

## PRRSV2 1C.2.45

### Situation Report of PRRSV Variant 1C.2.45, August 10, 2026

#### VUM: Category 1

PRRSV variant 1C.2.45, typically linked to RFLP pattern 1-2-4, has been classified as a variant under monitoring (VUM) Category 1 on August 2026. VUM Category 1 are those with predicted growth in the next 12 months and with <31 new sites affected in the past 6 months. This PRRSV-2 variant belongs to Lineage 1C and emerged from a split of variant 1C.2 in May 2026 (PRRS-Loom, 2026). Current evidence suggests variant 1C.2.45 is widespread in multiple U.S. production systems since it was first detected in 2022, based on the MSHMP sequence dataset.

[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 2022. A recent increase in cases was detected in early 2026. As of August 2026, over 290 sequences have been identified, linked to over 70 unique sites across 14 production systems in 6 states. This variant has been detected at similar frequencies in both breeding and growing pig herds, and the two most affected states are Iowa and North Carolina. |
| Production impact/severity | There are no reported or published studies on the impact of 1C.2.45 on clinical and production outcomes to date.                                                                                                                                                                                                                                                                                                                                      |

#### Nucleotide similarity to vaccines

The following summarizes median nucleotide percent identity between all non-identical 1C.2.45 sequences captured through MSHMP up to date and commercially available PRRSV2 vaccines.

Ingelvac ATP  
83.4%  
Prime Pac  
84.4%

Ingelvac MLV  
84.4%  
Prevacent  
86.4%

Fostera  
84.2%  
PRRSGard  
86.2%

#### 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

PRRS-Loom. PRRSV-2 Lineage-Variant Nomenclature: May 5, 2026 Update [Internet]. 2026. Available from: <https://stemma.shinyapps.io/PRRSloom-variants/>

