PRRSV2 1C.5.32

Situation Report of PRRSV Variant 1C.5.32, August 19, 2025

VUM: Category 4

PRRSV variant 1C.5.32, typically linked to RFLP pattern 1-4-4, has been designated a variant under monitoring (VUM)category 4 on August 2025.VUM category 4 are those with predicted growth in the next 12 months and with >100 new sites affected by this variat in the past 6 months. Current evidence suggests this variant is widespread in several U.S. states. PRRSV 1C.5.32 was first detected in 2023, based on the MSHMP sequence dataset. This PRRSV-2 variant belongs to Lineage 1C and emerged from a split of variant 1C.5 in early 2025 (PRRS-Loom, 2025).

Click here to access monthly epidemiological updates on PRRSV variants under monitoring.

Indicator	Evidence
Populational growth	Variant 1C.5.32 was first brought to attention in January 2025, when increased sequence-level detection of a subclade of variant 1C.5 was detected (Swine Health Information Center, 2025). This led to seven genetically distinct sub-groups receiving new variant IDs (PRRS-Loom, 2025). Initial investigations suggested a regional outbreak in Iowa (Swine Health Information Center, 2025). This variant has been consistently circulating across multiple production systems since late 2023, with a notable increase in the number of affected sites observed in spring 2024 and spring 2025. As of August 2025, over 1500 sequences have been identified, linked to over 700 unique sites across 22 production systems in 10 states. This variant has been most frequently detected in growing pig herds in Iowa and Minnesota. As of May 2025, this variant has been reported as the most predominant amongst PRRSV OF5 sequencing submissions (SDRS, 2025).
Production impact/severity	No systematic data analysis is available to date descibing this variant's impact in production parameters and diseases severity, particularly in contrast to other known variants. Initial investigations suggests that Ct values of samples submitted for diagnosis averages 16.8 for lung and 27.9 for oral fluid, which are generally lower than observed for submitted samples of PRRSV Lineage 1A (Swine Health Information Center, 2025).

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

Swine Health Information Center. SHIC Monitoring Emerging PRRSV-2 Lineage 1C.5 Clonally Expanded Clade [Internet]. 2025. Available from: https://www.swinehealth.org/shic-monitoring-emerging-prrsv-2-lineage-1c-5-clonally-expanded-clade/

PRRS-Loom. PRRSV-2 Lineage-Variant Nomenclature: March 6, 2025 Update [Internet]. 2025. Available from: https://stemma.shinyapps.io/PRRSLoom-variants/

SDRS. Swine Disease Reporting System Report #87 (May 06, 2025). 2025. Available from: https://www.swinehealth.org/wp-content/uploads/2025/05/SDRS-report-87.pdf

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