

PRRSV2 1C.5

Situation Report of PRRSV Variant 1C.5, August 10, 2026

VUM: Category 3

PRRSV variant 1C.5, typically linked to RFLP pattern 1-4-4, has been demoted to a variant under monitoring (VUM) Category 3 on August 2026. VUM Category 3 are those with predicted growth in the next 12 months and with 51-100 new sites affected in the past 6 months. Current evidence suggests this variant continues widespread in several U.S. states. PRRSV 1C.5 was first detected in 2018, based on the MSHMP sequence dataset. This PRRSV2 variant belongs to Lineage 1C. Studies suggests this variant is a descendant of a recombinant ancestor characterized by recombination at the ORF1a gene between two segments that would be otherwise classified as L1C and L1A in the ORF5 gene (Pamornchainavakul et al., 2022).

[Click here](#) to access monthly epidemiological updates on PRRSV variants under monitoring.

Indicator	Evidence
Populational growth	This variant has been consistently circulating across multiple production systems since 2020, with a notable increase in the number of affected sites observed in spring 2021 and winter 2022. Initial descriptions in early 2021 reported this as a regional outbreak affecting primarily the Midwest (Kikuti et al., 2021). As of August 2026, over 3900 sequences have been identified, linked to over 1100 unique sites across 32 production systems in 13 states. Research suggests its rapid spread was likely driven by a low infectious dose and high viral shedding rather than superior airborne stability compared to other variants (Torremorell et.al, 2025. As of November 2025, cumulative detection of this variant amonsgt VDL submitted samples in 2025 surpassed previous years detections (SRDS, 2025). This variant has been detected primarily in growing pig herds and the two most affected states continues to be Iowa and Minnesota.
Production impact/severity	PRRSV variant 1C.5 initial epidemiological investigations showed higher finishing mortality compared to sites affected by other PRRSV variants (Kikuti et al., 2021). Experimental studies also showed this variant to be highly virulent and infectious, causing higher mortality and more severe symptoms (Rawal et al., 2023; Melini et al., 2025). Veterinarians reported a sharp increase in abortion, sow mortality, and piglet mortality in both the farrowing and nursery phases, while average daily gain dropped significantly in finishing pigs (AASV, 2021). Studies also suggest that certain -1 programmed ribosome frameshift (PRF) stop codon patterns, which were identified as predominantly circulating in the field, may provide enhanced growth fitness for the virus (Yan et al., 2022).

Nucleotide similarity to vaccines

The following summarizes median nucleotide percent identity between all non-identical 1C.5 sequences captured through MSHMP up to date and commercially available PRRSV2 vaccines.

Ingelvac ATP
 85.4%
Prime Pac
 86.6%

Ingelvac MLV
 86.2%
Prevacent
 88.9%

Fostera
 86.2%
PRRSGard
 88.4%

Disclaimer

Diagnostic data should be interpreted with caution because surveillance efforts vary between production systems and phase of production. Variant classifications, based on predefined criteria, are meant to inform industry-wide discussions, not to replace specific on-farm risk assessments or expert advice. This information is compiled from publicly available publications that either use recent variant nomenclature or can be verified as referencing this specific variant. Consequently, the data may not be entirely comprehensive. It is important to note that confirmatory studies and their findings often take time to be published, and some variants may not yet have generated sufficient reporting on their impact.

References

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Suggested citation

National Surveillance Report. PRRSV Variants Under Monitoring Situation Report of PRRSV Variant 1C.5, August 2026 [Internet]. Available from: <https://mshmp.umn.edu/PRRS-variant-monitoring>