

SWINE HEALTH

Title: Temporal, spatial & phylogenetic analysis of PRRSV sequences, NPB project #15-156

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Scientific Abstract:

We explored the relations between the spatial risk of PRRS outbreaks and its phylodynamic history in the U.S during 1998–2016 using ORF5 sequences collected from swine farms in the Midwest region. We used maximum entropy and Bayesian phylodynamic models to generate risk maps for PRRS outbreaks and reconstructed the evolutionary history of three selected phylogenetic clades (A, B and C). High-risk areas for PRRS were best-predicted by pig density and climate seasonality and included Minnesota, Iowa and South Dakota. Phylodynamic models demonstrated that the geographical spread of the three clades followed a heterogeneous spatial diffusion process. Furthermore, PRRS viruses were characterized by typical seasonality in their population size. However, endemic strains were characterized by a substantially slower population growth and evolutionary rates, as well as smaller spatial dispersal rates when compared to emerging strains. We demonstrated the prospects of combining inferences derived from two unique analytical methods to inform decisions related to risk-based interventions PRRS in the US.

These research results were submitted in fulfillment of checkoff-funded research projects. This report is published directly as submitted by the project's principal investigator. This report has not been peer-reviewed.

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