

Cattle movement data: does it constitute a good predictor for disease spread?

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Introduction: Our knowledge about the precise routes of transmission of many infectious pathogens between farms and the role possible contacts between these farms may play in the spread of disease is limited. One of the most common and economically important diseases in dairy cattle in the UK is bovine mastitis. *Staphylococcus aureus* is one of the most frequently isolated contagious pathogens.

Overall Aim: To evaluate whether incorporating cattle movement data into mathematical models for disease spread can improve our predictions for the spatial and temporal dynamics of infectious diseases by comparing model predictions with the observed spread of a marker pathogen.

Materials and methods:

- 45 dairy farms recruited in Somerset.
- Collection of bulk milk samples from each farm at two time points (May 2007 and October 2007).
- Collection of quarter milk samples from a) cows not milked with the rest of the herd on the bulk milk sample collection day, b) purchased animals, and c) first calving heifers introduced to the milking herd during the study period.

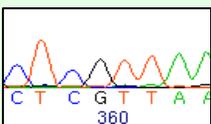
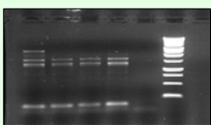
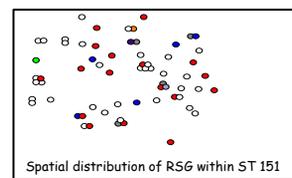
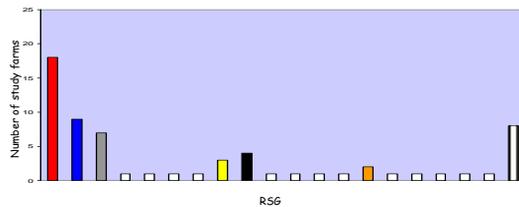
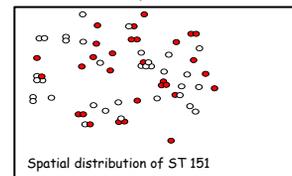
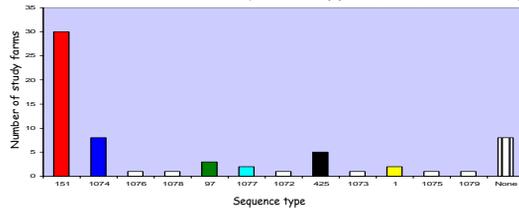
Phenotypic and genotyping techniques to identify *S. aureus*: culture of 2 ml of bulk milk sample on sheep blood aesculin agar → selection of up to 15 *S. aureus* colonies, identified by morphology on agar, use of Gram staining, catalase test and coagulase test → species confirmation by 16S PCR.

Novel typing protocol: Random Amplified Polymorphic DNA PCR with three different primers: combine results to create RAPD strain groups (RSG). One colony from each RSG isolated within a farm is then strain typed by Multi-locus Sequence Typing (MLST).

Preliminary results: May collection

Culture and isolation 490 colonies selected → 16S-PCR 490 isolates confirmed → RAPD-PCR 490 isolates typed → Final collection: MLST 56 isolates

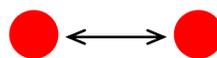
MLST sequence types (ST) and RSG present on study farms



Network analysis and mathematical modelling: create alternative models to explain strain distribution at each time point

Node attribute data:

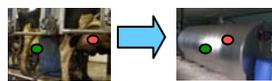
- Bio-security measures
- Handling of heifers at first calving
- Farming and housing systems
- On-farm mastitis profile
- Other species present on farm
- TB restrictions
- Questionnaire



Edge relationship data:

- Movement of dairy cattle between farms
- People or companies visiting the farm
- Contacts with other farms via sharing grazing land, relief milkers, agricultural equipment
- Movement of non-dairy and non-bovine animals between farms
- Movement derogations ('linked holding')
- Questionnaire and British Cattle Movement Service

Strain distribution data



Conclusions (based on analysis of May 2007 samples)

- We found a high prevalence of *S. aureus* within the study region (82%). Individual MLST strain type prevalence varied from 2-67%.
- RAPD-PCR is a technically simple method to compare isolates within a farm and has enabled further division of MLST strain types at a single time point. However, it is not suitable for comparison between time points.
- The observed strain distributions for the most prevalent strains suggest that the spatial spread of *S. aureus* cannot be explained by a pure diffusion process. Neither can direct cattle movements between the study farms explain the observed data as there are insufficient number of these movements. Some farms in the study with *S. aureus* have been closed to imports for several years.
- Further analysis of the cattle movement database will investigate the potential role of movements from outside the study set, however, disease spread between farms does not appear to rely solely on the reported movement of cattle.

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