

Making epidemiological sense out of large datasets of PRRS sequences

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Key Points

- Occurrence of PRRS lineages is not equal in different years, systems or production types
- Occurrence of specific PRRS lineages is associated with movement of animals
- Continuous surveillance for PRRS occurrence is important in understanding its determinants and might be able to provide insights that can help on its prevention

Factors associated with the occurrence and dynamics of specific genetic lineages of PRRSV are not fully determined. Identifying these factors and their role could provide insights into transmission routes and possible interventions that could decrease PRRS dissemination in the United States swine industry.

By utilizing a dataset of 1901 PRRS sequences provided by the Morrison Swine Health Monitoring Project (MSHMP) participants over 3 recent years, we described spatiotemporal patterns in the occurrence of different lineages of PRRSV and investigated the extent to which the network of pig movement between farms determines the occurrence of PRRS from similar lineages.

We showed that PRRS lineages occurred at different frequencies across geographically overlapping production systems. Preliminary analysis showed that the relative frequency in which specific lineages occur increase while others decrease over time. The rate at which these changes occur appears to be system-specific. Some lineages were also more common in farms of specific production types (i.e. sow farm or nurseries). As expected, farms that were connected via pig movements were more likely to share the same lineages than expected by chance across all years.

These findings suggest that system-specific characteristics partially drive PRRS occurrence over time and across farms of different production types. Our results also indicate that animal movement between farms is a driver of PRRS occurrence, strengthening this hypothesis of viral transmission. Additional research is needed to quantify risks and develop mitigation measures related to animal movement. Our analysis of this complex MSHMP PRRS dataset aids in describing trends in PRRS occurrence over time and provide novel insights into the dynamics of PRRS transmission, benefiting the development of decision making processes which ultimately result in regional prevention strategies.

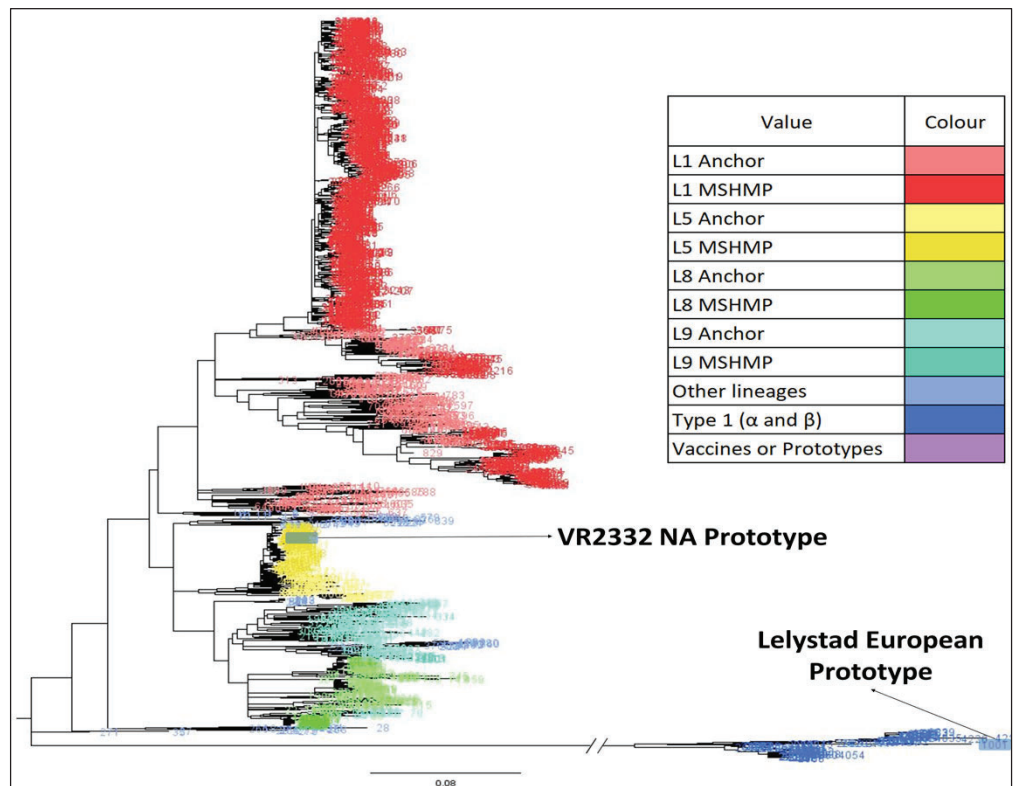


Figure 1: Phylogenetic tree of sequences used in this analysis. Different genetic groups of PRRS can be seen, as well as the preponderance of Lineage 1.

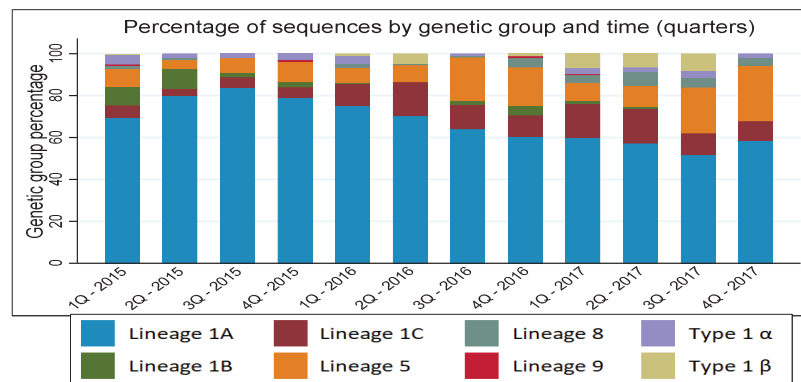


Figure 2: Temporal trend for PRRS occurrence according to genetic groups. The frequency in which different genetic groups occurs change over time.

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