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Culicoides imicola, biting midge species: a recent invader species in the Mediterranean basin ?

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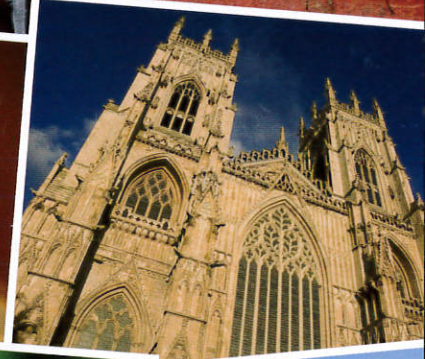
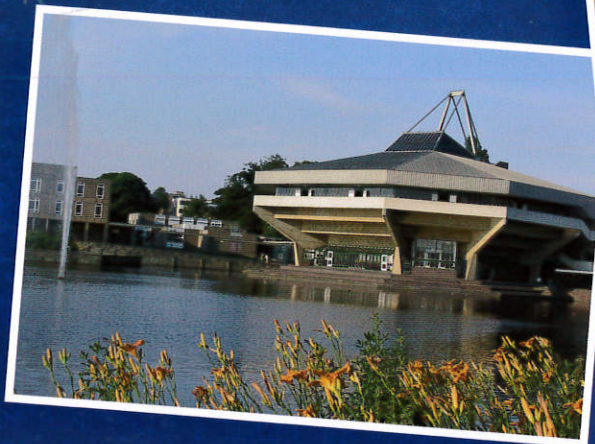
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ECE 2014

ABSTRACTS

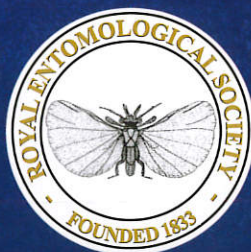


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during spontaneous activity. We found that activity in one neuron inhibits or delays the generation of a spike from the other neuron in the same sensillum by up to 7 ms. ORNs respond to odors with complex dynamics that have been thought to arise solely within an ORN from the kinetics of transduction and spike generation. We asked whether response dynamics in *Drosophila* are also shaped by interactions between the ORNs inhabiting a sensillum. As reported earlier by others, we found that an excited ORN inhibits its neighbor within a sensillum. Excitation of an ORN using optogenetic tools induced inhibition in the neighbor, arguing against an inhibitory mechanism that involves molecular interactions with the odorants, and our further experiments demonstrate directly that the inhibitory action can be explained by current flow through the extracellular space. We discuss the function of the inhibitory interaction in an ecological context.

S37.6 Understanding and exploiting vector-pathogen-host interactions

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Infectious diseases affecting human health that involve mosquito-borne pathogens are a global problem. Investigating mosquito behaviour is an essential part of understanding the transmission cycle and could lead to the development of effective tools for the monitoring and control of diseases, including malaria. We have recently demonstrated that *Anopheles gambiae* mosquitoes infected with *Plasmodium falciparum* malaria parasites are significantly more attracted to human odours than uninfected mosquitoes. Additionally, in collaboration with Wageningen University, Radboud University in The Netherlands and Rothamsted, we are investigating the ability of malaria parasites to alter human body odour making it more attractive to *Anopheles* mosquitoes. The aims of these studies are to understand the olfactory and chemical mechanisms underlying the behavioural manipulation of mosquitoes, and odour manipulation of human beings, by malaria parasites and how this knowledge can be exploited to develop novel monitoring and control tools, or to improve the use of those already available. These studies also raise the question of the importance of parasite manipulation of vectors, from an epidemiological perspective, and whether it is present in other arthropod-host-pathogen systems.

S37.7 Weather forecasting by insects: sexual behavior changes as atmospheric pressure varies

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Abrupt fall of barometric pressure presage storms which can cause high mortality of small and short-lived organisms, such as insects. We studied changes in mating behaviours of three taxonomically unrelated insects, *Diabrotica speciosa* (Coleoptera), *Pseudaletia unipuncta* (Lepidoptera) and *Macrosiphum euphorbiae* (Hemiptera), when subjected to natural or manipulated changes in atmospheric pressure. In response to decreasing barometric pressure, male beetles exhibited decreased locomotory activity with female pheromone. However, when in proximity to females, they exhibited reduced courtship sequences and the precopulatory period. Under the same situations, moth and aphid females exhibited significantly reduced calling behaviour. In the case of the armyworm there was a significant decrease in the incidence of mating under rising atmospheric conditions, suggesting an effect on male behaviour. When atmospheric pressure rose, very few *M. euphorbiae* oviparae

called. This was similar to the situation observed under decreasing conditions, and consequently very little mating was observed in this species except under stable conditions. All species exhibited behavioural modifications, but there were interspecific differences related to size-related flight ability and the diel periodicity of mating activity. We postulate that the observed behavioral modifications, especially under decreasing barometric pressure would reduce the probability of injury or death under adverse weather conditions.

S38 PERSPECTIVES ON THE GLOBAL EMERGENCE OF CULICOIDES-BORNE ARBOVIRUSES

Convenors: Simon Carpenter (UK) and Tim Lysyk (Canada)

S38.1 *Culicoides* Research Progress: What is the State of Our Art? [Keynote lecture]

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Relative to many vector groups like mosquitoes or ticks, *Culicoides* spp. (biting midges) have received far less research attention. The recent increases in activity of *Culicoides*-borne animal viruses have changed that. Bluetongue, epizootic hemorrhagic disease and an entirely new orthobunyavirus, Schmallenberg, have been appearing, and persisting, in places where they were historically unknown. Entomological research activity has exploded particularly in Europe over the past 10-15 years, ranging from field monitoring and control trials to pending description of the first *Culicoides* genome. This has provided wonderful opportunities to expand our knowledge of the European fauna, and hopefully will help promote appreciation for entomology and reinvigorate European training programs in the field. Further, we have been able to explore fundamental and important aspects of the biology of the genus globally (e.g. dispersal, relationships with symbionts, genetic correlates of vector competence). Here I will try to provide an overview of where we stand in *Culicoides* research across the basic-applied continuum, particularly as relates to our knowledge of disease epidemiology and the possibilities of improved disease control through vector management or manipulation.

S38.2 Modelling impacts of ecological complexity and environmental changes on *Culicoides*-borne diseases – how much detail do we need?

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The recent invasion and spread of exotic strains of *Culicoides*-borne arboviruses in both endemic and epidemic situations worldwide has emphasised the dynamic nature of virus – midge vector – host interactions in these systems and implicated global changes in climate, land use, trade and animal husbandry in disease emergence. *Culicoides*-borne arbovirus systems tend to be ecologically complex with multiple midge species and multiple hosts that are often involved in transmission in a single region. This is in part due to the wide host and habitat preferences of key livestock-associated *Culicoides* vector species. Drawing on case studies from both temperate and tropical situations, this talk addresses the degree of ecological complexity that must be represented in model frameworks for us to better understand and predict disease emergence. We describe how and why key ecological processes are being incorporated into models of transmission and spread including (i) seasonally changing host-midge vector interactions (ii) landscape features and trade networks (iii) diversity of host communities including reservoir wild mammal species. Key knowledge gaps and relevance of ecological model outputs to mitigation policies will be highlighted.

S38.3 *Culicoides imicola*, a recent invader in the Mediterranean Basin?

Claire Garros, Stéphanie Jacquet, Karine Huber, Sylvain Guichard, Annelie Tran, Hélène Guis, Marie-Laure Setier-Rio, Jean-Claude Delécolle, Thomas Balenghien
Cirad, Control of Exotic and Emerging Animal Diseases, France; INRA, Control of Exotic and Emerging Animal Diseases, France; Cirad, Animal and Integrated Risk Management, France; EID-Méd, France; Strasbourg Université, IPPTS, France
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The biting midge *Culicoides imicola* (Diptera: Ceratopogonidae) is a major vector of two important Orbiviruses: bluetongue (BT) virus, which affects wild and domestic ruminants, and African Horse Sickness virus, a lethal disease of horses. Historically, *C. imicola* presented an Afrotropical distribution but from the 90s, it spread apparently into the Mediterranean Basin, resulting in epizootic BT outbreaks on insular territories and eventually on the European mainland. While the exact historical limits of this species in southern Europe were unknown before the first BT outbreaks, this species was then considered as an 'invasive' species for the Mediterranean basin. However our knowledge about newly colonized areas and introduction pathways are based largely on historical and entomological survey data, which are often incomplete and, sometimes, misleading. We present a background of the current knowledge on *C. imicola* distribution. Indeed, distribution studies suggest that the species has spread into new regions during the last 20 or 30 years, although recent studies have found little evidence for further expansion since 2000. Recent population genetics studies based on mitochondrial DNA support a recent European expansion, while the hypothesis of an ancient presence of the insect vector was strongly favored by microsatellite analysis. To investigate whether *C. imicola* is truly an invasive species, we present an ecoclimatic niche model and multi-marker population genetic approach. The local progression of the settled populations in the south of France is also presented.

S38.4 A model for long-distance dispersion of *Culicoides* and its role in the management of arbovirus spread

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Recent years have seen the emergence and spread of the *Culicoides*-borne arboviruses bluetongue (BTV) and Schmallenberg (SBV) throughout much of Europe. *Culicoides* have the potential to disperse semi-passively on prevailing winds, rapidly spreading virus into new areas many hundreds of kilometres away. We describe how an atmospheric dispersion model (the Met Office NAME model) has been modified to simulate *Culicoides* flight activity based on dedicated entomological data sets collected in the UK. The model played a significant role in aiding policy responses to BTV outbreaks in the UK in 2007 and 2008, and was subsequently used to assess the areas of the UK exposed to SBV in 2011. The model has further been applied to retrospective analyses of BTV case origins in the EU and for risk assessment exercises in the UK and New Zealand.

S38.5 Measuring between-farm variation in *Culicoides* (Diptera: Ceratopogonidae) density, the vectors of bluetongue virus*

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Culicoides midges are ubiquitous on farms in the UK, but little research has explored their abundance, an important determinant of disease risk. Models to explain and predict variation in their abundance are needed for effective targeting of control methods against bluetongue (BT) and other *Culicoides*-borne diseases. Midge abundances were estimated using light traps on 35 farms in north Wales. *Culicoides* catches were combined with remotely-sensed

ecological correlates, and on-farm host and environment within a general linear model. Local-scale variation in exhibited an almost 500-fold difference between farms Obsoletus Group catches. The variance explained was high for the BT vector species (81% for Obsoletus Group; Pulicaris Group, 73% for *C. pulicaris*, 74% for *C. punctatus*). The abundance of all vector species increased with the number of sheep on farms, but this relationship was missing from any of the non-vector models. At a large spatial scale, there is significant variation in *Culicoides* Obsoletus Group abundance, which undermines attempts to record their nationwide distribution in larger scale models. A prior survey should be undertaken for farms with high *Culicoides* catches within a sampling area and stability in catch size should be checked between seasons and years.

S38.6 Identification of vector competence traits in *Culicoides sonorensis*, the North American vector of bluetongue virus

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Culicoides biting midge are a major vector of arboviruses that cause serious livestock and human disease. These include bluetongue virus (BTV) which causes an acute disease in sheep with high rates of morbidity and mortality. The ability of *Culicoides* to develop a transmissible arbovirus infection varies significantly both between and within species and has been linked to both viral and vector genetics. The current *Culicoides sonorensis* genomic project will provide an unprecedented opportunity to identify genetic traits and individual genes which play a significant role in BTV dissemination within the insect host. Comparison at the genome and transcriptome level between individual *C. sonorensis* is already providing a significant insight into the genetic and cellular mechanisms involved in infection and dissemination and these studies will be discussed during this presentation. Enhancing our understanding of host-vector interactions at the cellular level may lead eventually to vector surveillance techniques to identify indigenous *Culicoides* populations with the potential to transmit arboviruses.

S39 [THURSDAY PM]

INSECT DIVERSITY AND ECOSYSTEM FUNCTION Convenor: Wolfgang W Weisser (Germany)

S39.1 Distribution and persistence of red wood ant nests: a geostatistical approach to 45 years of settlement

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The occurrence of hill-building wood ants of the Formica rufa-group was censused 11 times over the period 1966 - 2010 in 1640 ha area (250 - 800 m a.s.l.) east of Freiburg / Br. (SW-Germany) and their settlement pattern analyzed. Most occupied nests (average density 16 nests per 100 ha) belonged to *F. rufa* and *F. polyctena*; *F. pratensis* and *F. lugubris* occurred distinctly less. In spite of changes in nest numbers, their spatial distribution remained remarkably stable during this 45 year period, always maintaining the same non-random pattern, according to point-pattern-analyses. High-density spots and ant-free areas did not differ consistently in habitat composition, contrary to common expectations. Poisson-point-process-based distribution analyses were employed to elucidate the role of several habitat factors as well as geological and topographic conditions.

S39.2 Diversity in a detritivore community: an agroecosystem context

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