Contrasting PRRSV lineage patterns from 2017 to 2021 at the individual farm, production system, and regional levels in Ohio and neighboring states

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Key Point:

- Individual farm and production system-level PRRSV-2 lineage patterns do not necessarily correspond to regional-level patterns.
- Analysis of differences in lineage distribution across time at the regional, production system, and individual farm levels highlight the importance of decisions made at the production system and individual farm levels for PRRSV prevention and control.

Introduction:

Porcine reproductive and respiratory syndrome virus (PRRSV) has been challenging to control due to its high mutation rates and genetic diversity. This retrospective study aimed to describe and compare the distribution of PRRSV lineages obtained at the individual farm, production system, and regional levels.

Methods:

PRRSV type 2 (PRRSV-2) sequences (n = 620) between 2017 – 2021 were collected from one collaborating production system and swine farms across Ohio and neighboring states, including Indiana, Michigan, Pennsylvania, and West Virginia. The ORF5 region of collected PRRSV-2 sequences were aligned with 169 lineage anchors and six PRRSV live attenuated vaccine strains including Ingelvac PRRSV ATP and MLV, Fostera PRRSV, Prime Pac PRRSV RR, Prevacent, and PRRSGard. PRRSV-2 sequences were assigned to the most identical lineage anchors/vaccine strains.

Results and Discussion:

In 2017 – 2021, ~30% of submitted sequences were identified as vaccine strains. Non-vaccine sequences (n = 435) were mostly classified as the L1A lineage (79.8%) at the regional level, followed by L1H, L1C, L5, L8, and L1F (Figure 1). Similar to the regional level, L1A was the most identified lineage (64.3% - 100.0%) among five systems that submitted the greatest number of sequences (n = 7 – 195), followed by L1H, L1C, L5, L8, and L1F; however, the lineage distribution was distinct. At the individual farm level, there was less diversity in sequences from five farms that submitted the greatest number of sequences (n = 14 – 28) compared to system and regional levels; the majority was classified as either L1A or L5. Throughout the five years of study, we also found co-existence of L1A and L5 in three individual farms and co-existence of L1A, L1H, and L5 in one farm, indicating that lineages likely co-exist in individual farms.

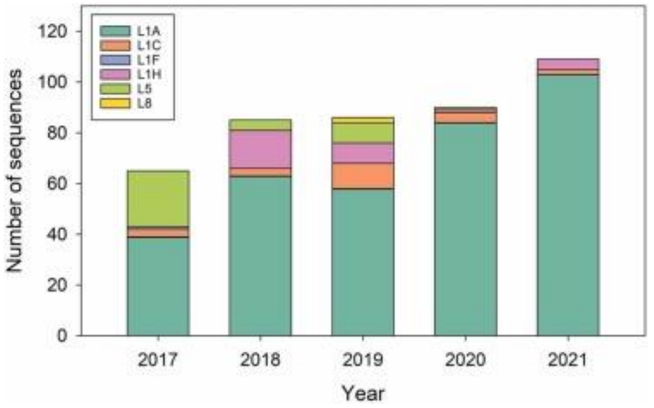

Figure 1. Annual lineage distribution of PRRSV-2 ORF5 non-vaccine sequences between 2017 and 2021 (n = 620).

Overall, our results show that individual farm and production system-level PRRSV-2 lineage patterns do not necessarily follow regional-level patterns. This highlights the influence of individual farms and systems in shaping PRRSV occurrence and suggests the importance of within-farm system monitoring and early detection for accurate knowledge on PRRSV-2 lineage occurrence and emergence.

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