

Epidemiological models for controlling porcine respiratory and reproductive syndrome in the United States

Perez, A.M.¹, Zu Dohna, H.¹, Montecino, D.¹, Brito Rodriguez, B.P.¹, Cano, J.P.², Polson, D.², Mondaca, E.² and Whedbee, Z.¹, ¹University of California in Davis, Center for Animal Disease Modeling and Surveillance, USA, ²Boehringer Ingelheim Vetmedica Inc., USA; amperez@ucdavis.edu

Porcine Respiratory and Reproductive Syndrome (PRRS) is a viral disease of swine that causes annual losses for US\$ 664 million in the United States. Here, we present features of a new surveillance system for PRRS developed in partnership with the United States swine industry. The objective of the surveillance system is to support disease control at a regional scale. Data are collected and organized using a web-based system referred to as Disease BioPortal. Phylogenetic analysis is used to identify in-contact farms and companies. The web-based system is used to map, display, and analyze the data, using models for epidemiological display and analysis. Techniques and methods for identification of disease clusters and anomaly detection were developed and incorporated into the web-based system. Rule- and model-based anomaly detection models are used to identify unusual or unexpected changes in the data, based on results of one or more of the cluster tests (model based detection; e.g. a high risk of cases in a given area and time) or to recognize a situation previously unrecorded in a given region (rule based detection; e.g. the first case in a given county). Contact-rates are computed for pig farms and companies, to determine clusters (compartments, zones) at similar risk for the disease. Systematic sequencing and phylogenetic analysis of PRRS samples is conducted in near-real time in a regional basis to identify compartments or zones in which virus transmission exist, which is prerequisite for the implementation of a regionalization strategy for controlling the disease.