An online monitoring and surveillance system for the early detection and identification of emerging animal diseases: www.moss.be

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To cite this version:

Pierre Kerkhofs, Anouk Veldhuis, Jacques Barnouin, Libo Ren, Marc Dispas. An online monitoring and surveillance system for the early detection and identification of emerging animal diseases: www.moss.be. 1. International One Health Congress, Feb 2011, Melbourne, Australia. hal-02749283

HAL Id: hal-02749283
https://hal.inrae.fr/hal-02749283
Submitted on 3 Jun 2020

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at the people who live and work within the poultry value chains. Using research done in the Greater Mekong Sub-region, this paper argues that value chains and trade flows play an important role in HPAI virus maintenance, spread and hence disease control. Value chain analysis can provide information on volume, on type of products, on the people engaged, the relationships linking people, and the practices at each node. How these value chains operate is dictated by human behaviour and actions, which if understood provide critical insights into risk management. There are two benefits from looking more closely at the poultry value chains:

- Poultry product (specific bird types and products) movement can be assessed through an understanding of supply and demand between consumption centres and production clusters. This can then be utilised to refine the epidemiological understanding of risk points, spatial and temporal and identification of intervention points.
- Once risky points and interventions have been identified with the people involved at the important points, information on their behaviour and rule structures provide a much stronger basis to plan how to work with them in order to add value to their livelihoods and hence reducing the risks that an intervention will be rejected.

This paper presents how to approach often complex poultry sectors, breaking them down into manageable chains that provide income and food to a many people, in order that the one health disease risks they can pose can be managed and minimised in a sustainable manner.

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Emergency Vaccines Against Viral Hemorrhagic Fevers

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Numerous viral diseases have emerged/re-emerged over the past decades. Aside from many others, the so called ‘viral hemorrhagic fevers’ present a particular threat to our health systems. Most of the causative agents of viral hemorrhagic fevers are zoonotic in origin and remain a major challenge for animal (wildlife, livestock) and human health worldwide. Many countries have established infectious disease centers with primary responsibility for disease surveillance, reference microbiology and quality assurance, and preparedness and response to these threat agents. However, the development of countermeasures is still in early stages and has not yet produced effective licensed products. This paper discusses the development of proper animal disease models and the utilization of live attenuated and replication-deficient vaccines for prophylaxis and treatment of viral hemorrhagic fevers caused by hantaviruses, filoviruses and arenaviruses. Despite promising vaccine candidates the mechanisms of protection remain largely unknown, but certain correlates of protection have been identified. Remaining issues such as safety and licensure are either currently addressed or need to be addressed in the future. The minimum goal would be the approval of emergency vaccines for the use in humans within the next few years.

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An Online Monitoring and Surveillance System for the Early Detection and Identification of Emerging Animal Diseases: www.moss.be

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To ease the early detection of (re)emerging animal diseases, the Belgian sanitary authorities promoted the study on and the implementation of a web based application designed to manage with three categories of diseases: unknown emerging diseases, diseases with an unusual clinical expression and identified diseases when usual treatment seems to be inefficient.
This “Monitoring and Surveillance System” website (MoSS) allows for the detection of unusual syndromes in domesticated and wild animals, via an online notification system to be used by veterinary field practitioners. The web application, developed in PhP-MySql, aims at managing clinical description, animal typology, epidemiologic data and spatio-temporal proximity to run a hierarchical ascending classification process (HACP) that results into the identification of “clusters” of cases grouped by similarity.

The configurable HACP will be optimized using recorded information in previously identified cases of emerging diseases in Belgium.

The identification of a new cluster automatically generates an alert in the system, linked with the sending of emails to the sanitary authorities and expert(s). The selection of expert(s) is automated taking into account fields of expertise, geographical proximity and the mainly affected anatomo-physiological system in the specific animal species involved in the new cluster.

Additional information about the evolution of the disease, lab results and treatments can be published on dedicated Forum pages and read by authorized veterinarians.

The whole website has been designed to be easily managed by non-IT professionals. The application runs now in English, French and Dutch and supports the cross-border reporting.

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**OFFLU: Contributions Toward Improved Vaccine Strain Selection for Poultry**

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In Egypt and Indonesia, where highly pathogenic avian influenza subtype H5N1 (H5N1 HPAI) has become enzootic, FAO has undertaken two technical projects under the OFFLU banner in collaboration with national agencies to understand the characteristics and epidemiology of circulating viruses, determine efficacy of available influenza vaccines for poultry, and to develop national systems to support the use of efficacious poultry vaccines as part of a comprehensive strategy to combat HPAI. To further understand the evolution of the H5N1 HPAI virus in Indonesia and the subsequent impact of vaccines applied to poultry, the OFFLU project pioneered the application of antigenic cartography, developed to characterise human influenza viruses, for avian influenza viruses. The resulting map can be used help assess vaccine immunity against circulating strains. Laboratory capacity building and technology transfer supports these activities in national veterinary laboratories to develop a sustainable mechanism to monitor viruses and inform vaccine selection. This is the first coordinated effort of its kind for monitoring of influenza in animals at a national level.

The majority of the clade 2.1 viruses characterised from Indonesian village-based poultry during 2007-2008 cluster together in subclade 2.1.3, suggesting that little variation has occurred among this group of viruses; however, a few significant outliers have been detected that represent viruses capable of escaping the protection afforded by current vaccines against H5 avian influenza. Overall, the outcome of biologic, genetic and antigenic analyses of these viruses in Indonesia has contributed to the identification of updated candidate vaccine strains for poultry.