

## **THE CHALLENGES OF LINKING GENETIC AND EPIDEMIOLOGICAL DATASETS TO RECONSTRUCTING TRANSMISSION TREES FOR LIVESTOCK VIRAL DISEASES**

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Reconstructing transmission trees that accurately reflect the relationships between infected individuals or populations during a disease outbreak can provide valuable insights into both the nature of disease transmission and the overall dynamics of the underlying epidemiological process. Genetic data are becoming increasingly important in the estimation of pathogen transmission trees, particularly with regard to RNA viruses because of their inherently high mutation rate. Using foot and mouth disease virus (FMDV) as an example, this presentation reviews the application of full-genome sequence data as a practical tool to the reconstruction of farm-to-farm level transmission dynamics within recent FMD outbreaks in Europe. Bayesian and statistical parsimony analysis of sequenced field samples (UK 2007, Bulgaria 2011, as well as historical cases from 1967–68 in the UK) have demonstrated that full-genome sequences exhibit clustering that is consistent with transmission scenarios describing the herd-to-herd spread of the virus. Such data also have the potential to predict undisclosed infected premises, and can provide evidence of the involvement of fomites in transmission chains. Furthermore, these farm-level relationships do not appear to be influenced by the genetic diversity of FMD viruses that exist between individual animals in different epidemiological units. However, the ability of these approaches to confidently reconstruct transmission trees is still complicated by difficulties in defining farm-level ownership to evolutionary ancestors that arise due to intra-host evolution, subsequent to FMDV transmission from farms. To tackle this problem, new analytical tools have recently been developed to accommodate spatial and temporal epidemiological information, together with the genetic data to provide a more robust framework to infer probable transmission trees. Work to validate these models is currently underway using empirical data from a large sequence dataset derived from the 2001 epidemic in the UK. These approaches can now be applied to the development of sampling strategies during FMD outbreaks, and provide data to monitor the spread of FMDV in endemic settings, as well as guide the development of new analytical tools to support control policies in the event of virus incursions into FMD-free countries.