

Porcine reproductive and respiratory syndrome virus dissemination across pig production systems in the United States

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Learn more about our work at <https://machado-lab.github.io/>

Background

Despite improvements in virus characterization, mainly by viral sequencing, it is unclear whether most PRRSV infections are a product of viral circulation within a farm, between farms within a production system (local) or between farms across production systems (external).

Objective

To investigate the dissemination dynamics of PRRSV among pig farms in three production systems. The understanding of PRRSV transmission routes has the potential to inform targeted strategies for its prevention and control, however, further studies are needed to identify the contribution of known local routes of transmission.

Materials and methods

ORF5 PRRSV sequences derived from the PRRSV MSHMP database were obtained from three commercially unrelated systems of sow-to-finish swine farms collected during 2014-2019 in a defined dense pig populated region of the United States.

To determine the spatiotemporal patterns of PRRSV spread, the impact of different potential predictors on PRRSV spread, as well as to infer the migration rates between internal vs external introductions (between farm systems) we used a Bayesian phylodynamic approach. This methodology considers the observed genetic diversities to estimate, for example the volume of PRRSV spread among farms of different production systems.

Results

1. PRRSV evidenced high levels of transmission between non-commercially related pig production systems, especially, from November until May when PRRSV tends to peak in the studied region. These results reinforce the importance of farm proximity on PRRSV spread.
2. Sow farms were found to be the most dominant spreaders of PRRSV, however, significant number of samples collected in sow and nursery farms most likely originated from finisher farms.
3. Between-farm dissemination becomes easier when farms are located in highly populated pig areas (from 500 to 1000 pig/km²), as well as farms located at a range within 0.5 km and 0.7 km from major roads showed more likelihood to be infected by PRRSV.
4. On the other hand, PRRSV evidenced more difficulty reaching farms at higher elevation surrounded by dense vegetation, which acted as dissemination barriers.

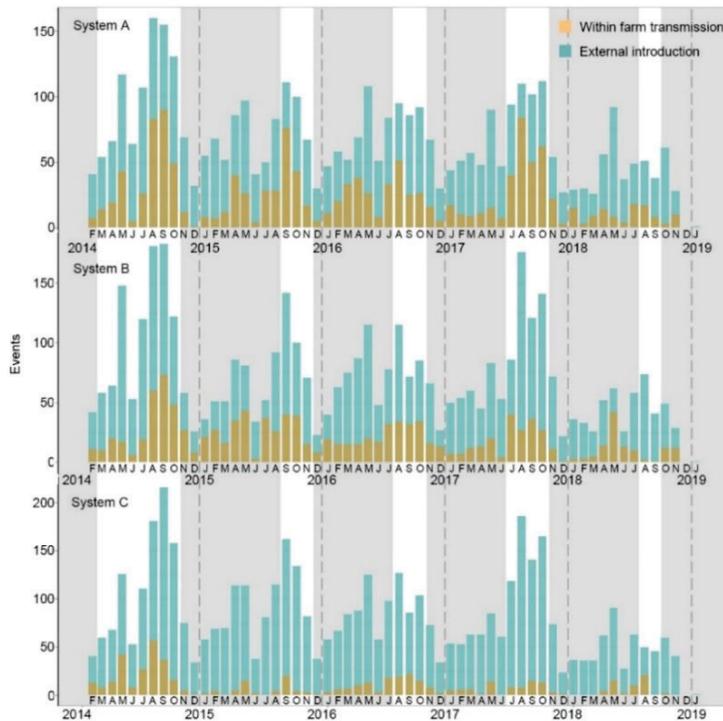


Figure 1. PRRSV migration events among pig systems inferred through a structured coalescent model. Number of dissemination events originated in farms that belong to the same pig system compared to the events coming from farms integrated to another pig system. The grey background represents the months where the exponentially weighted moving average epidemic monitor surpassed the established PRRSV epidemic threshold (based on the February 2020 MSHMP report), while dashed lines represent the beginning of each year.

Conclusions and implications

The understanding of PRRSV transmission routes has the potential to inform targeted strategies for its prevention and control, where reinforcement in biosecurity considering farm proximity as a relevant route for virus dissemination may be the best tool to prevent PRRSV spread.

For more details please read the full paper here (<https://onlinelibrary.wiley.com/doi/abs/10.1111/tbed.13728>)