurred in 23 (92.6%) experimentally challenged calves and in 0 control calves. The mean onset of fecal oocyst shedding was 5.6±2 days across all doses, but occurred later at lower doses. The pattern of fecal oocyst shedding over time was curvilinear; the log-total oocysts counted/g of feces increased with age (P<0.007), reached a peak, and declined (P<0.0001). The mean number of days with diarrhea was 6.5±1.8. As dose increased, the frequency of diarrhea-days increased (P=0.14), but there was no difference in other clinical signs. The ID₅₀ of *C. parvum* in dairy calves was 64 oocysts, based on fecal oocyst detection. These results indicate a positive dose-response relationship, that the amount of oocysts to which calves are exposed contributes to the length and severity of diarrhea, and that a very low dose of oocysts can cause infection. Therefore, efforts to reduce the incidence of diarrhea in neonatal dairy calves associated with cryptosporidiosis and environmental contamination should focus on improved husbandry and management in order to minimize exposure to the parasite.

Reducing the transmission of *Salmonella Typhimurium* in pigs with a DIVA vaccine and feed with coated butyrate

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This study evaluated the effect of 2 control measures on *Salmonella* transmission in pigs. *Salmonella*-negative weaned piglets were randomly assigned to 3 groups (n=3×16): A) oral vaccination with an inactivated *Salmonella Typhimurium* DIVA-strain; B) vaccination as in A + feed with coated butyrate; C) no vaccination or supplemented feed (control). At 9 weeks of age, 4 pigs/group were challenged with *S. Typhimurium*. Blood was analyzed weekly with a commercial LPS-ELISA (detection of infection-induced antibodies) and an in-house whole cell-ELISA (detection of infection- and vaccination-induced antibodies). Feces (2×/week) and tissue samples (necropsy at age 15 weeks) were bacteriologically examined for *Salmonella*. Based on these results, a transmission ratio R_a was calculated to quantify the average number of secondary cases caused by 1 infectious animal during the observation period. The negative control (n=8) remained negative throughout the study. Vaccination did not induce a detectable seroconversion in the LPS-ELISA, while the whole cell-ELISA detected an earlier antibody response in A and B when compared to C. More pigs were excreting *Salmonella* in the feces in C (22.7%) than in A (19.7%) and B (7.4%) (P>0.05). A similar trend was observed for the isolation results in the organs (P>0.05). Following R_a values were obtained: A (1.76[1.02;9.01]), B (2.52[1.02;9.01]) and C (+∞[1.88;+∞]). In conclusion, both interventions were able to diminish the transmission of *S. Typhimurium*, but the highest reduction was obtained by vaccination with the DIVA-vaccine. Moreover, vaccination with this vaccine allowed to differentiate between infected and vaccinated animals.

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