

## Monitoring the detection of PRRSV variant 1H.18

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Restriction Fragment Length Polymorphism (RFLP) may erroneously group genetically dissimilar PRRS viruses while segregating closely related ones. Phylogenetic methods organize PRRS viruses into ancestral "families," commonly called lineages and sub-lineages, tend to form broad groups. Recognizing the need for a comprehensive fine-scale variant classification system across all sub-lineages, an AASV-funded working group, comprising researchers from UMN, ISU, and USDA, is developing and testing a new variant classification. This variant nomenclature will be used throughout this science page, since lineage/sub-lineage and RFLP (either separately or combined) were not accurate when used as case definition to identify this clade.

In December 2023/January 2024, the increase in occurrence of a novel PRRSV variant came to our attention. Initially, sequences belonging to this group were classified as a somewhat rare RFLP pattern (1-12-2) and were assigned to sub-lineages L1C or L1H, depending on the classification method employed (PRRSView or distance to the nearest reference). When the new variant classification was applied, a clade comprised of sequences positioned between sub-lineages L1H and L1C on the phylogenetic tree was identified. These observations underscore the challenge faced by either RFLPs and sub-lineages in confidently labeling sequences belonging to this group. With a recent influx of sequences belonging to this variant, we have compiled current available data to ensure stakeholders and industry are informed.

A total of 61 sequences belonging to this variant (1H.18) have been identified as of week 19 of 2024 on the MSHMP database, most of them classified as either RFLP 1-8-4 (n=32), 1-12-2 (n=20), or 1-12-1 (n=1). This variant has been identified in nine production systems located mostly in IA (n=23) and MN (n=22), although one sequence was detected in IL. While sporadic detections of the 1H.18 variant date back to 2018 (Figure 1), a slight uptick in cases has been noted since late 2023. Notably, the surge in 1H.18 sequences in 2020 likely went undetected due to all of the sequences at the time being classified as RFLP 1-8-4, a common RFLP type that occurs in many different lineages and sub-lineages, and many of the sequences originated from a single site. The 61 1H.18 sequences originated from 46 unique sites (5 breeding, 10 grow-finish, 11 others, and 20 unknown). The production impact of this variant has not yet been formally assessed, although both mild and more severe clinical presentation have been reported.

**Currently we don't have enough evidence suggesting this variant is of immediate concern to the swine industry, but prospective monitoring is warranted.** Although not comprehensive, the MSHMP provides a representative picture of the situation. Careful consideration when interpreting isolated case reports and sequence counts is necessary, as they may lead to erroneous conclusions due to reporting biases.

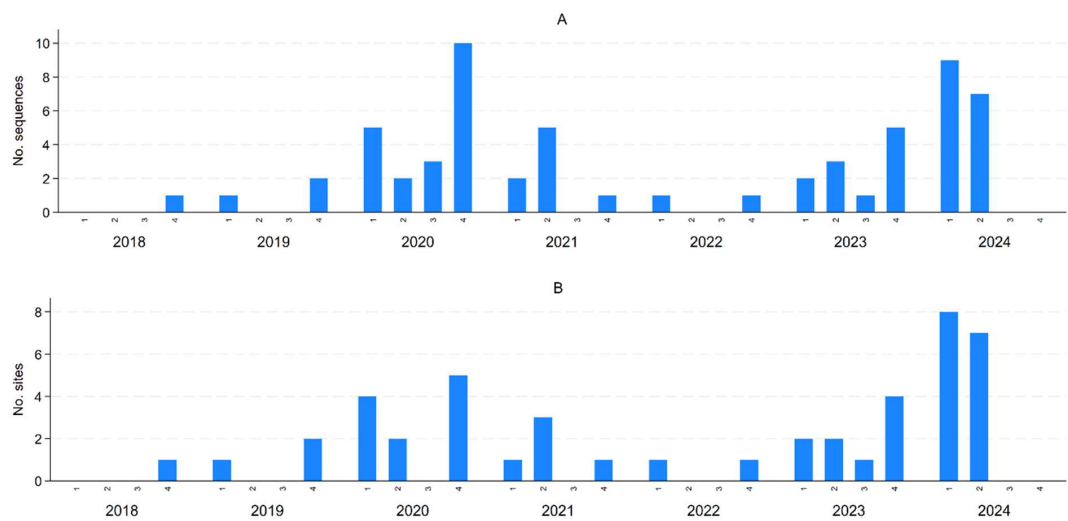


Figure 1. (A) Number of 1H.18 sequences detected by quarter and (B) number of 1H.18 affected sites based on the quarter in which the sequence was first detected on each farm.

**MSHMP will continue to prospectively monitor this variant, and additional reports will be issued as the situation unfolds.** Don't hesitate in contacting MSHMP in case you have questions.