

Evaluation of the role of cattle movements in the spread of *Staphylococcus aureus* strain types between dairy farms

Garcia-Alvarez L, Webb CR, Lindsay H and Holmes MA

Department of Veterinary Medicine, University of Cambridge, UK

Our knowledge of the precise routes of transmission of many infectious pathogens between farms, and the role possible contacts between these farms play in the spread of disease, is limited. The introduction of national cattle tracing systems at individual animal level has enabled the parameterisation of mathematical models for infectious disease spread with explicit contact networks. These data are both computationally intensive to include in models and expensive to collect. A key question therefore is: do reported animal movements adequately capture the structure of the risk-potential network for disease spread between cattle farms?

In this study we used a marker pathogen *Staphylococcus aureus*, a causative agent of bovine mastitis, to map the spread of infectious bacteria between dairy farms. We then compared the observed spread with predicted spread based on mathematical models using alternative parameterisations for the risk-potential network linking farms.

We present a novel protocol to capture the strain profile within a farm using milk collected from the bulk tank. The typing protocol combines the use of Random Amplified Polymorphic DNA PCR and Multi-locus sequence typing (MLST) to maximise the chance of identifying all strains present on a farm whilst keeping the time and cost involved viable to enable a greater number of farms to be included in the study. Movement data for both cattle and sheep were obtained from the British Cattle Movement Service and the Animal Movements Licensing Service via RADAR to create a "reported risk-potential network". A questionnaire was administered to all study farms to identify other potential routes of transmission of infection between farms, and create a "non-reportable risk-potential network". These included human contacts, the use of shared equipment and collection companies.

A total of 16 strain types of *S. aureus* were identified, with 42 out of the 45 study farms infected with at least one strain type at one or both time points. The observed strain distributions for the most prevalent strains suggest that the spatial spread of *S. aureus* cannot be explained by a nearest neighbour model (based on spatial location). Initial analysis of the "non-reportable risk-potential networks" shows that indirect animal-animal contacts via people visiting the farm may contribute to certain strain distributions. Furthermore, preliminary analysis of the "reported risk-potential network" indicates that the distribution of observed strain types cannot be accurately modelled using only this data to parameterise the model. In conclusion, the use of animal movement data is likely to capture many of the essential elements of disease spread between dairy farms. However, the solely use of these data, without allowance for other non-reported contacts between farms, may result in little improvement in the accuracy of prediction of the spatial dynamics of infectious diseases over more parsimonious modelling approaches.