

Porcine reproductive and respiratory syndrome virus 2 (PRRSV-2) genetic diversity and occurrence of wild type and vaccine-like strains in the United States swine industry

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Key Points:

- The mean PRRSV ORF5 genetic distance was generally smaller in years in which there was a relative higher frequency of a dominant lineage.
- Vaccine-like sequences comprised about one fourth of all sequences, most lineage 5 sequences were Ingelvac PRRS MLV-like.
- A reduction in the frequency of wild-type lineage 8 sequences from 2012 onwards was observed.

Nucleotide sequencing of the open reading frame 5 (ORF5) region of the viral genome has become a popular methodology to differentiate genotypes and strains, and to understand viral diversity across time. Efforts in immunizing the herds have been made in the past few decades, particularly in high density swine regions. Current PRRSV vaccines main outcome is to reduce and mitigate economic losses due to the disease. However, the use of live vaccines implies viral replication with the potential of vaccine-derived virus shedding through the process. We describe the porcine reproductive and respiratory syndrome virus genotype 2 (PRRSV-2) genetic diversity and occurrence of vaccine-like strains in the U.S. over the course of 10 years.

Methods

Four commercially available vaccines are utilized in the United States (Ingelvac PRRS MLV, Ingelvac PRRS ATP, Fostera PRRS, and Prevacent PRRS). These four vaccines were introduced into the swine market in 1994, 2004, 2012 and 2018, respectively. For each lineage associated with a commercially available vaccine, the ORF5 percent nucleotide difference between sampled sequences and the ORF 5 of the associated vaccine was calculated. This data was plotted by year to illustrate the diversification patterns of vaccine lineages and the occurrence of vaccine-like isolates through time. A total of 26,831 ORF5 PRRSV-2 sequences obtained from 34 swine production systems participating in the Morrison Swine Health Monitoring Project (MSHMP), a Swine Health Information Center funded project, and conducting routine monitoring and outbreak investigations between 2009–2019 were included in this analysis. Within group mean genetic distance (mean proportion of nucleotide differences) per year according to herd type was calculated. The percent nucleotide difference between each sequence and the ORF5 sequences from the four commercially available PRRSV-2 vaccines within the same lineage over time was used to classify sequences as wild-type or vaccine-like. A 5% percent nucleotide difference to a vaccine strain cutoff was used to classify sequences as vaccine-like or wild-type.

Results

The mean ORF5 genetic distance fluctuated from 0.09 to 0.13. The yearly increase and decrease in mean genetic distance, regardless of herd type, is possibly explained by the change in frequency of the dominant lineages and sub-lineages over time. Vaccine-like sequences comprised about one fourth of sequences obtained through routine monitoring of PRRS. We found that 99% lineage 5 sequences were Ingelvac PRRS MLV-like (Fig 1). Lineage 8 sequences up to 2011 were 62.9% Ingelvac PRRS ATP-like while the remaining were wild-type viruses. From 2012 onwards, 51.9% of lineage 8 sequences were Ingelvac PRRS ATP-like, 45.0% were Fostera PRRS-like, and only 3.2% were wild-type. For lineage 1 sequences, 0.1% and 1.7% of the sequences were Prevacent PRRS-like in 2009–2018 and 2019, respectively.

Conclusion

These results suggest that usage of vaccine-like viruses through use of modified live vaccines might have contributed to decrease within-lineage viral diversity as vaccine-like strains become more prevalent. However, it is also important to consider the broader context of PRRSV in the United States, where Lineage 1A emerged in 2014 and quickly became the most prevalent PRRS lineage, which might have led to viral competition with wild-type lineage 5 and lineage 8 sequences. Possible implications of a high frequency of vaccine-like viruses sequenced from field samples are: 1) a more comprehensive understanding of PRRSV diversity in the field is hindered since whether this represents vaccine shedding or that a vaccine strain is favored during sequencing of samples originating from pigs with mixed PRRSV infections remains to be elucidated; 2) Concerns about vaccine strain evolution in the field, potential recombination with wild-type viruses and vaccine-like strains causing clinical disease might arise; or 3) Given that vaccines have been associated with decreased clinical manifestations, an increase in vaccine-like sequences occurrence in the field might be beneficial in terms of predictability of PRRS economic impact.

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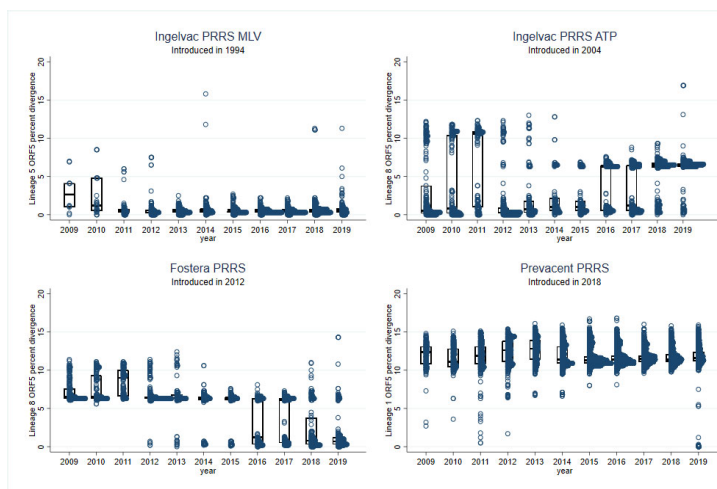


Fig 1. Yearly percent nucleotide differences between lineage 5 ORF5 sequences to Ingelvac PRRS MLV; lineage 8 sequences to either Ingelvac PRRS ATP or Fostera PRRS; and lineage 1 sequences to Prevacent PRRS.