

PRRSv ORF5 difference from VR2332 by herd type

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- Breeding herd sequences differ 8%-16% while in other herd types they differ 1%-15% from VR2332 at the ORF5 level.
- The larger nucleotide identity (%) range compared to VR2332 in growing pigs suggests a higher viral diversity within this group.

The Morrison Swine Health Monitoring Project (MSHMP) involves periodically analyzing PRRSv sequence data voluntarily shared by participants. As a continuation of these series of preliminary data exploration, here we describe viral diversity of PRRSv according to the herd type (e.g. breeding, wean-to-finish) the sequences originated from as a factor that can potentially play a role in diversity. Factors that influence viral persistence in a farm may also have different relative importance depending on herd type. Examples of these factors are that the acute phase of the infection does not necessarily lead to seroconversion of all animals within the herd at the same time, that the introduction of new susceptible pigs (e.g. gilts, weaners or growers) can boost virus activity, and that the passive immunity in young pigs is of short duration allowing piglets to be susceptible to infection or even re-infection by 4 to 10 weeks of age.¹ This is important because molecular mechanisms involved in RNA viral diversity are mutation and genome recombination.² Whenever there is an opportunity of co-circulation of different viruses, the probability of re-infections, co-infections, and/or recombination likely increases, as it does immunity driven selection.

Out of the current 31,457 sequences in the MSHMP dataset, approximately 50% of these contain information on herd type. As described in previous science pages, PRRSv type 1 (PRRSv1) comprises less than 5% of our dataset and is currently classified as a different viral species than PRRSv type 2 (PRRSv2),³ thus it was excluded from this analysis. After removing partial sequences and PRRSv1 sequences, we ended up with a dataset (n= 12,921) comprised of 57% of the sequences coming from breeding herds (n=7,321), 19% from nurseries (n=2,488), 16% from finishing sites (n=2,121), and 8% from wean-to-finish sites (n=991). The percent identity, number of nucleotide characters that match exactly, and its complement, percent nucleotide difference, between each sequence and the reference VR2332 (the first North American PRRSv2 isolate in 1992)⁴ was calculated.

A statistically significant difference was found in the percent nucleotide difference from VR2332 between the herd types (Kruskall-Wallis $p < 0.001$). Additionally, if we stratify the differences in 0-5%, 6-10%, 11-15%, and >15% we found that the distributions were unequal between herd types ($\chi^2 p < 0.001$). Out of all the sequences from breeding, nursery, wean-to-finish and finisher herds, 7%, 27%, 24% and 20% of those had a 0-5% difference when compared to VR2332. However, out of all the sequences from breeding, nursery, wean-to-finish and finishers herds, 88%, 67%, 58% and 75% of those had a 11-15% difference when compared to VR2332 (Table 1). This suggests a higher viral diversity within growing pigs that could potentially be the result of a new introduction or vaccination use.

There are several possible contributing factors that could help explain these results. The lower biosecurity of these types of farms compared to sow-farms could increase this population's vulnerability to new viral introductions. Commingling of animals from different sources could increase the chances of re-infections, co-infections and viral recombination, if more than one virus is present. Vaccination is not an uncommon practice with that population, which can also explain part of the diversity since animals not only become viremic but can also shed vaccine virus. However, before any conclusions may be drawn, further analysis of these results is needed. These findings highlight some of the challenges in understanding PRRSv transmission and evolution, particularly in growing pigs.

Table 1. ORF5 percent nucleotide differences from VR2332 by herd type.

ORF5 difference from VR2332	Herd Type							
	Breeding		Nursery		Wean-to-finish		Finisher	
	n	%	n	%	n	%	n	%
≤ 5%	489	6.7	676	27.2	241	24.3	434	20.5
6-10%	180	2.4	71	2.8	103	10.4	58	2.7
11-15%	6,449	88.1	1,657	66.6	575	58.0	1,581	74.5
> 15%	203	2.8	84	3.4	72	7.3	48	2.3

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