# Swine Disease Reporting System
# Report # 98 (April 07, 2026)

**What is the Swine Disease Reporting System (SDRS)?** SDRS includes multiple projects that aggregate data from participating veterinary diagnostic laboratories (VDLs) in the United States of America, and reports the major findings to the swine industry. Our goal is to share information on activity of endemic and emerging diseases affecting the swine population in the USA, assisting veterinarians and producers in making informed decisions on disease prevention, detection, and management.

After aggregating information from participating VDLs and summarizing the data, we ask for the input of our advisory group, which consists of veterinarians and producers across the US swine industry. The intent is to provide an interpretation of the observed data, and summarize the implications to the industry. Major findings are also discussed in monthly podcasts. All SDRS reports and podcasts are available at https://fieldepi.org/sdrs/.

**Swine Health Information Center (SHIC)-funded Domestic Swine Disease Surveillance Program:** collaborative project among multiple VDLs, with the goal to aggregate swine diagnostic data and report it in an intuitive format, describing dynamics of pathogen detection by PCR-based assays over time, specimen, age group, and geographical area. Data is from the Iowa State University VDL, South Dakota State University ADRDL, University of Minnesota VDL, Kansas State VDL, Ohio ADDL, and Purdue ADDL.

**Collaborators:**

*Swine Disease Reporting System office*: Principal investigators: Daniel Linhares & Giovani Trevisan; Project coordinator: Quyen Thuc Le; Software Developer: Kinath Rupasinghe; Data Analyst: Sajan Kumar Thallapelly and Likhitha Nakka.

*Iowa State Uni.*: Gustavo Silva, Marcelo Almeida, Bret Crim, Eric Burrough, Phillip Gauger, Christopher Rademacher, Darin Madson, Michael Zeller, Rodger Main.

*Uni. of Minnesota*: Cesar Corzo, Albert Rovira, Matt Sturos, Hemant Naikare.

*Kansas State Uni.* and Kansas Dept. of Agr.: Rob McGaughey, Franco Matias-Ferreyra, Jamie Retallick, Jordan Gebhardt, Sara McReynolds.

*South Dakota State Uni* and South Dakota AIB: Jon Greseth, Darren Kersey, Travis Clement, Angela Pillatzki, Jane Christopher-Hennings, Eric Nelson, Mendel Miller and Marc Hammrich.

*Ohio Animal Disease and Diag. Lab.* and *The Ohio State Uni*: Melanie Prarat, Dennis Summers, Andréia Arruda.

*Purdue Uni* and *Indiana State BOAH*: Craig Bowen, Kenitra Hendrix, Joseph Boyle, James Lyons, Kelli Werling.

**Disease Diagnosis System**: Consisting of reporting disease diagnosis (not just pathogen detection by PCR), based on diagnostic codes assigned by veterinary diagnosticians from ISU-VDL and OH-ADDL.

PRRSView and FLUture and : Aggregates PRRSV and influenza A virus diagnostic data from the ISU-VDL. PRRSLoom-Variants: PRRSV-2 variant classification from UMN.

PRRS virus Genotyping report and BLAST tool: Benchmark PRRSV ORF5 sequences and compare your PRRSV sequence with what have been detected in the U.S.

**Audio and video reports:** Key findings from SDRS projects are summarized monthly in a conversation between investigators and is available in the Spotify, Apple Podcast, YouTube, LinkedIn, and the SDRS webpage. In addition to this report, interactive dashboards and educational material are publicly available.

**Advisory Group:** Mark Schwartz, Megan Niederwerder, Paul Yeske, Deborah Murray, Brigitte Davenport, Peter Schneider, Sam Copeland, Luc Dufresne, Daniel Boykin, Corrine Fruge, William Hollis, Rebecca Robbins, Thomas Petznick, Kurt Kuecker, Lauren Glowzenski, Brooke Kitting and Dustin Oedekoven.

**Note:** This report contains data up to March 31, 2026.

# Topic 1 – Detection of PRRSV RNA over time by RT-qPCR.

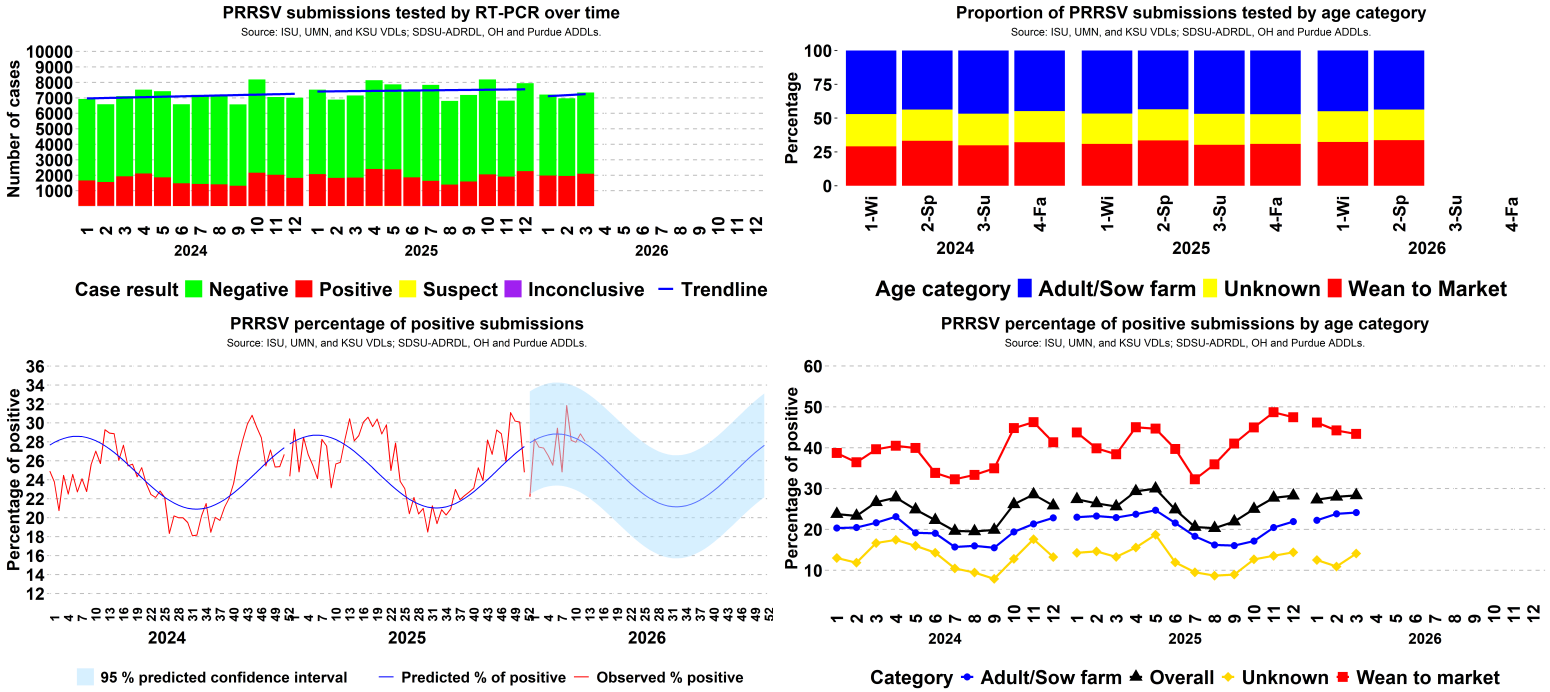
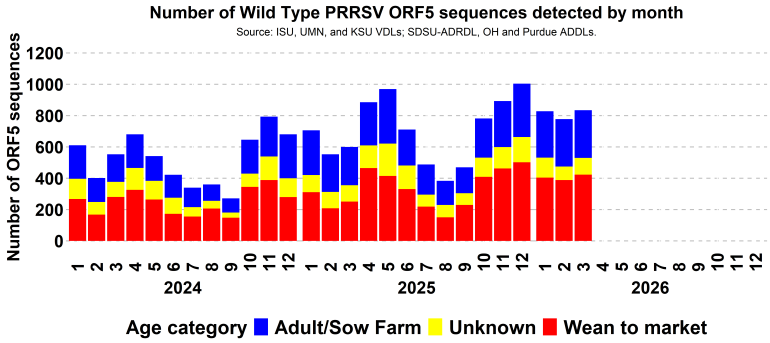


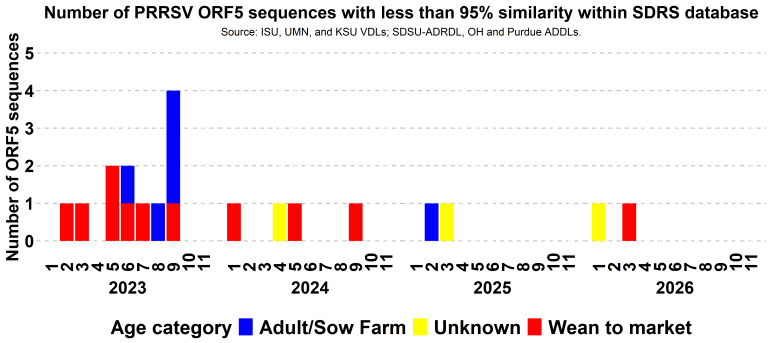

**Figure 1. Top**: *Left*: Results of PRRSV RT-PCR cases over time; *Right*: Proportion of accession ID cases tested for PRRSV by age group per year and season. **Bottom**: *Left* Expected percentage of positive results for PRRSV RNA by RT-qPCR, with 95% confidence interval band for predicted results based on weekly data observed in the previous 4 years; *Right*: Percentage of PRRSV PCR-positive results, by age category, over time. Wean to market corresponds to nursery and grow-finish. Adult/Sow correspond to Adult, boar stud, breeding herd, replacement, and suckling piglets. Unknown corresponds to not informed site type or farm category.

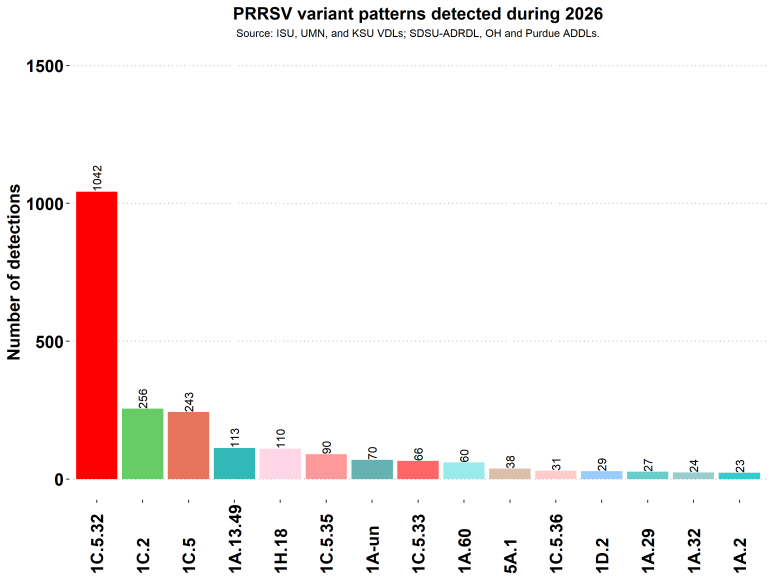
## SDRS Advisory Group highlights:

- Overall, 28.35% of 7,350 cases tested PRRSV-positive in March, similar to 27.99% of 6,971 in February.
  - Positivity in the adult/sow category in March was 24.16% (776 of 3,212), similar to 23.84% (748 of 3,137) in February.
  - Positivity in the wean-to-market category in March was 43.37% (1,073 of 2,474), similar to 44.22% (1,041 of 2,354) in February.
  - Overall PRRSV-percentage of positive cases was 3 standard deviations above state-specific baseline in IA, IL and NC.

# Topic 1.1 – PRRSV ORF5 sequences detection over time




**Most frequent PRRSV variants detected across U.S. states in 2026**

Source: ISU, UMN, and KSU VDLs; SDSU-ADRDL, OH and Purdue ADDLs.

| SiteState | First Most Frequent | Second Most Frequent | Third Most Frequent |
|---|---|---|---|
| IA | 1C.5.32 - 676 | 1C.5 - 149 | 1C.2 - 118 |
| IL | 1C.5.32 - 125 | 1C.5.35 - 8 | 1A.5 - 6 |
| IN | 1C.5.35 - 35 | 1A.54 - 11 | 1C.5 - 11 |
| KS | 1A.58 - 2 | 1C.5.32 - 1 | 1H.28 - 1 |
| MN | 1C.5.32 - 125 | 1H.18 - 38 | 1A.13.49 - 11 |
| MO | 1C.5.32 - 50 | 1C.5 - 39 | 1C.2 - 7 |
| NC | 1C.2 - 93 | 1A-un - 48 | 1A.60 - 34 |
| NE | 1C.5.33 - 44 | 1C.5 - 19 | 1A.2 - 10 |
| OH | 1C.5.35 - 39 | 1C.5.32 - 21 | 1C.5 - 5 |
| OK | 1C.5.32 - 10 | 1A.2 - 2 | 1E.1 - 2 |
| SD | 1C.2 - 10 | 1A.13.49 - 7 | 1C.5 - 3 |

**Figure 1. Top**: **Left**: Number of PRRSV ORF5 sequences detected by age category; **Right**: Number of PRRSV ORF5 sequences with less than 95% similarity after BLAST analysis with the sequences in the SDRS database (Sequences with more than 6 ambiguities, sequences with less than 597 nucleotides or higher than 606 nucleotides are not included in this analysis); **Bottom** *Left*: 15 PRRSV ORF5 sequences most frequent detected by variant; *Right*: Most frequently detected PRRSV ORF5 sequences in 2026, shown by variant at the U.S. state level along with their respective detection counts **Note: un indicates unclassified**.

### SDRS Advisory Group highlights:

- During March, the states with higher number of PRRSV 1C.5.32 detections were detected in IA, IL, MN, MO, IN, OK, NC, OH, NE (respective number of sequences: 245, 62, 36, 20, 6, 6, 4, 3, 1);
- In March, 1C.5.32 (385) was the PRRSV variant most detected in the U.S., followed by 1C.5 (82), and 1C.2 (80);
- SDRS database identified first-time detection of PRRSV variants according to provided site state:
  - February 2026: 1A.13.49 (KY, TN), 1A.5 (MO), 1C.5.33 (ID), 1C.2.39 (MN), and 1C.5.32 (MI)
  - March 2026: 1C.2 (NV, VA), 1A.13.49 (NE, MO), 1C.2.39 (NE, OK), and 1C.5.35 (MI)
- Some of the Advisors noted that both the 1C.2 and 1A.13.49 variants have been associated with significant morbidity and mortality, though not to the same severity as variant 1C.5.32. However, there has been a notable uptick in cases linked to variant 1A.13.49;
- Click on the links below to access the PRRSV genotype dashboard and the SDRS BLAST tool to compare your PRRSV ORF5 sequence with the SDRS database.

# Topic 2 – Enteric coronavirus RNA detection by RT-qPCR

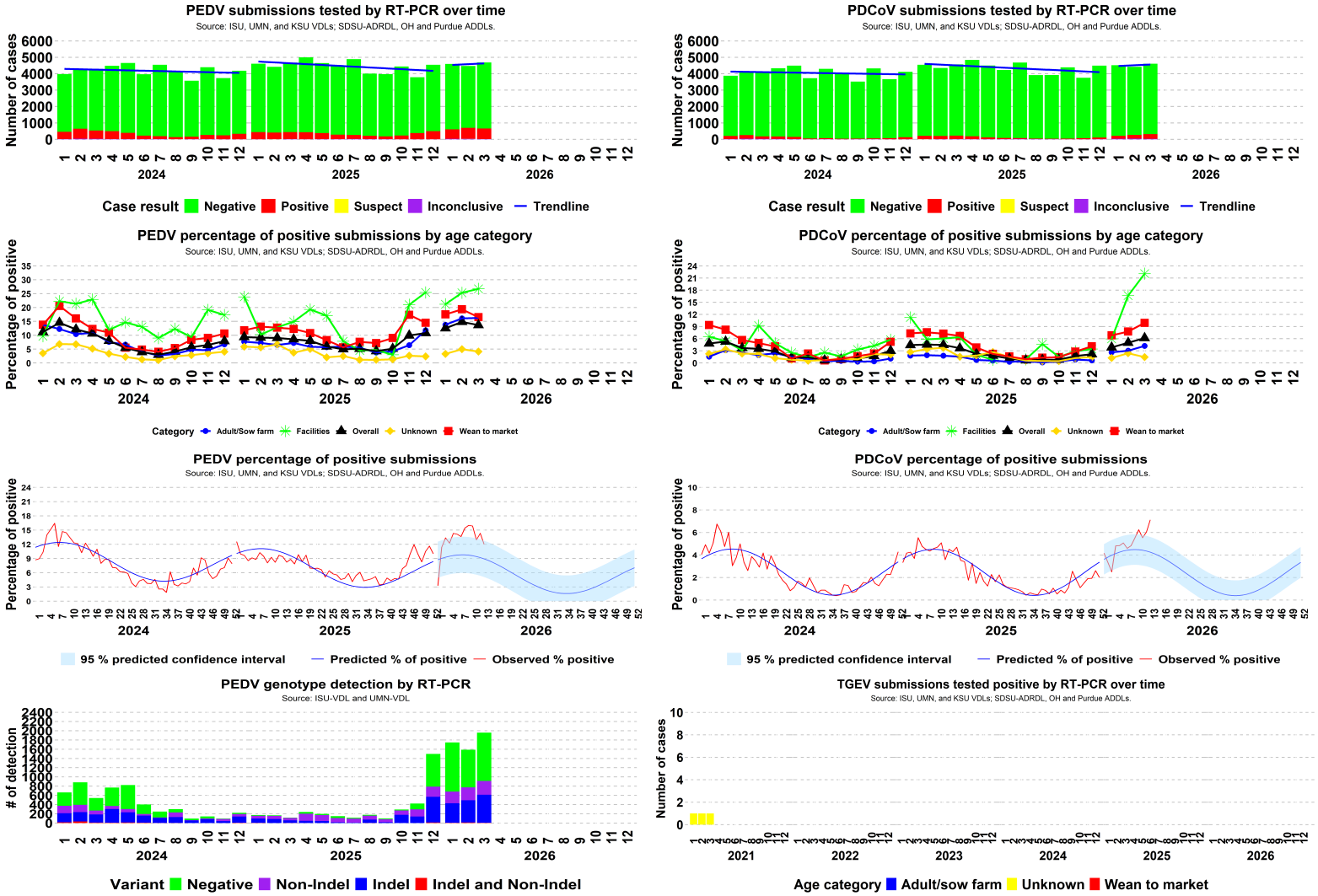



**Figure 1. Top**: Left PEDV; Right PDCoV cases tested by RT-PCR over time. Second from top: Left PEDV; Right PDCoV percentage of positive RT-PCR results by age category. Third from top: Left PEDV; Right PDCoV expected percentage of positives with 95% CI for 2026 prediction. Bottom: Left PEDV genotype detection over time; Right TGEV positive cases by age category.

### SDRS Advisory Group highlights:

- Overall, 13.65% of 4,687 cases tested PEDV-positive in March, similar to 14.84% of 4,475 in February.
  - Positivity in the adult/sow category in March was 16.25% (276 of 1,698), similar to 16.08% (269 of 1,673) in February.
  - Positivity in the wean-to-market category in March was 16.52% (269 of 1,628), a moderate decrease from 19.36% (303 of 1,565) in February.
  - Positivity in the facilities category in March was 26.74% (46 of 172), similar to 25.33% (38 of 150) in February.
  - Overall PEDV-percentage of positive cases was 3 standard deviations above state-specific baseline in IL.
  - Overall, 0.26% of 1,959 samples had mixed PEDV genotype detection in March, similar to 0.75% of 1,590 in February.
- Overall, 6.16% of 4,611 cases tested PDCoV-positive in March, similar to 5.02% of 4,424 in February.
  - Positivity in the adult/sow category in March was 4.22% (71 of 1,681), similar to 3.05% (50 of 1,642) in February.
  - Positivity in the wean-to-market category in March was 9.92% (158 of 1,593), a moderate increase from 7.78% (121 of 1,556) in February.
  - Positivity in the facilities category in March was 22.09% (38 of 172), a substantial increase from 16.67% (25 of 150) in February.
  - Overall PDCoV-percentage of positive cases was 3 standard deviations above state-specific baseline in IL.
- There was 0 positive case for TGEV RNA-PCR in March, 2026 over a total of 4,439 cases tested. It has been 60 months (with a total of 229,501 cases tested) since the last TGEV PCR-positive result.

# Topic 3 – Detection of *M. hyopneumoniae* DNA by PCR.

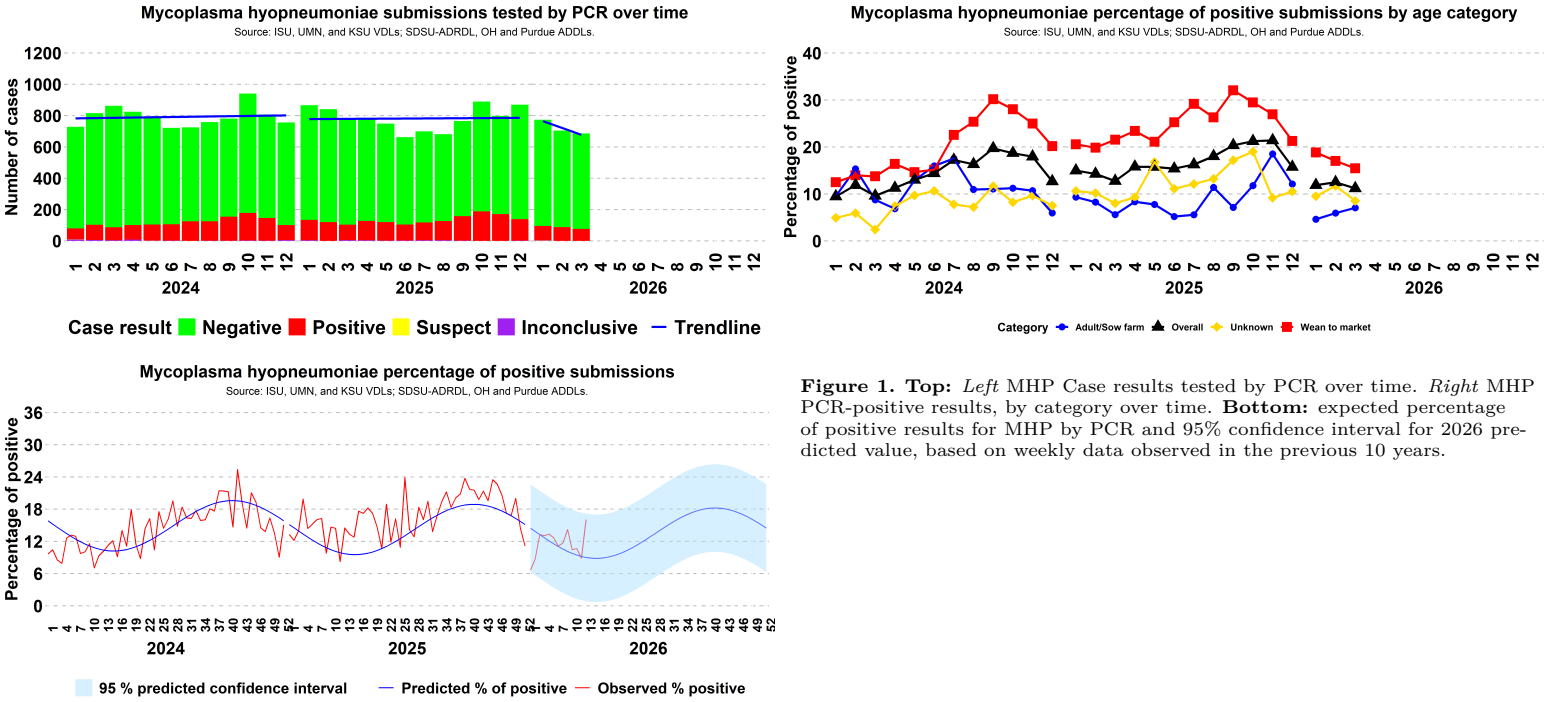
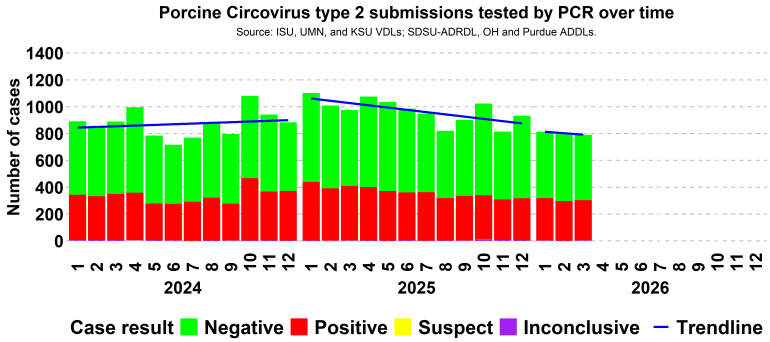


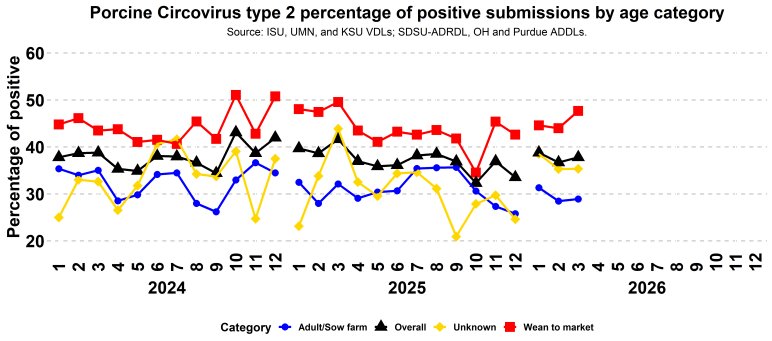

**Figure 1. Top:** *Left* MHP Case results tested by PCR over time. *Right* MHP PCR-positive results, by category over time. **Bottom:** expected percentage of positive results for MHP by PCR and 95% confidence interval for 2026 predicted value, based on weekly data observed in the previous 10 years.

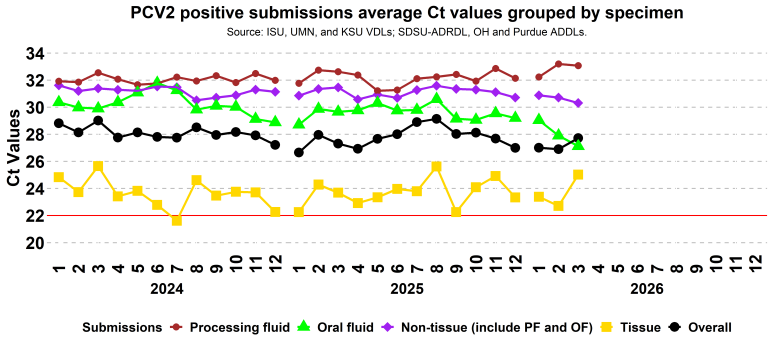
### SDRS Advisory Group highlights:

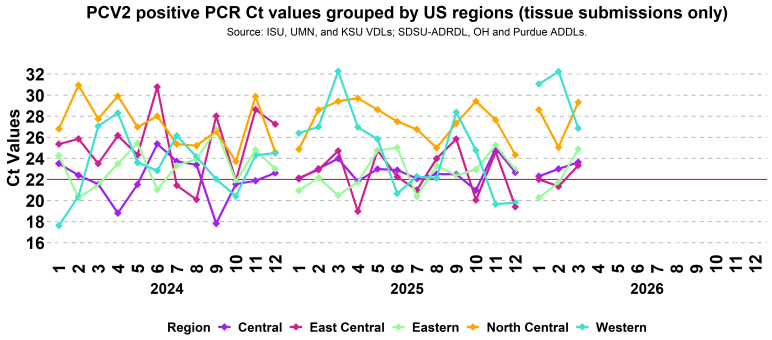
- Overall, 11.21% of 687 cases tested *M. hyopneumoniae*-positive in March, similar to 12.48% of 705 in February.
  - Positivity in the adult/sow category in March was 7.05% (17 of 241), similar to 5.93% (14 of 236) in February.
  - Positivity in the wean-to-market category in March was 15.46% (49 of 317), similar to 17.04% (61 of 358) in February.
  - Overall MHP-percentage of positive cases was within state-specific baselines in all 11 monitored states.

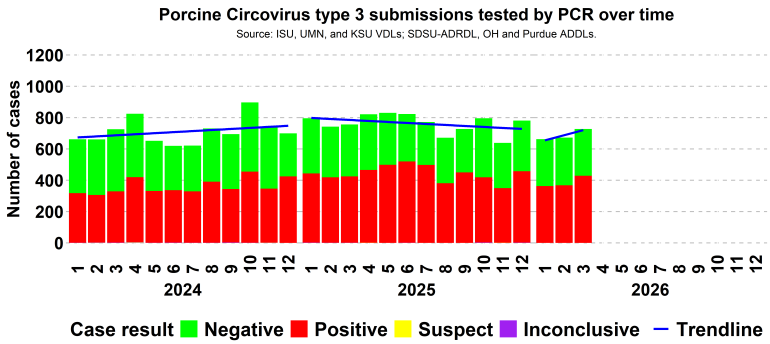
# Topic 4 – Detection of Porcine Circoviruses type 2 and 3 DNA by PCR.



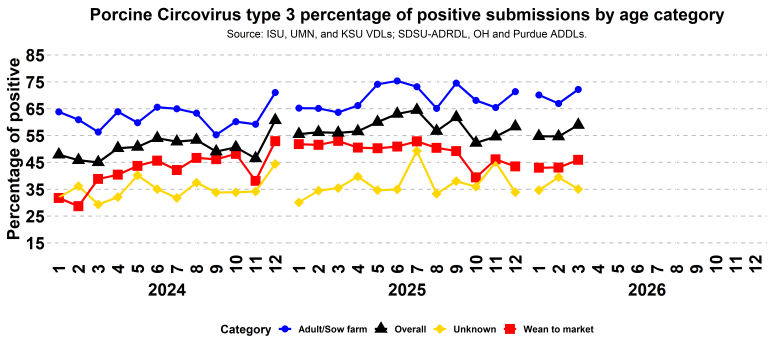




**Figure 1. Top**: *Left*: Results of PCV2 PCR cases over time; *Right*: PCV2 PCR-positive results, by category over time. **Middle**: *Left*: Average Ct values of PCV2 submissions by specimen; *Right*: Average Ct values of PCV2 tissue submissions by U.S. region; Central (IA), East Central (IL, IN, MO and WI), Eastern (AL, AR, CT, DE, FL, GA, KY, LA, MA, ME, MD, MI, MS, NC, NH, NJ, NY, OH, PA, RI, SC, TN VA, VT and WA), North Central (MN, ND and SD), Western (AK, AZ, CA, CO, HI, ID, KS, MT, NM, NV, OK, OR, TX, UT, WA and WY). Red line represent Ct threshold calculated using methodology based on Dx codes. **Bottom** *Left*: Results of PCV3 PCR cases over time; *Right*: PCV3 PCR-positive results, by category over time.

### SDRS Advisory Group highlights:

- Overall, 37.8% of 791 cases tested PCV2-positive in March, similar to 36.72% of 806 in February.
  - Positivity in the adult/sow category in March was 28.93% (105 of 363), similar to 28.48% (94 of 330) in February.
  - Positivity in the wean-to-market category in March was 47.69% (165 of 346), a moderate increase from 43.99% (172 of 391) in February.
  - In the month of March, the regions with the lowest PCV2 average Ct values in tissue submissions were East Central (18 submissions; average Ct 23.3), Central (46 submissions; average Ct 23.6), Eastern (21 submissions; average Ct 24.9), Western (10 submissions; average Ct 26.9), and North Central (31 submissions; average Ct 29.3).
- Overall, 58.93% of 728 cases tested PCV3-positive in March, a moderate increase from 54.68% of 673 in February.
  - Positivity in the adult/sow category in March was 72.19% (283 of 392), a substantial increase from 66.96% (227 of 339) in February.
  - Positivity in the wean-to-market category in March was 45.95% (119 of 259), a moderate increase from 43.08% (109 of 253) in February.

# Topic 5 – Detection of Influenza A Virus (IAV) RNA by RT-PCR.

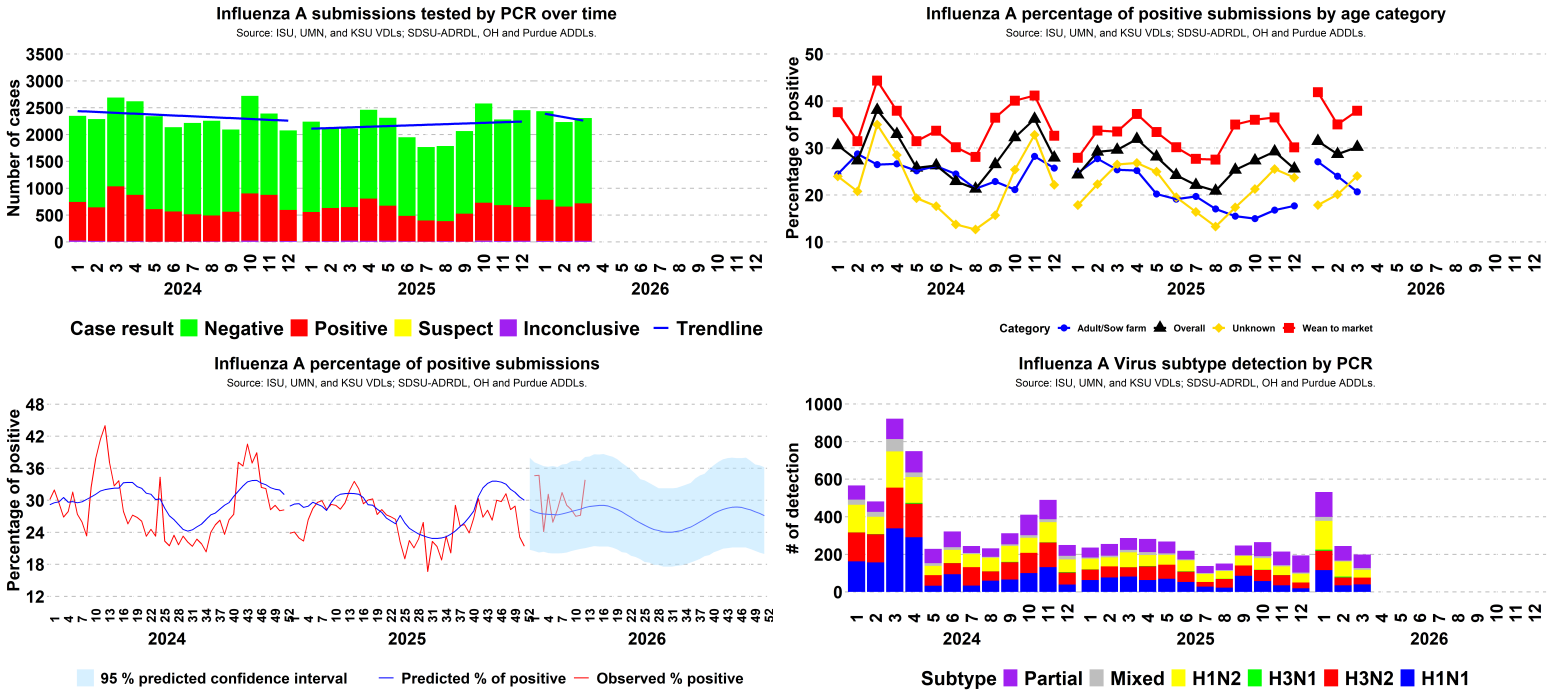
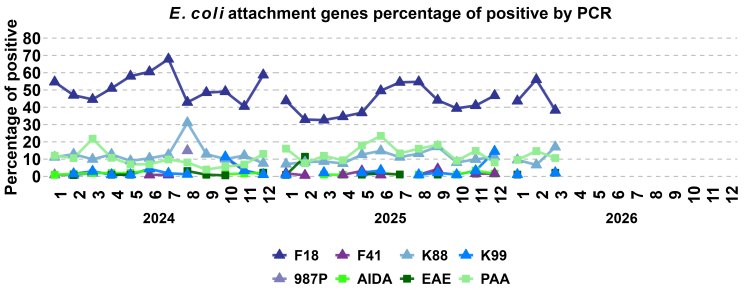


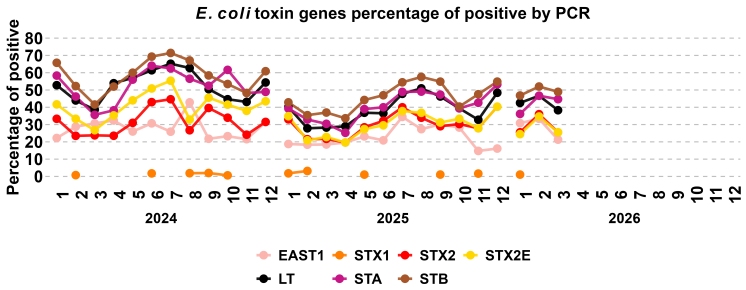

**Figure 1. Top:** *Left* Results of IAV PCR cases over time. *Right* Percentage of IAV PCR-positive results, by category over time. **Bottom:** *Left* expected percentage of positive results for IAV by PCR and 95% confidence interval for 2026 predicted value, based on weekly data observed in the previous 4 years. *Right* Number of IAV subtyping PCR detection over time; (Partial - only hemagglutinin or neuraminidase region detected; Mixed - 3 or more haemagglutinin and neuroamnidase regions detected. i.e., "H1 H3 N1").

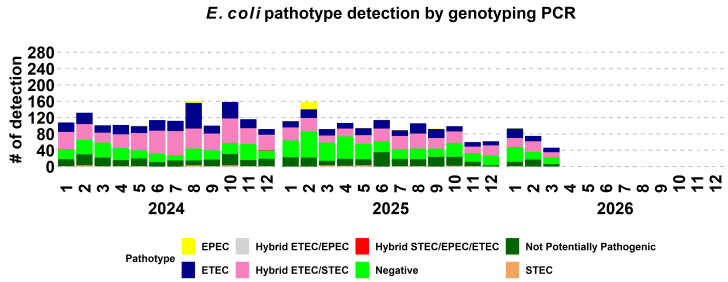
### SDRS Advisory Group highlights:

- Overall, 30.2% of 2,308 cases tested IAV-positive in March, similar to 28.69% of 2,234 in February.
  - Positivity in the adult/sow category in March was 20.67% (105 of 508), a moderate decrease from 24% (120 of 500) in February.
  - Positivity in the wean-to-market category in March was 37.93% (435 of 1,147), a moderate increase from 35% (405 of 1,157) in February.
  - Overall IAV-percentage of positive cases was 3 standard deviations above state-specific baseline in OK and NC.
- Overall, 4.52% of 199 samples had mixed subtype detection in March, a moderate increase from 2.05% of 244 in February.

# Topic 6 – Detection of *E. coli* DNA by Genotyping PCR.




**Most frequent *E. coli* virotypes detected by State in 2026**

Source: ISU, UMN, and KSU VDLs; SDSU-ADRDL, OH and Purdue ADDLs.

| SiteState | First Most Frequent | Second Most Frequent | Third Most Frequent |
|---|---|---|---|
| IA | F18;LT;STa;STb;Stx2e | EAST1 | F18;Paa;EAST1 |
| IL | F18;LT;STa;STb;Stx2e | F18;EAST1;LT;STb;Stx2e | F18;LT;Stx2e |
| IN | F18;LT;STa;STb;Stx2e | F18;EAST1;LT;STb | |
| KS | F18;EAST1;LT;STa;STb | | |
| MN | F18;LT;STa;STb;Stx2e | K88;Paa;EAST1;LT;STa;STb | STa;STb |
| MO | F18;LT;STa;STb;Stx2e | F18;LT;STa;STb | K88;EAST1;LT;STb |
| NC | F18 | K88;Paa;EAST1 | F18;EAST1;LT;STa;STb |
| NE | F18;LT;STa;STb;Stx2e | K88;STa;STb | F18;STa;STb |
| OH | F18;Paa;EAST1 | F18;Paa;EAST1;LT;STb | |
| SD | K88;STa;STb | F18;LT;STa;STb;Stx2e | K88;EAST1;LT;STb |

**Figure 1. Top:** *Left E. coli* PCR-Positive results by attachment genes over time. *Right E. coli* PCR-Positive results by toxin genes over time. **Bottom:** *Left E. coli* number of samples tested by PCR genotype and their respective pathotype classification. *Right* Most frequent detected *E. coli* virotype by PCR in 2026 at U.S. state level (color code on table cells associated with the pathotype legend).

### Education Material:

- Click on the links here to access the *E. coli* PCR Genotyping Interpretation Tool
- **Attachment genes: Fimbriae** – F18, K88(F4), K99(F5), 987P(F6), F41; **Adhesins** – EAE (Intimin), PAA, AIDA
- **Toxin genes: Heat-labile** – LT; **Heat-stable** – STa and STb; **Shiga toxins** – Stx1, Stx2 and Stx2e; and EAST1
- **Enterotoxigenic *E. coli* (ETEC):** Has fimbriae and toxin (not Stx2e) genes. Associated with neonatal and post-weaning diarrhea
- **Shiga toxin-producing *E. coli* (STEC):** Has fimbriae (F18) and toxin (must be Stx2e) gene. Associated with edema disease
- **Enteropathogenic *E. coli* (EPEC):** Presence of the EAE (Intimin) adhesin
- **Hybrids (ETEC/STEC, ETEC/EPEC, STEC/EPEC, ETEC/STEC/EPEC):** Combination of characteristics of more than one pathotype

### SDRS Advisory Group highlights:

- Overall, 47 samples were tested for *E. coli* PCR in March.
  - In March, the *E. coli* pathotypes with higher number of sample detections were Hybrid ETEC/STEC (12 detections), ETEC (11 detections), and Not Potentially Pathogenic (6 detections).
  - In March, the *E. coli* attachment genes with higher detection rate were F18 (38.30%), K88 (17.02%), and PAA (10.64%).
  - In March, the *E. coli* toxin genes with higher detection rate were STB (48.94%), STA (44.68%), and LT (38.30%).

# Topic 7 – Confirmed tissue cases etiologic/disease diagnosis at the ISU-VDL and OH-ADDL

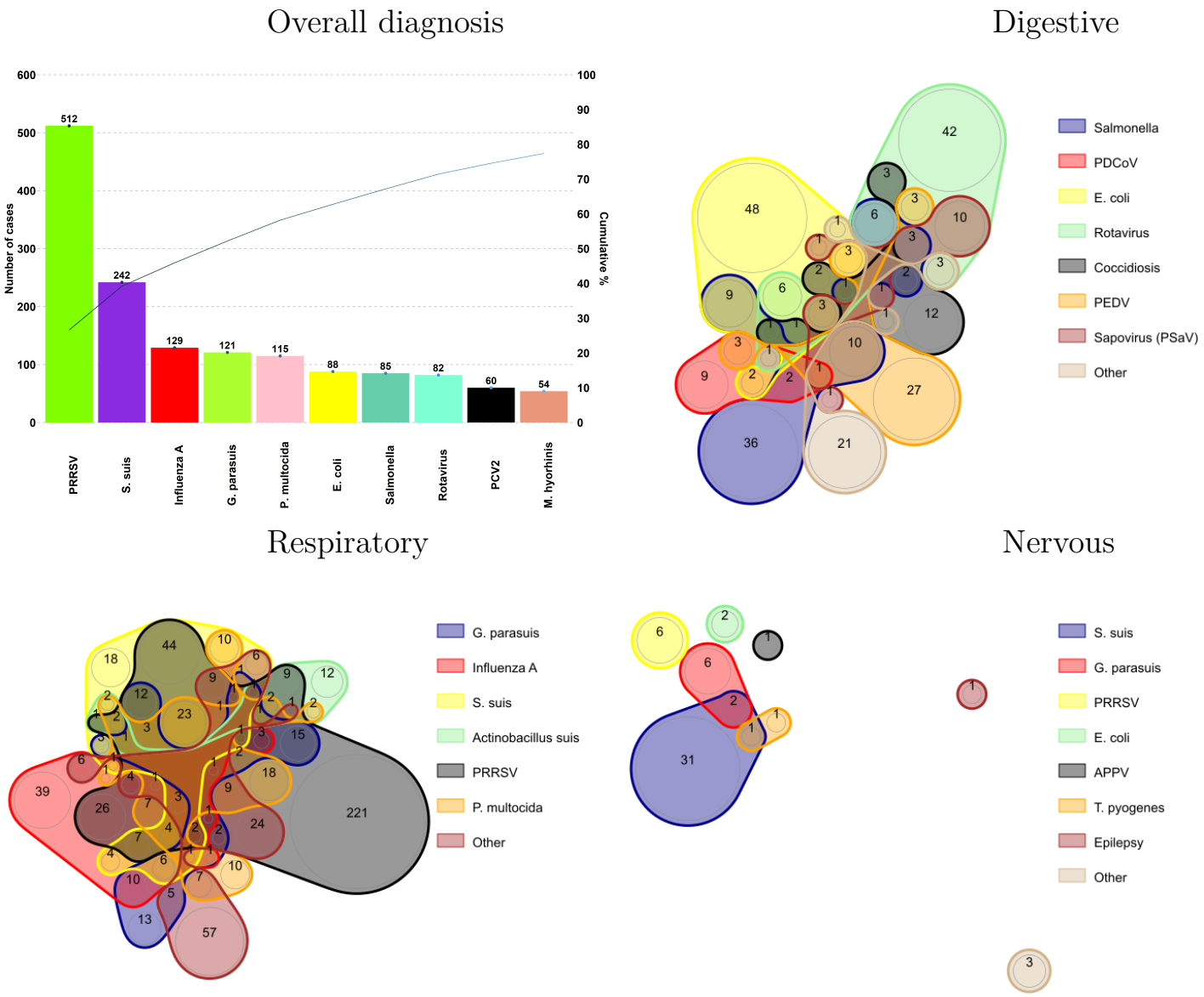



**Figure 4.** ISU-VDL and OH-ADDL most frequent overall confirmed tissue disease diagnosis. The presented system is described in the title of the chart. Colors represent one agent; line intersections present diagnosis of 2 or more agents within a submission. Only the most frequent etiology/disease are presented. Less frequent etiology/disease are grouped as "other". Non-confirmed diagnoses are not presented. This work is made possible due to the commitment and teamwork from the ISU-VDL and OH-ADDL diagnosticians who assign standardized diagnostic codes to each case submitted for histopathology: Drs. Almeida, Burrough, Derscheid, Gauger, Magstadt, Piñeyro, Siepker, Madson, Thomas, Gris, Yanez and previous VDL diagnosticians who have contributed to this process.

Note: Disease diagnosis takes 1 to 2 weeks to be performed. The graphs and analysis contain data from February 01, 2026 to March 27, 2026

**SDRS Advisory Group highlights:**

• PRRSV (512) led cases with confirmed etiology, followed by *S. suis* (242), and Influenza A (129). PRRSV (462 of 1147) led the number of confirmed respiratory diagnoses, Rotavirus (82 of 365) lead the number of confirmed digestive diagnoses, and *S. suis* (34 of 57) led the number of confirmed neurological diagnoses.

**Note:** *The SDRS is a collaborative project among multiple VDLs in the US swine industry. The VDL collaborators and industry partners are all invited to submit content to share on this bonus page related to disease prevention, control, and management. Stay tuned for more content in future editions.*

# Insights From Two Decades of PRRSV Evolution

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Analysis of the SDRS PRRSV Sequencing Database reveals a clear shift in the circulation of wild type PRRSV lineages over the past two decades, marked by the decline of historically dominant groups and the emergence of several expanding L1C sublineages. L8 (**L8A**–**L8E**) recorded **181 detections in 2006**, rose to a peak of **886 detections in 2009**, and then declined over time to **5 detections in 2026**. Similarly, L9 (**L9A**–**L9E**) began with **330 detections in 2006**, peaked in **2009 at 889 detections**, and subsequently declined to **no detections after 2024**. L1F (**n = 4,387**) remained highly detected through the late 2000s (e.g., **607 detections in 2007**) before gradually decreasing to **four detections in 2026**. The **wild-type European lineages** followed a comparable pattern, with **81 detections in 2006, a peak of 400 in 2011, and a decline to 6 detections in 2026**. Among the lineages with longer-term circulation, L1A (**n = 24,090**) maintained widespread circulation through the mid 2010s, rising steadily from **134 detections in 2006** to a peak of **2,632 detections in 2017**, before entering a sustained decline that reached **267 detections in early 2026**. L1H (**n = 10,442**) increased gradually after its first detection in 2010, reaching **1,617 detections in 2022**, and then decreased in the following years. L1E (**n = 3,111**) showed an early peak in **2012 (402 detections)**, followed by a brief resurgence in **2022 (299)** and a continued decline thereafter. L1C-others (**n = 6271**) peaked in **2012 at 986 detections** and subsequently declined to **a single detection in 2026** (Figure 1).

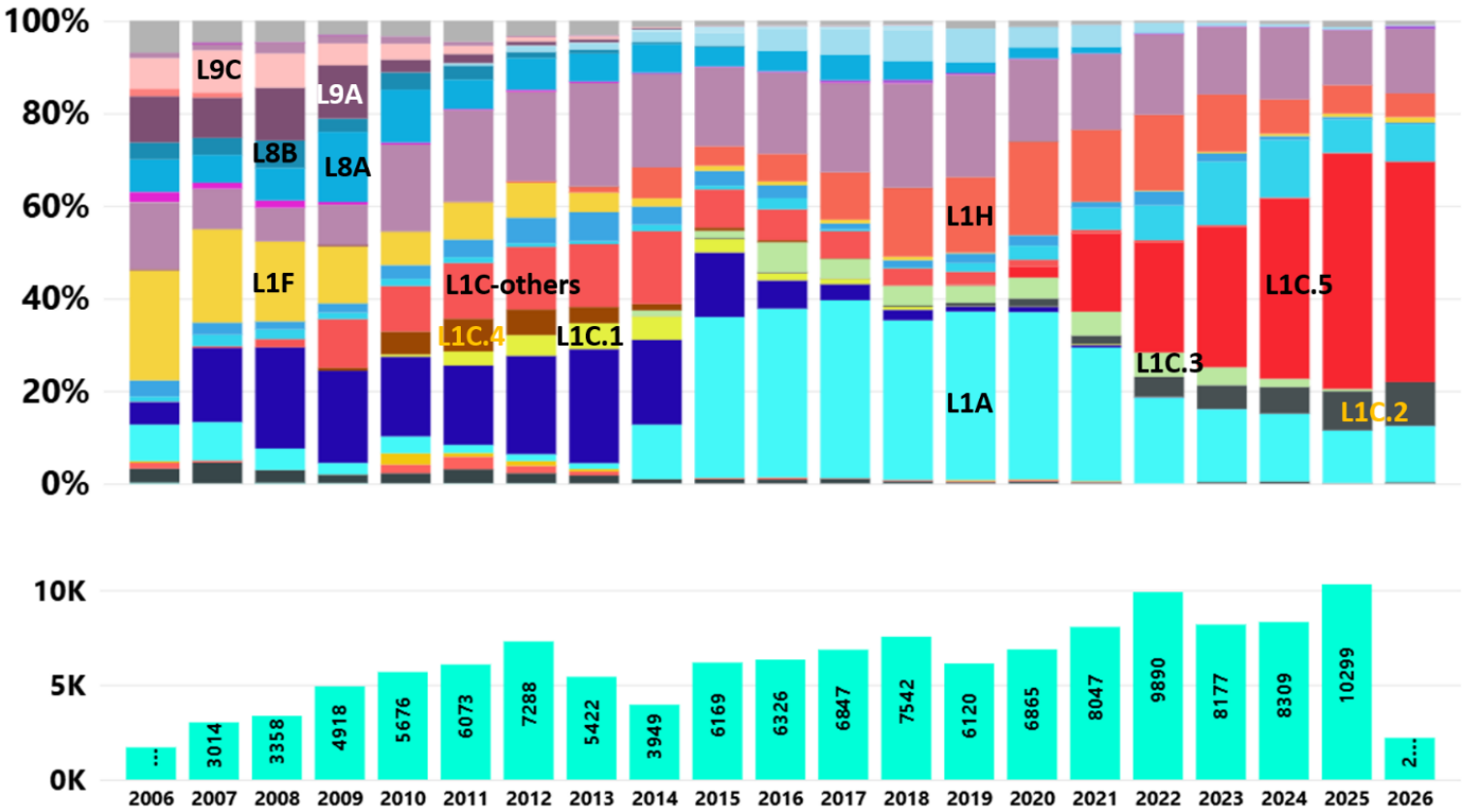


**Figure 1.** PRRSV ORF5 sequences dynamic over time and lineage distribution from 2006-2026, available at SDRS dashboards. Bottom: number of PRRSV ORF5 sequences. Top: proportion of sequences by Lineage

L1C-associated lineages showed a range of temporal patterns, with several displaying distinct waves of activity over time. L1C.1 (**n = 1,494**) rose rapidly after emerging in 2010 and peaked in **2012 (327 detections)** before steadily declining to **a single detection in 2023**. L1C.3 (**n = 3,147**) peaked later at **520 detections in 2022**, followed by sharp declines to **no detections in 2026**. L1C.4 (**n = 1,475**) emerged in **2008 with 1 detection**, increased to a peak of **431 detections in 2011**, and has not been detected since **2023**. In contrast to these declines, two L1C sublineages – **L1C.2** and **L1C.5** – have continued to expand. **L1C.2**, first detected in 2014, reached **870 detections in 2025** and remains active with **208 detections in 2026**. **L1C.5** has shown the most dramatic rise: after emerging in 2014, had an aggressive 1C.5 variant detected in 2020 with become predominant in the field and grew rapidly to **5,241 detections in 2025** and has already accumulated **1,048 detections in the first quarter of 2026**, with **variant 1C.5.32 alone has made up 966 detections** (Figure 2), making it the **dominant wild type lineage** in recent years. Collectively, these trends reflect substantial lineage turnover, with long standing lineages receding and newer L1C sublineages – **especially L1C.5** – now shaping contemporary PRRSV circulation.

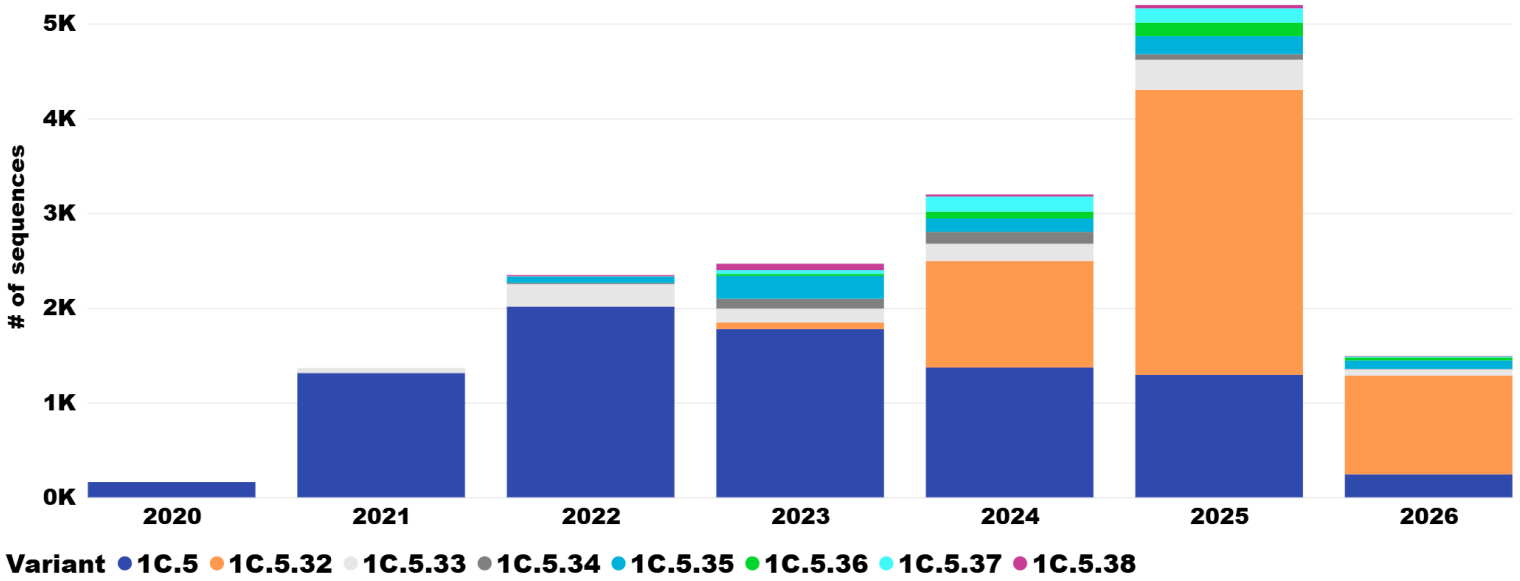


**Figure 2.** PRRSV variants distribution from L1C.5

To further clarify these recent changes, variant level trends were examined using a rolling 12 month window, defined as the 12 months preceding the most recent detection and compared with the previous 12 month interval. Among **82 variants** active in the most recent period, only **32 declined**, indicating that **most variants (n = 50)** are currently expanding. Several variants exhibited particularly strong growth. Variant **1C.5.32** showed the most pronounced increase, accumulating **3,437 detections** in the current period – **a 150% increase** compared with the prior interval. Variant **1C.2** climbed to **872 detections**, rising by **406 (87%)**, and variant **1H.18** increased to **404 detections, a 127% rise**. Variant **1C.5.33** rose to **327 detections**, increasing by **122 detections (59%)**. Variant **1A.13.49** also expanded markedly, reaching **102 detections – a 175% increase**.

A smaller group of variants showed notable declines during the same period, with decreases **exceeding 30 detections** in variants **1C.5, 1A.2, 1A.28, 1C.5.34**, and **1H.9**, suggesting waning circulation or displacement by more rapidly expanding variants. Overall, these variant-level results highlight finer-scale patterns within the broader lineage changes, with several rapidly increasing variants disproportionately shaping current PRRSV detections.

Taken together, these lineage and variant level patterns highlight substantial shifts in the PRRSV population structure, raising the question of how these recent detections are organized evolutionarily. To place these trends within a broader genomic context the phylogenetic relationships of all PRRSV-2 sequences detected in 2026 was conducted, along with a focused analysis of the rapidly expanding L1C.5 sublineage. The 2026 phylogeny shows clear separation among major PRRSV lineages, with multiple well-defined clusters and **a prominent grouping of L1C sublineages** reflecting their increased activity during this period (Figure 3).

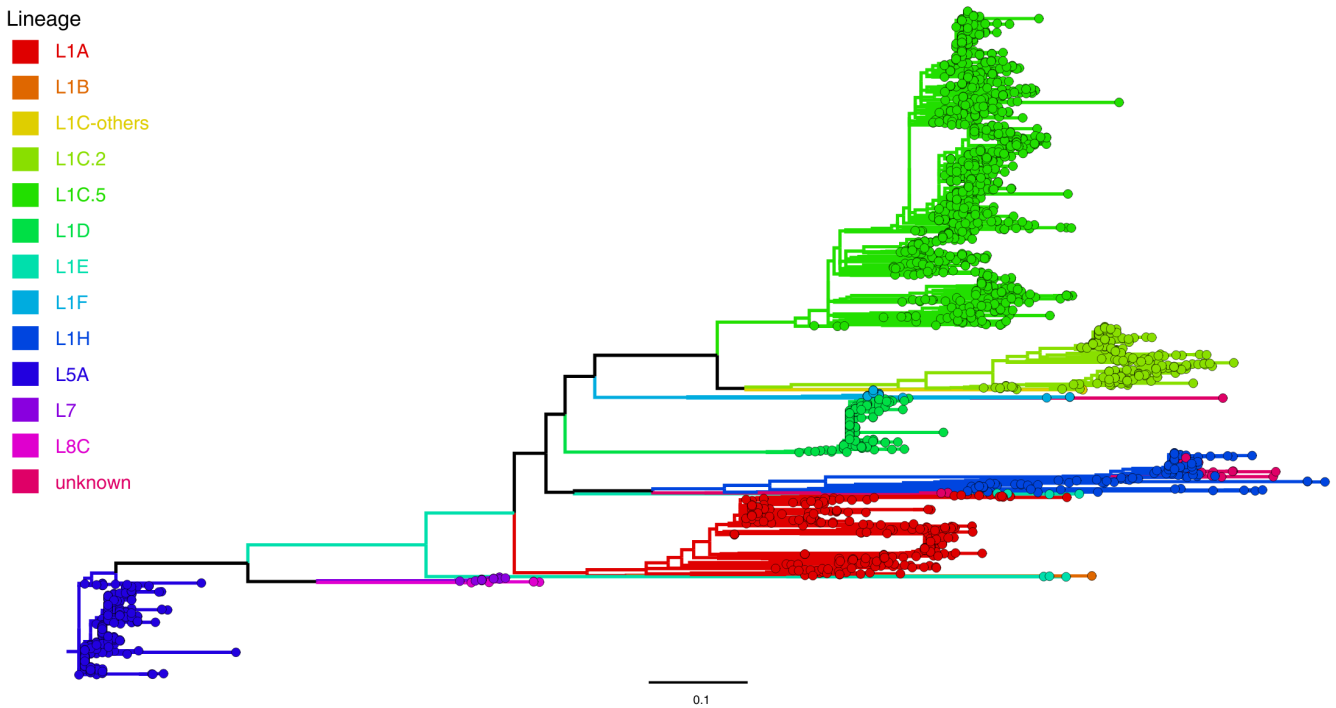


**Figure 3.** Phylogenetic tree for PRRSV sequences detected in 2026. The phylogenetic tree is rooted by the PRRSV-2 prototype strain VR-2332 a L5A virus.

The L1C.5 sublineage focused phylogeny provides higher-resolution insight into this expanding group of PRRSV-2. Most 2026 L1C.5 sequences cluster fall within a single large group corresponding to variant **1C.5.32**, reflecting its strong expansion during this period. However, differentiation among the 1C.5.32 exists and is currently forming two large predominant groups (Figure 4). Additional smaller but distinct clusters representing **1C.5.33 to 1C.5.38** variants are also visible, indicating continued diversification within the sublineage in 2026 (Figure 4).

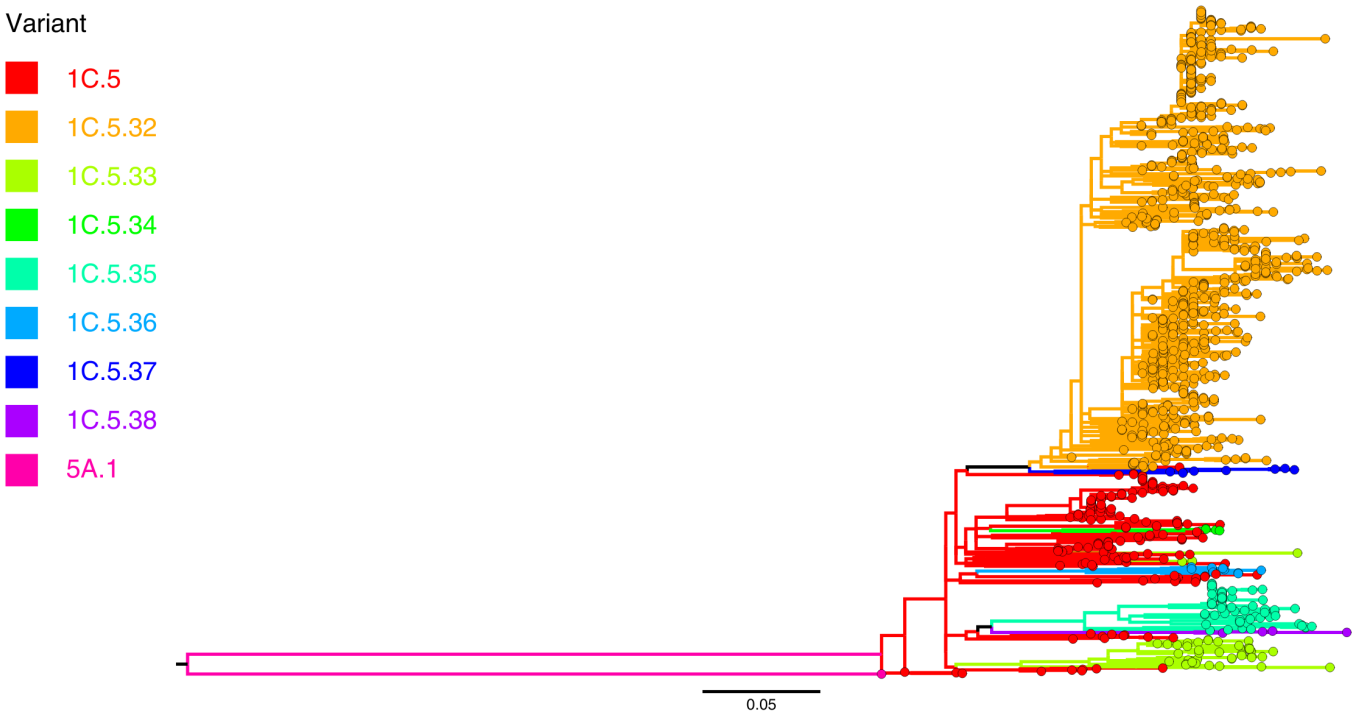


**Figure 4.** Phylogenetic tree of 1C.5 variants sequences detected in 2026. The phylogenetic tree is rooted by the PRRSV-2 prototype strain VR-2332 a 5A.1 virus.