

Presentation Abstract

Add to Itinerary

Print

Presentation: 237 - Modelling the spatial distribution of *Culicoides* biting midges at the local scale

Location: Uxmal 1 (5)

Pres. Time: Friday, Nov 06, 2015, 5:15 PM - 5:30 PM

Category: +A9. Vector-borne and parasitic diseases

Author(s): **Georgette Kluiters**¹, David Sugden¹, Helene Guis², K. Marie McIntyre¹, Karien Labuschagne³, Matthew Baylis¹, ¹University of Liverpool, Neston, United Kingdom; ²CIRAD, Montpellier, France; ³ARC - Onderstepoort Veterinary Institute, Onderstepoort, South Africa. Contact: g.kluiters@liverpool.ac.uk

Abstract: Purpose: The *Culicoides* midge vectors of bluetongue (BT) are ubiquitous on farms in the UK, but little research has explored their spatial abundance, an important determinant of disease risk. Models to explain and predict variation in their abundance are needed for effective targeting of BT control methods. Although epidemiological models are commonplace at the national scale, no investigations have taken place at a finer spatial scale. Our aim is to identify determinants of midge abundance at a local 1 km scale.

Methods: 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 environmental data, within a general linear model. Drivers of local scale variation were determined at the 1 km resolution.

Results: Local-scale variation in Obsoletus Group abundance exhibited an almost 500-fold difference (74 to 33,720) between farms, but the Obsoletus Group model explained 81% of this variance. The variance explained was consistently high for the Pulicaris Group, *C. pulicaris* and *C. punctatus* (80%, 73%, and 74%), the other possible BTV vector species in the UK. 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. Performance of the non-vector models was also high (65-87% variance explained), but species differed in their associations with satellite variables.

Conclusions: At a large spatial scale, there is significant variation in *Culicoides* Obsoletus Group abundance, undermining attempts to record their nationwide distribution in larger scale models, which have historically explained the abundance of these vectors poorly. Satellite data can be used to explain a high proportion of this variation and may produce effective predictive models of disease vector abundance.

Relevance: This work highlights how novel local-scale modelling of disease vectors can explain a large degree of spatial variation that national-scale models fail to explain. This should be of note to policy makers when deciding upon guidelines for entomological surveys before, during and after disease outbreaks.

Technical Support

Phone: 217-398-1792

[Helpdesk](#)



The Online Abstract
Submission and Invitation
System

© 1996 - 2016 Coe-Truman
Technologies, Inc. All rights
reserved.



Coe-Truman Technologies, Inc.