

## PRRS 174 Sequence Project

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### Overall Objective:

To monitor and understand the evolution of PRRS virus. Specifically, to identify the location and time of new virus strains developing and have the opportunity to respond.

That objective requires a long term approach to develop the infrastructure for data collection, analysis and interpretation. We have made baby steps in the last several years as we build the participation of Swine Health Monitoring Program and share diagnostic information. But this is only the first of many steps. We start developing the analytic approach, we have started to build a dataset of PRRS virus sequences and invite your participation. We are requesting all your PRRS virus sequences with corresponding locations. As a very preliminary first step, Professor Alkhamis selected sequences collected from 2013 – 2015 from 2 systems. He describes his approach in the next paragraph. We have no results yet and I present this so you can get an inkling for the complexity involved.

A convenience sample of 84 isolates was selected for this analysis. High-risk areas (probability > 0.6) were identified by presence-only maximum entropy method to be the most suitable locations for the spread and maintenance of PRRS in systems 55 and 66. The most important environmental predictor that contributed to the ecological niche of PRRS was global pig density for both systems, followed by temperature seasonality and altitude for systems 55 and 66 respectively. The Bayesian phylodynamic method estimated that the divergence time of PRRS strain 174 ORF-5 gene isolated from systems 22 and 66 was between late xxxx and early xxxx. Furthermore, significant viral dispersal routes were identified between both systems, while system 22 was the most likely source of the spread into systems 66. Ecological Niche modeling results suggest that more information related to climate, land cover and pig farm demographics is needed to further improve the risk prediction for PRRS in the United States, whereas the methodology presented here, may be useful in guiding the design of surveillance programs and to identify areas in which under-reporting may have occurred. However, results of the phylodynamic modeling was able to quantify the evolutionary dynamics of newly emerging PRRS strains and substantiates the ability of such methodological approach to improve molecular surveillance of novel swine viral diseases.

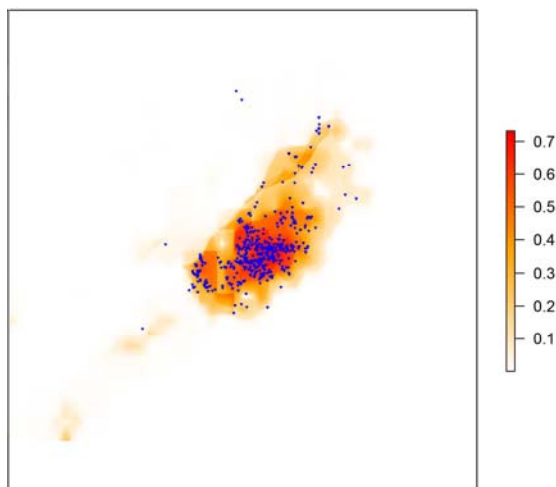


Fig. 1. Predicted geographical risk for PRRS outbreaks detected in system 66 between 2012 and 2015

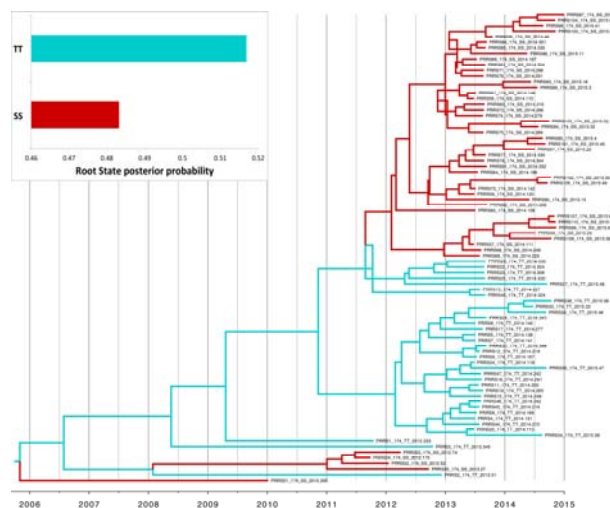


Fig. 2. Maximum clade credibility (MCC) phylogenies of ORF-5 gene of PRRS strain 174 isolated from systems 22 and 66. The color of the branches represents the most probable system state of their descendent nodes. The color coding corresponds to the upper left figure, which represents the root location state posterior probability distributions.

Moh Alkhamis is a DVM, with MPVM and PhD degrees awarded by the University of California, Davis. Moh has recently joined the College of Veterinary Medicine, University of Minnesota faculty as an Adjunct Assistant Professor. His PhD involved modeling and surveillance of highly infectious diseases and in the past decade, he has worked with a number of global reference laboratories analyzing surveillance data, with special emphasis on animal viral diseases. His research interest include spatial, spatiotemporal, and Bayesian phylodynamic modeling of disease surveillance data.