

January 2026 Report

About the project

Variants of PRRSV continue to emerge, causing issues for the industry. To support proactive decision-making, we developed a national surveillance report designed to identify and communicate variants showing signs of wider spread, which we refer to as Variants Under Monitoring (VUMs). Our approach employs [PRRS-Loom](#) variant classifications for ORF5 sequences alongside with an algorithm that predicts which variants are likely to expand over the next 12 months (defined as an anticipated increase of >20% based on sequence counts). These predictions are combined with near-real-time national data from the [Morrison Swine Health Monitoring Project \(MSHMP\)](#) to track the number of currently affected sites. This project provides several key benefits, including proactive monitoring of circulating variants, enhanced situational awareness for stakeholders, and the promotion of faster, more coordinated responses to emerging threats.

What are PRRSV variants and VUMs

PRRSV variants are groups of viruses that are closely related based on their ORF5 gene. Viruses within the same variant typically differ by less than 2.5% from one another and by less than 5% from the nearest related variant ([click here](#) to find more about PRRSV variants). Variants under monitoring (VUMs) are PRRSV-2 variants currently circulating in the U.S. that, based on genetic and epidemiological data, are predicted to have potential for widespread transmission. The prediction algorithm, developed using retrospective data, leverages early indicators to forecast increases in variant sequencing within the following year, with an accuracy of 77% ([Pamornchainavakul et al., 2024](#)). Sites affected by each VUM are identified through MSHMP by linking genetic sequences to their corresponding Premises ID. VUMs are further classified into four categories based on the number of new sites affected over the past six months. Variants that do not show sequence-based potential for widespread transmission are not considered variants under monitoring (VUM).

Summary of Variants Under Monitoring (VUMs) as of January 13, 2026

This month's report identified the following number of VUMs in each category:

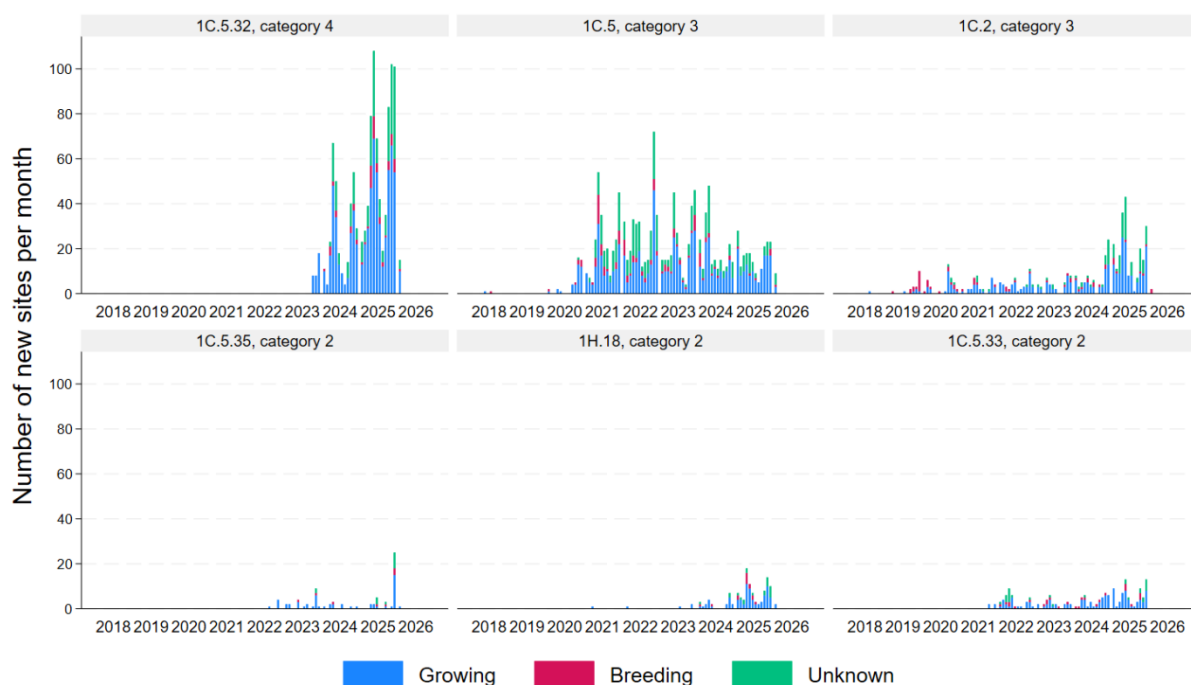
PRRSV variant class	Predicted growth in next 12 months	Number new sites in past 6 months	Number of variants	Percent sequences in past 6 months
No enhanced monitoring	Low	-	168	53
VUM Category 1	High	<=30	16	1
VUM Category 2	High	31-50	3	2
VUM Category 3	High	51-100	2	16
VUM Category 4	High	>100	1	28

Six PRRSV variants are classified as Variants Under Monitoring (VUMs) category 2 or higher and are described in this month's report: Variants 1C.5.32 remains a VUM Category 4, 1C.2 and 1C.5 remains VUM Category 3, 1H.18 remains VUM category 2, 1C.5.32 and 1C.5.35 were promoted to VUM category 2 from a previous category 1 status (this change is reflected in a new variant-specific situation report). Previous reports for all variants ever classified as VUM Category 2 or higher remain available.

Currently circulating PRRSV variants under monitoring (VUMs) as of January 13, 2026

The table and epidemiological curves below bring additional information on currently circulating VUMs that are category 2 or higher. Epidemiologic curves show the weekly number of new sites (including breeding and growing sites) affected by each variant, based on unique Premises ID.

Variant	VUM category	Total sequences	Total sites	Total new sites in previous 6 months	Total systems	Total states	States in which circulation was detected
1C.5.32	4	2317	1112	355	22	11	IA IL KS MI MN MO OH OK SD TX WI
1C.5	3	3716	1368	96	32	13	IA IL IN KS MN MO NE OH OK PA SC SD WI
1C.2	3	1286	529	80	26	14	AR CO IA IL KS MN MO NC ND NE OH OK SD TX
1H.18	2	353	139	40	15	6	IA IL IN MN OH PA
1C.5.35	2	260	110	40	15	8	IA IL IN MN MO OH PA SD
1C.5.33	2	533	202	31	20	7	AR CO IA IN MN NE SD



VUMs Situation Reports

Situation reports describing existing scientific evidence and field reports on production impact/severity are provided for each VUM category 2 or higher. Information is gathered when a variant is first listed as a VUM category 2 or higher and updated as new information becomes available.

[Situation Report of PRRSV Variant 1C.5.35, January 2026](#)

[Situation Report of PRRSV Variant 1C.5.33, January 2026](#)

[Situation Report of PRRSV Variant 1C.5.32, January 2026](#)

[Situation Report of PRRSV Variant 1C.5, January 2026](#)

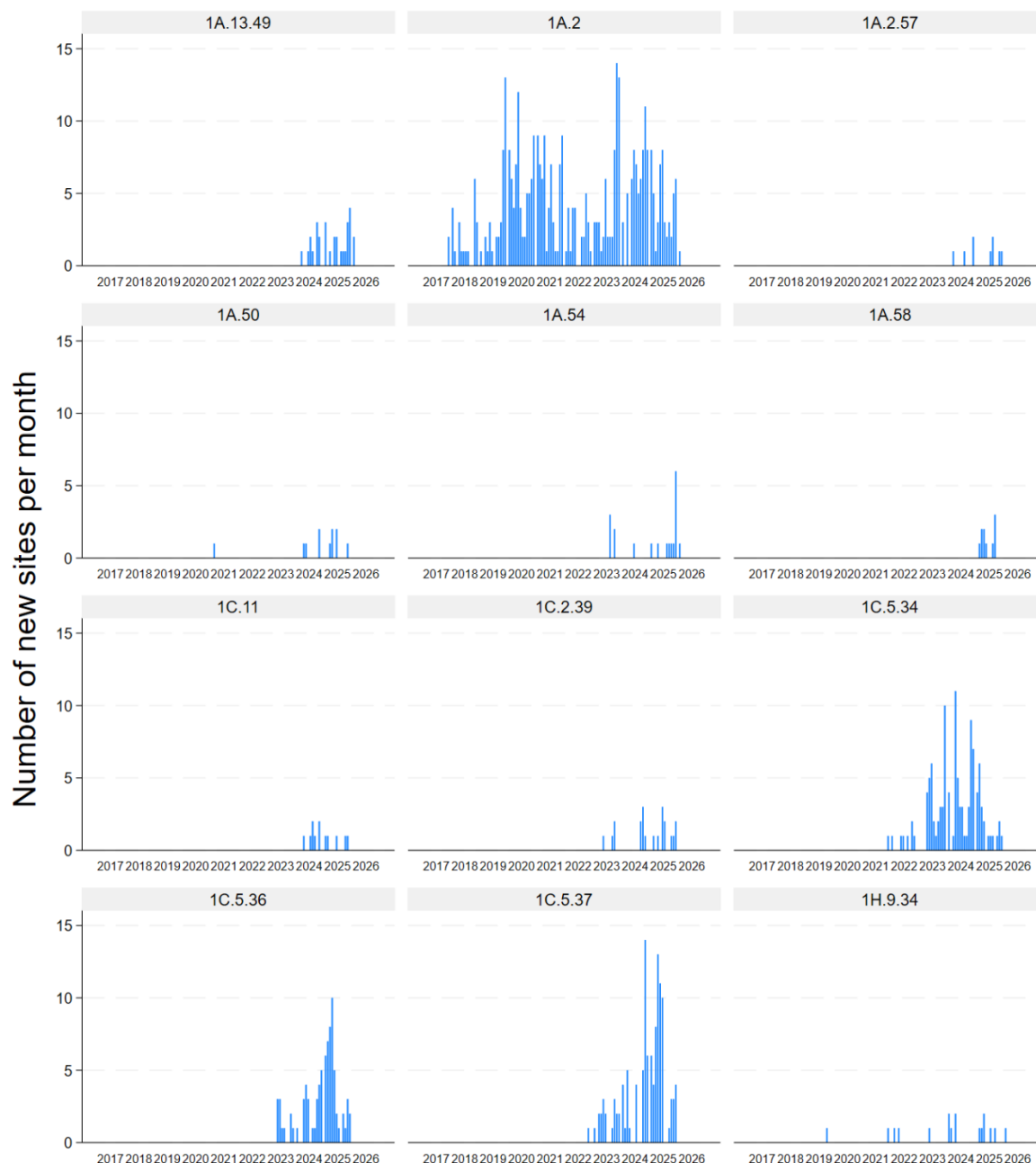
[Situation Report of PRRSV Variant 1H.18, December 2025](#)

[Situation Report of PRRSV Variant 1C.2, October 2025](#)

[Situation Report of PRRSV Variant 1C.5.37, October 2025](#)

Category 1 Variants Under Monitoring (VUMs) as of January 13, 2026

Epidemiologic curves below show the weekly number of new sites affected by all VUMs category 1 (i.e., flagged by the sequence-level model for predicted growth potential with low number of new sites affected in the previous six months) as of January 2026.



The figure consists of three bar charts, each representing a different scenario. The y-axis for all charts is 'Number of new sites per month', ranging from 0 to 15. The x-axis shows the years 2023, 2024, and 2025.

- Scenario 1A (1A.2.56):** Shows a significant number of new sites in early 2024, peaking at approximately 4 sites in March. There are also smaller peaks in early 2023 and early 2025.
- Scenario 1E (1E.5):** Shows a small number of new sites in early 2023, peaking at approximately 1 site in January. There are no new sites in 2024 or 2025.
- Scenario 1H (1H.9.51):** Shows a small number of new sites in early 2024, peaking at approximately 2 sites in January. There are no new sites in 2023 or 2025.

General disclaimers

The information presented in this report is based on data shared voluntarily by MSHMP-participating systems and diagnostic laboratories. While efforts have been made to ensure accuracy and timeliness, findings may be subject to reporting delays, variability in sampling strategies, and limitations inherent to diagnostic testing and sequencing. VUM categories are based on MSHMP data, which, while broadly representative of the U.S. swine industry, are not comprehensive. Interpretation of diagnostic laboratory data for pathogen detection should be made with caution, as surveillance efforts differ between breeding and growing sites, with greater sampling effort typically focused on breeding herds. Designations such as Variants Under Monitoring (VUMs) and their assigned categories are intended to support situational awareness and facilitate informed discussions among veterinarians, producers, researchers, and other stakeholders. They do not constitute definitive assessments of risk at the farm level and should not replace site-specific diagnostics, expert consultation, or context-specific decision-making.

Project Team and Institutional Affiliations

This report was developed by a collaborative team of researchers at the University of Minnesota, including [Dr. Mariana Kikuti](#), [Dr. Cesar Corzo](#), [Dr. Kimberly VanderWaal](#), [Dr. Igor Paploski](#), and Dr. Nakarin Pamornchainavakul. It builds upon two key initiatives: the [Morrison Swine Health Monitoring Project \(MSHMP\)](#), which provides ongoing monitoring data across U.S. swine production systems, and [PRRS-Loom](#), a platform for PRRSV-2 variant classification and early trend detection.

Suggested citation

National Surveillance Report PRRSV Variants Under Monitoring, January 2026 [Internet]. 2025. Available from: <https://mshmp.umn.edu/PRRS-variant-monitoring>

References and related sources

[Morrison Swine Health Monitoring Project](#)

[PRRSloom-Variants](#)

VanderWaal K, Pamornchainavakul N, Kikuti M, Zhang J, Zeller M, Trevisan G, Rossow S, Schwartz M, Linhares DCL, Holtkamp DJ, da Silva JPH, Corzo CA, Baker JP, Anderson TK, Makau DN, Paploski IAD. PRRSV-2 variant classification: a dynamic nomenclature for enhanced monitoring and surveillance. mSphere 0:e00709-24. <https://doi.org/10.1128/msphere.00709-24>

Pamornchainavakul N, Kikuti M, Paploski IAD, Corzo CA, Vanderwaal K. Predicting Potential PRRSV-2 Variant Emergence through Phylogenetic Inference. Transboundary And Emerging Diseases, v. 2024, p. 1-15, 2024. <https://doi.org/10.1155/2024/7945955>