

## Reducing clusters and breaking chains of BVD infection in the GB Cattle network

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Bovine Viral Diarrhoea (BVD) is an endemic disease of cattle in Great Britain, but in Scotland a BVD eradication programme has been running since 2010 and since 2014 includes compulsory testing, culling of infected animals and movement restrictions on non-negative herds. BVD epidemiology is driven by a small number of super spreading individuals where transmission from dam to foetus in the first trimester of pregnancy results in a persistently infected (PI) animal, which can shed virus throughout its lifetime.

Here we examine methods for detecting reduction of transmission within Scotland as a result of the eradication programme using surveillance and sequence data. The surveillance data consists of individual animal test results linked to the Cattle Tracing System movement records, and the sequence data is from the short 5'UTR genomic region from >2000 animals, representing a large fraction of known PIs in Scotland from 2012-2017. From the surveillance data we can calculate the spatial and temporal distribution of BVD infections, and can trace where the dams of the PIs were at the time of infection. From the sequence data, information linking different infections, potentially from disparate geographic regions can be obtained.

The sequence data set revealed at least 50 clusters of genetically identical short 5'UTR sequences from animals on different farms. An initial mutation rate analysis showed that the time to most recent common ancestor of these clusters was 1-5 years, implying that these genetic clusters represent recent transmissions. The expected distribution of genetic cluster sizes varies as a function of underlying contact network properties and population scale epidemiological parameters. By simulating transmission between farms we found that the distribution of animal infections and cluster size could be informative about changes in transmission coefficient. Analysing the genetic clusters together with the Cattle Tracing System data in different years showed a marked reduction in cluster size and numbers of clusters, correlating with increased movement restrictions of the eradication programme and an overall reduction in infections transmitting within Scotland. In summary, this study shows how combining sequence data from PI cattle with movement data can yield useful extra information to help measure the progress of eradication.