





Detection of PRRSV RFLP type 1-7-4 over time

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Key Points:

- PRRSV RFLP type 1-7-4 was first identified in our MSHMP dataset in 2003.
- An increasing trend up to 2014 has been observed and is now on a decreasing trend.

Restriction fragment length polymorphisms (RFLP) has been extensively used as an approach to diversity classification. Briefly, this technique uses the patterns created by three restriction enzymes (*Mlul*, *Hincll*, and *Sacll*) when cutting the ORF5 region of the viral genome to classify PRRSV strains in a 3-digit RFLP code¹. An RFLP has limitations since it does not accurately determine genetic relatedness of PRRSV², it is still a valuable tool in assessing viral diversity as a first step.

PRRSV RFLP type 1-7-4 has been described as one of the most virulent strains due to its association with high mortality in piglets, severe morbidity in sows, and longer time to reach stability (to wean negative piglets) ^{3,4}. Here, we describe the frequency of PRRSV RFLP type 1-7-4 detection over time among MSHMP participant systems. The MSHMP dataset comprises 23,414 sequences from 1998 to 2018. For this analysis, 4,260 sequences were excluded due to inconsistences in the initial or stop codons in the sequences provided. An additional 19 sequences were excluded due to missing date of collection information. After these exclusions 19,135 sequences were analyzed and the most frequent RFLP pattern identified was 1-7-4 (24.0%), followed by 1-4-4 (20.5%), 2-5-2 (11.2%), 1-4-2 (8.5%), and 1-18-2 (5.7%).

RFLP type 1-7-4 was first identified in our MSHMP dataset in 2003 with an increasing trend up to 2014 (p<0.01). Occurrence peaked in 2015 at 47.7% of all sequences submitted from our MSHMP participants that year. From then on, the 1-7-4 RFLP type has shown a decreasing trend (p<0.01) with an overall detection frequency of 29.6% in 2018.

Location was available for 70.1% of the initial 19,135 sequences. Among those, most of the sequences were submitted from states divided into two regions. Region 1 and 2 comprise 13.3% and 86.7% of the data, respectively. In Region 1, 1-7-4 was first identified in 2008 and its frequency followed the same trend patterns of our overall analysis, increasing until 2014 (p<0.01) and decreasing from 2015 onwards (p<0.01). In Region 2, 1-7-4 was first identified in 2010 showing an increasing trend until 2014 (p<0.01) and a decreasing trend from 2015 onwards (p<0.01). However, the frequency of 1-7-4 in Region 2 has increased during the last year compared with the year before (36.8% in 2017 vs 44.0% in 2018); p<0.01), suggesting that a possible change in the trend might be occurring.

It is important to mention that the MSHMP database represent a proportion of the industry. In addition, available sequences are the reflection of sample collection, diagnostics and sequencing which introduces selection bias.

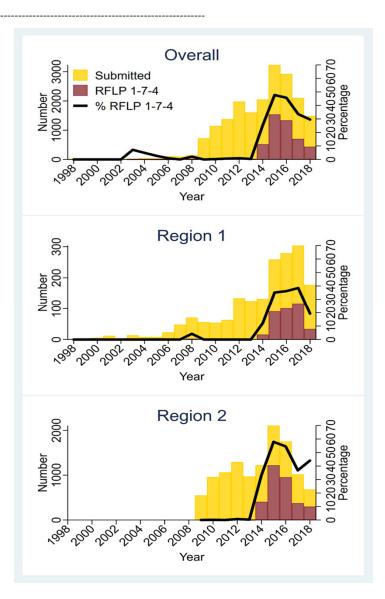


Figure 1. Absolute and relative frequency of PRRSV RFLP type 1-7-4 over time among

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