Swine Disease Reporting System
Report # 89 (July 01, 2025)

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 www.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; Data Analyst: Quyen Thuc Le; Project coordinator: Guilherme Cezar

Iowa State Uni.: Edison Magalhães, Gustavo Silva, Marcelo Almeida, Bret Crim, Kinath Rupasinghe, Srijita Chandra, Eric Burrough, Phillip Gauger, Christopher Rademacher, Darin Madson, Michael Zeller, Rodger Main.

Uni. of Minnesota: Mary Thurn, Paulo Lages, Cesar Corzo, Stephanie Rossow, 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, Beth Thompson.

Ohio Animal Disease and Diag. Lab. and *The Ohio State University*: 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.

PRRSView and FLUture: Aggregates PRRSV and influenza A virus diagnostic data from the ISU-VDL.

PRRS virus RFLP/Lineage 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, Google podcast, YouTube, LinkedIn, and the SDRS webpage. In addition to this report, interactive dashboards and educational material are publicly available.

Advisory Group: Providing their comments and perspectives monthly: Mark Schwartz, Megan Niederwerder, Paul Yeske, Deborah Murray, Brigitte Mason, Peter Schneider, Sam Copeland, Luc Dufresne, Daniel Boykin, Corrine Fruge, William Hollis, Rebecca Robbins, Thomas Petznick, Kurt Kuecker, Lauren Glowzenski, and Brooke Kitting.

Note: This report contains data up to June 30, 2025.

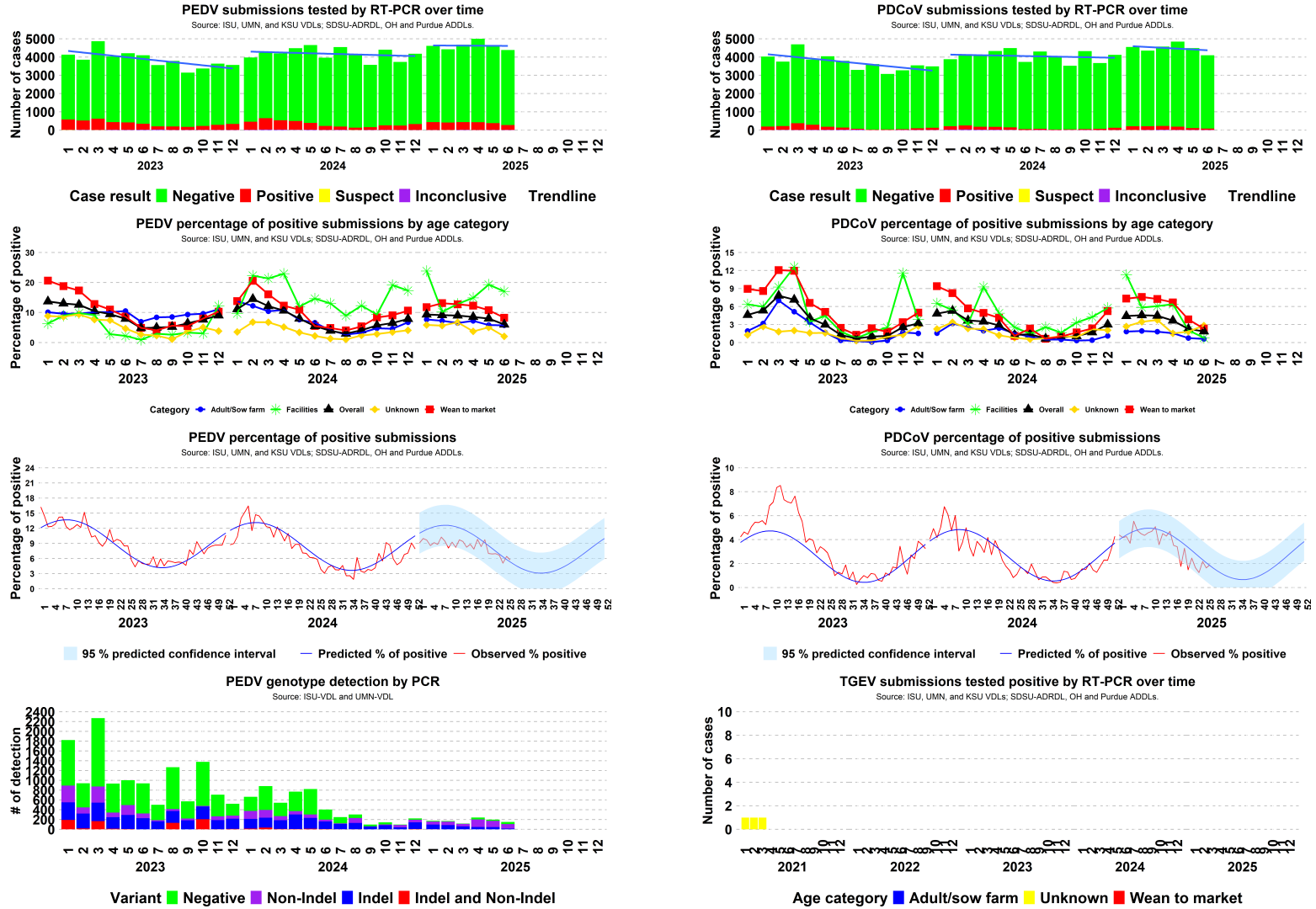# Topic 1 – Detection of PRRSV RNA over time by RT-qPCR.
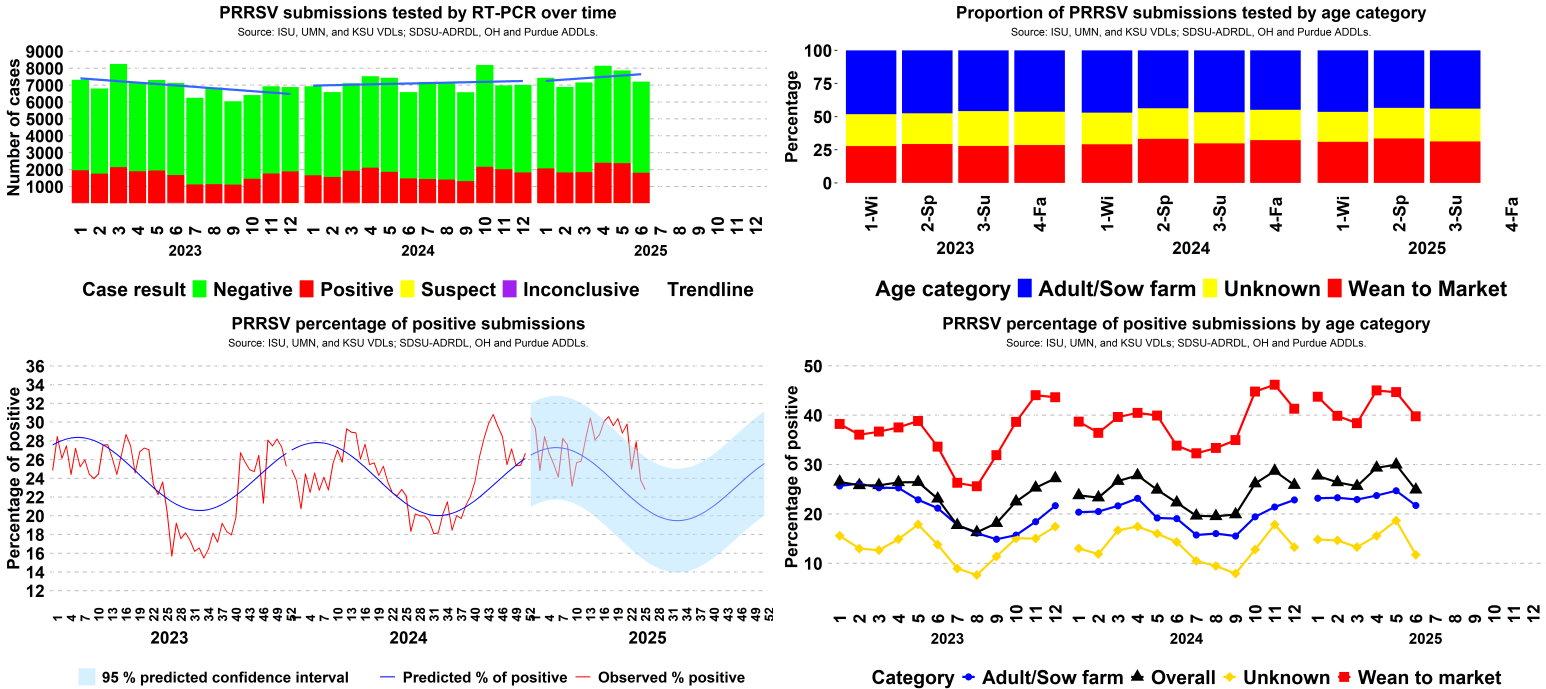
Figure 1. Top: *Left*: Results of PRRSV RT-PCR cases over time; *Right*: Proportion of accession ID cases tested for PRRSV by age group per year and season. **Bottom**: *Left* Expected percentage of positive results for PRRSV RNA by RT-qPCR, with 95% confidence interval band for predicted results based 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, 24.9% of 7,202 cases tested PRRSV-positive in June, a substantial decrease from 29.97% of 7,871 in May;
- Positivity in the adult/sow category in June was 21.71% (688 of 3,169), a moderate decrease from 24.71% (840 of 3,400) in May;
- Positivity in the wean-to-market category in June was 39.77% (896 of 2,253), a moderate decrease from 44.66% (1,176 of 2,633) in May;
- Overall PRRSV-percentage of positive cases was 3 standard deviations above state-specific baseline in IA, MN, SD and MO;
- The advisory group highlighted the importance of enhancing biosecurity for PRRSV since several cases might be attributed to biosecurity breaches connected with transport, feed deliveries, and manure hauling as possible causes of lateral transmission in finishing sites;
- In addition, specific in Minnesota, there was a spike in PRRSV + Influenza A virus-positive cases observed in May, with a decline noted in June, but still captured as more than expected in the state-level specific baseline.

Topic 2 – PRRSV ORF5 sequences detection over time

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 Lineage and RFLP; *Right*: Most frequent detected PRRSV ORF5 sequences in 2025 by lineage and RFLP at U.S. state level.

SDRS Advisory Group highlights:

- During June 2025, The states with higher number of PRRSV L1C.5 (variant) detections were detected IA, MN, MO, NE, IL, SD, IN, OH, CO, PA (respective number of sequences: 256, 43, 31, 28, 10, 9, 5, 5, 2, 1).
- In June L1C.5 1-4-4 (289) was the PRRSV sequence most detected in the U.S., followed by L1C.2 1-2-4 (62), and L1C.5 1-3-4 (37);
- Click on the links here to access the PRRSV genotype dashboard and the SDRS Blast tool to compare your PRRSV ORF5 sequence with the SDRS database.
- First detection of PRRSV Lineage 1C.2 RFLP 1-2-4 in North Carolina. The detection in North Carolina is the first time in history that a PRRSV Lineage 1C.2 has been detected in the state (more information in Bonus Page).

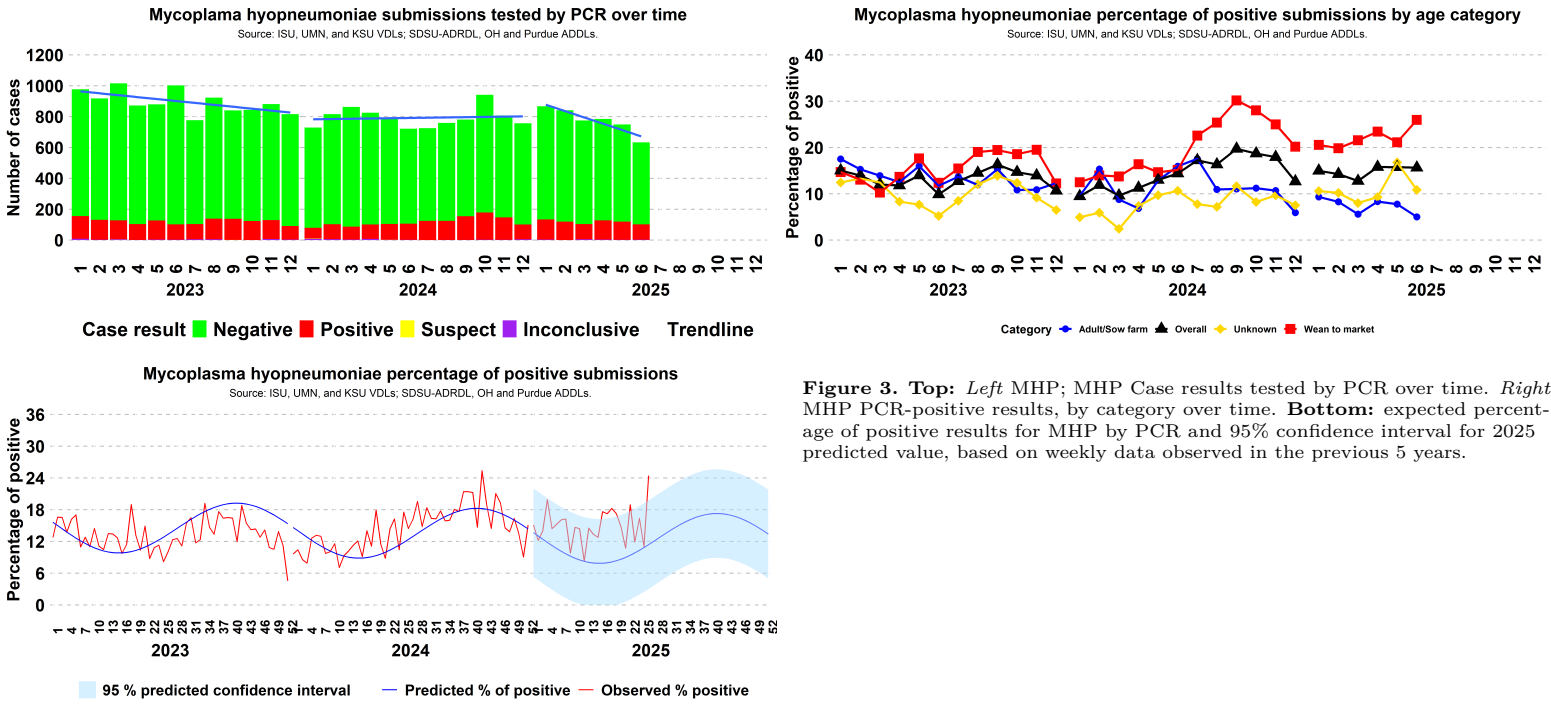# Topic 2 – Enteric coronavirus RNA detection by RT-qPCR

Figure 1. Top: *Left PEDV*; *Right PDCoV* cases tested by RT-PCR over time; **Second from top**: *Left PEDV*; *Right PDCoV* percentage of positive PCR positive results, by age category over time. Facilities are cases submissions from packing plants, truck washes, and vehicles. **Third from top**: *Left PEDV*; *Right PDCoV* expected percentage of positive results for cases tested by RT-PCR and 95% confidence interval for 2025 predicted value. **Bottom** *Left*: Number of PEDV genotype detection over time; *Right*: Number of TGEV positive cases by age category.

SDRS Advisory Group highlights:

- Overall, 6% of 4,382 cases tested PEDV-positive in June, similar to 7.99% of 4,646 in May;
  - Positivity in the adult/sow category in June was 5.75% (79 of 1,375), similar to 5.84% (88 of 1,507) in May;
  - Positivity in the wean-to-market category in June was 8.25% (137 of 1,660), a moderate decrease from 10.79% (195 of 1,808) in May;
- Positivity in the facilities category in June was 17.05% (22 of 129), a moderate decrease from 19.31% (28 of 145) in May;
  - Overall PEDV-percentage of positive cases was 3 standard deviations above state-specific baseline in IN;
  - Overall, 0% of 150 samples had mixed PEDV genotype detection in June, similar to 0% of 198 in May;
- Overall, 1.85% of 4,099 cases tested PDCoV-positive in June, similar to 2.27% of 4,492 in May;
  - Positivity in the adult/sow category in June was 0.6% (8 of 1,331), similar to 0.75% (11 of 1,458) in May;
  - Positivity in the wean-to-market category in June was 2.32% (35 of 1,510), similar to 3.85% (67 of 1,741) in May;
- Positivity in the facilities category in June was 0.78% (1 of 128), similar to 2.07% (3 of 145) in May;
- Overall PDCoV-percentage of positive cases was 3 standard deviations above state-specific baseline in MO, IN, OH and NC;
- There was 0 positive case for TGEV RNA-PCR in June, 2025 over a total of 4,012 cases tested. It has been 51 months (with a total of 191,709 cases tested) since the last TGEV PCR-positive result;
- The advisory group highlighted that PDCoV cases had been seen in the field, but as less severe than PEDV. However, these cases of PDCoV may indicate a biosecurity breach. According to the advisory group, both viruses continue to cause disruptions at the sow farm level, with PEDV remaining the more concerning.

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SDRS — Domestic Swine Disease Surveillance | Iowa State University Veterinary Diagnostic Laboratory | University of Minnesota Veterinary Diagnostic Lab | South Dakota ADRDL Animal Disease Research & Diagnostic Laboratory, Brookings, South Dakota | Kansas State Veterinary Diagnostic Laboratory | Ohio Animal Disease Diagnostic Laboratory | Purdue University Animal Disease Diagnostic Laboratory | USDA | SHIC Swine Health Information Center

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

Mycoplama hyopneumoniae submissions tested by PCR over time
Source: ISU, UMN, and KSU VDLs; SDSU-ADRDL, OH and Purdue ADDLs.
Case result: Negative / Positive / Suspect / Inconclusive / Trendline

Mycoplasma hyopneumoniae percentage of positive submissions by age category
Source: ISU, UMN, and KSU VDLs; SDSU-ADRDL, OH and Purdue ADDLs.
Category: Adult/Sow farm / Overall / Unknown / Wean to market

Mycoplasma hyopneumoniae percentage of positive submissions
Source: ISU, UMN, and KSU VDLs; SDSU-ADRDL, OH and Purdue ADDLs.
95 % predicted confidence interval / Predicted % of positive / Observed % positive

Figure 3. Top: *Left* MHP; 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 2025 predicted value, based on weekly data observed in the previous 5 years.

SDRS Advisory Group highlights:

- Overall, 15.64% of 633 cases tested *M. hyopneumoniae*-positive cases in June, similar to 15.75% of 749 in May;
  - Positivity in the adult/sow category in June was 5.02% (11 of 219), a moderate decrease from 7.78% (20 of 257) in May;
  - Positivity in the wean-to-market category in June was 25.96% (74 of 285), a moderate increase from 21.13% (75 of 355) in May;
- Overall MHP-percentage of positive cases was 3 standard deviations above state-specific baseline in MN;
- Even though on the week of June 23rd, *Mycoplasma hyopneumoniae* weekly positivity was above the expected result, 27 of 33 positive cases were deep tracheal swabs in finishing sites or lungs collected for producing homogenate with the purpose of sow farm exposure, which might not represent new clinical breaks in the field.

# Topic 4 – Detection of Porcine Circoviruses type 2 and 3 DNA by PCR.
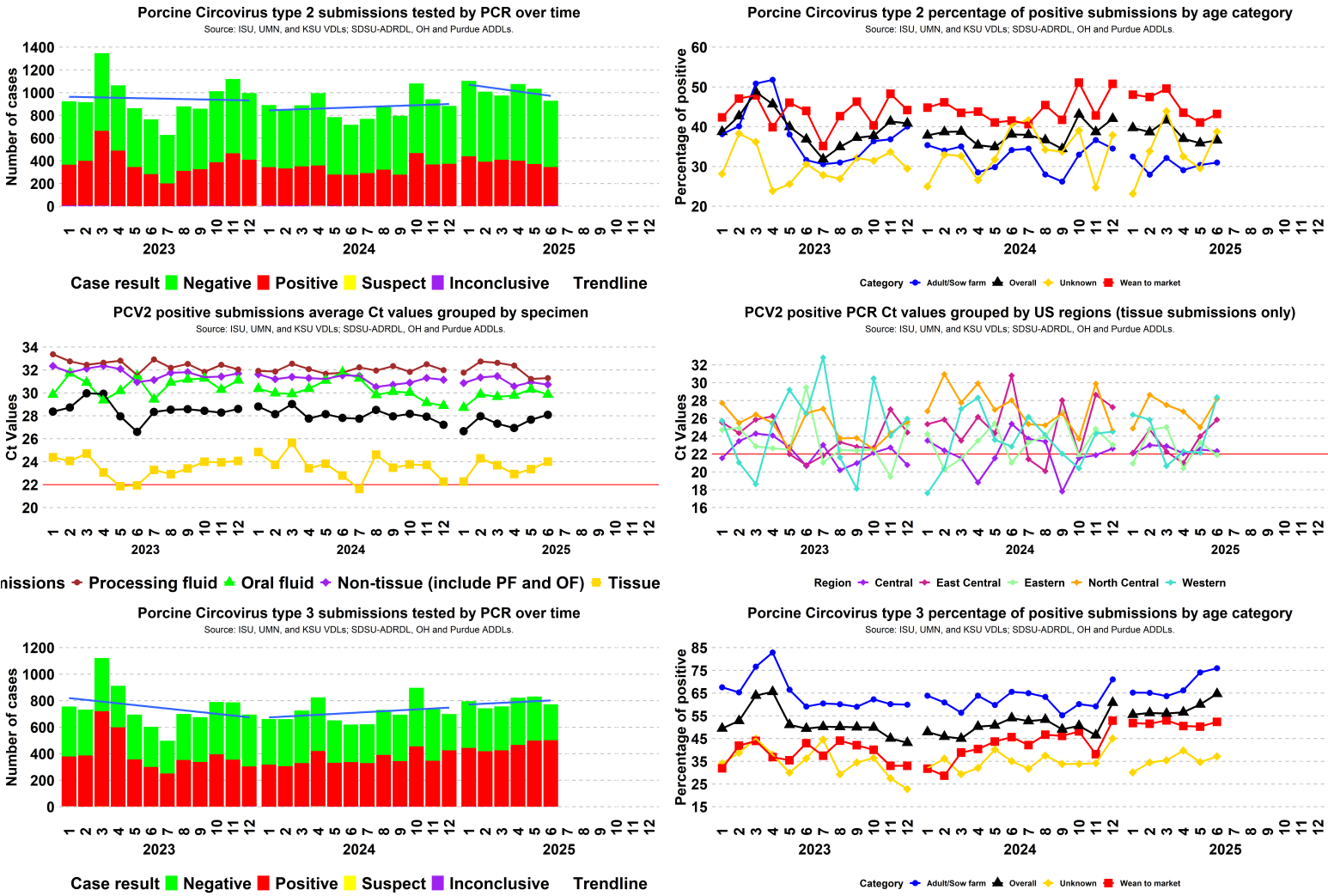
Figure 1. Top: *Left*: Results of PCV2 PCR cases over time; *Right*: PCV2 PCR-positive results, by category over time. **Middle**: *Left*: Average Ct values of PCV2 submissions by specimen; *Right*: Average Ct values of PCV2 tissue submissions by U.S. region; Central (IA), East Central (IL, IN, MO and 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, 36.6% of 929 cases tested PCV2-positive in June, similar to 35.88% of 1,034 in May;
  - Positivity in the adult/sow category in June was 31.01% (147 of 474), similar to 30.39% (124 of 408) in May;
  - Positivity in the wean-to-market category in June was 43.2% (162 of 375), a moderate increase from 41.08% (221 of 538) in May;
  - In the month of June, the regions with the lowest PCV2 average Ct values in tissue submissions was Eastern (24 submissions; average Ct 21.9), Central (47 submissions; average Ct 22.3), East Central (8 submissions; average Ct 25.8), North Central (27 submissions; average Ct 28.2), and Western (9 submissions; average Ct 28.4);
- Overall, 64.68% of 773 cases tested PCV3-positive in June, a moderate increase from 60.05% of 831 in May;
  - Positivity in the adult/sow category in June was 75.95% (341 of 449), similar to 74.1% (289 of 390) in May;
  - Positivity in the wean-to-market category in June was 52.36% (133 of 254), a moderate increase from 50.27% (184 of 366) in May.
- The advisory group highlighted that despite the increased percentage of positive submissions, no unusual PCV2/PCV3 clinical issues have occurred beyond typical patterns. However, the advisory group reported more PCV2d cases, with one advisory member having a PCV2e case in one farm.

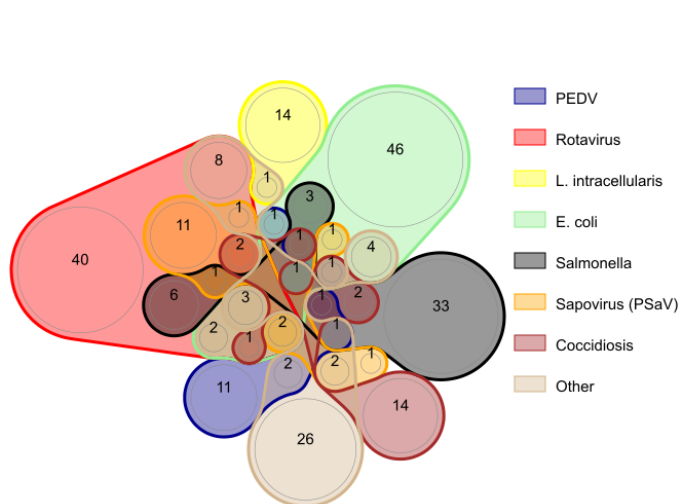# Topic 5 – Detection of Influenza A Virus (IAV) RNA by RT-PCR.
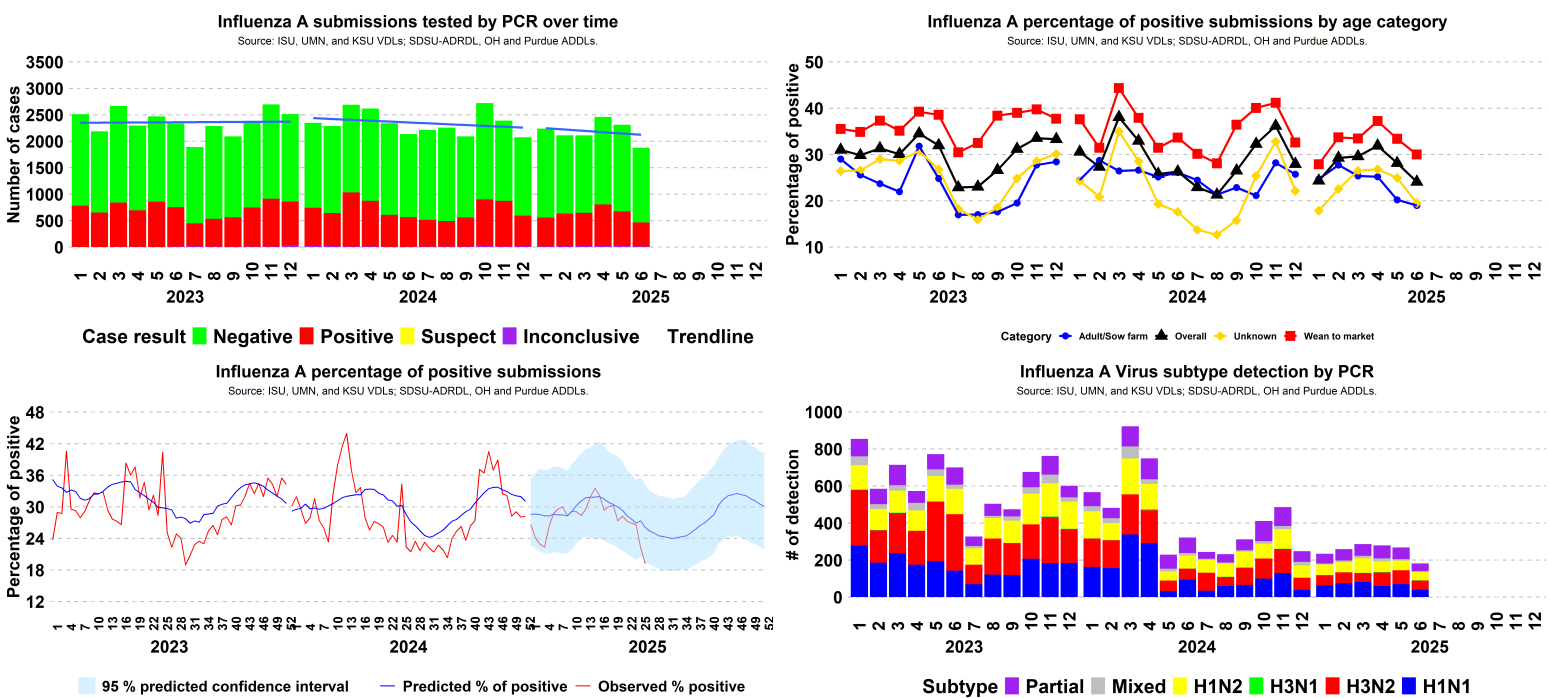
Figure 3. Top: *Left* Results of IAV PCR cases over time. *Right* Percentage of IAV PCR-positive results, by category over time. **Bottom:** *Left* expected percentage of positive results for IAV by PCR and 95% confidence interval for 2025 predicted value, based on weekly data observed in the previous 5 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").
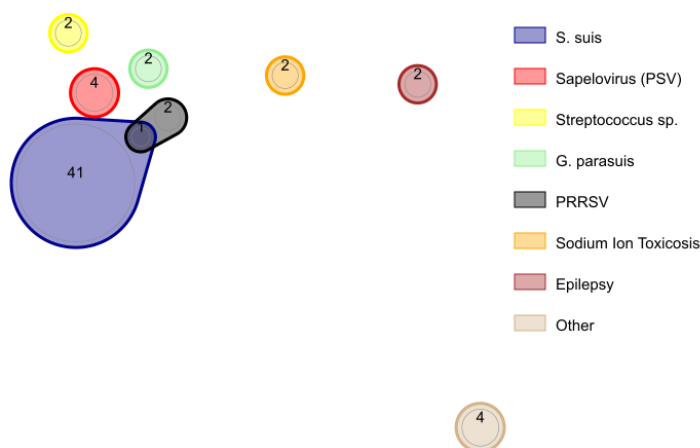
SDRS Advisory Group highlights:

- Overall, 24.09% of 1,876 cases tested IAV-positive cases in June, a moderate decrease from 28.15% of 2,313 in May;
  - Positivity in the adult/sow category in June was 19% (84 of 442), similar to 20.22% (94 of 465) in May;
  - Positivity in the wean-to-market category in June was 30% (252 of 840), a moderate decrease from 33.39% (379 of 1,135) in May.
- Overall IAV-percentage of positive cases was within state-specific baselines in all 11 monitored states;
- Overall, 2.2% of 182 samples had mixed subtype detection in June, similar to 2.99% of 268 in May.

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Topic 6 – Confirmed tissue cases etiologic/disease diagnosis at the ISU-VDL.

Overall diagnosis

Digestive

Respiratory

Nervous

Figure 4. ISU-VDL 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 diagnosticians who assign standardized diagnostic codes to each case submitted for histopathology: Drs. Almeida, Burrough, Derscheid, Gauger, Magstadt, Piñeyro, Siepker, Madson, Thomas, Gris 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 May. 1 to June. 23, 2025.

SDRS Advisory Group highlights:

• PRRSV (522) led cases with confirmed etiology, followed by *S. suis* (293), and *G. parasuis* (122). PRRSV (487 of 1245) led the number of confirmed respiratory diagnoses, Rotavirus (77 of 318) lead the number of confirmed digestive diagnoses, and *S. suis* (42 of 61) led the number of confirmed neurological diagnoses.

• A 25.5% increase in PRRSV cases co-diagnosed with other pathogens was observed in May–June 2025 (368) compared to the same period in 2024 (293 cases).

• In multiple instances, PCV2 and PCV3 were identified as co-diagnosed with PRRSV—an unusual trend not seen in 2023 and 2024 during May-June. Still, the leading pathogen co-diagnosed with PRRSV was *Streptococcus suis*.

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Spatiotemporal dynamics of PRRSV variants emergence and production phase progression across U.S. States

Quyen Le Thuc[1], Guilherme Cezar[1], Kinath Rupasinghe[1], Daniel Linhares[1], Giovani Trevisan[1]

1 - Iowa State University, Ames, IA, USA.

The SDRS has adopted algorithms for PRRSV lineage and variant classification to methodically organize incoming PRRSV ORF5 sequences within its PRRSV Sequencing Database. This structured approach improves the capacity for tracking detection patterns, new variants, and understanding the genetic connections among sequences over time. Therefore, more data analysis can be done regarding the order of detection of these variants and the detection among states.

The SDRS PRRSV Sequencing Database has processed a total of 5,186 sequences only for 2025, which span 14 distinct lineages and 61 unique variants, with Iowa notably reporting 39 distinct variants. Lineage 1C.5 was the most frequently detected, accounting for 46.99% (n = 2,098) of all sequences (Figure 1). This was followed by lineage 1A at 12.75% (n = 661) and lineage 5A at 10.86% (n = 563). Among the variants, the most frequent detected were 1C.5.32 (n = 1,267), 1C.5 (n = 697), and L1C.2 (n = 438).

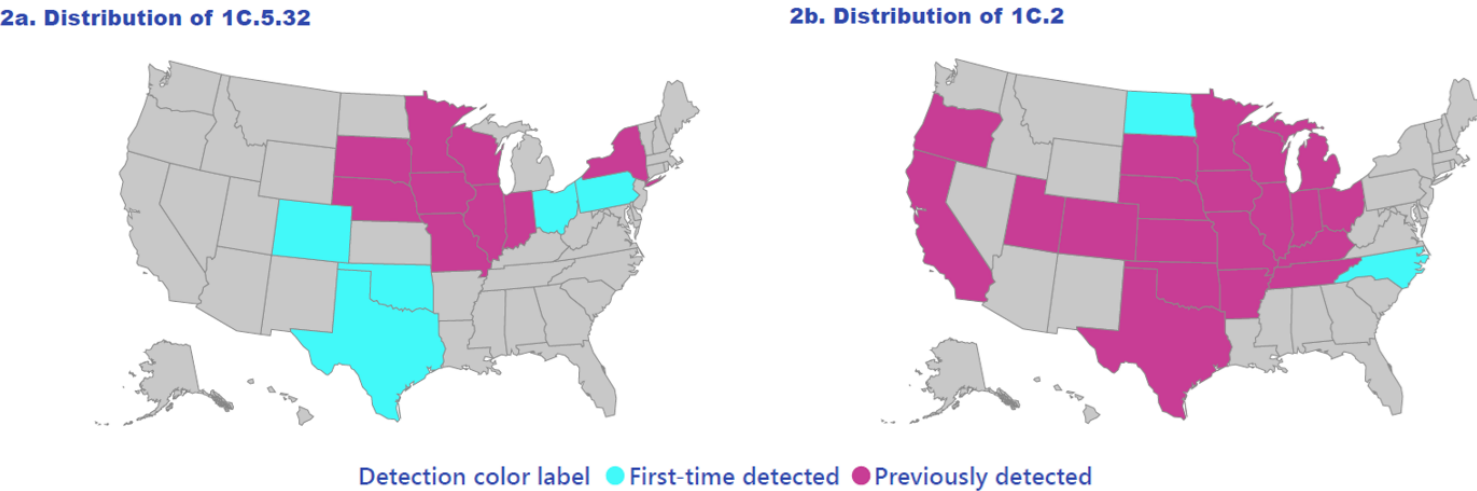**Figure 1.** Total number of sequences detected on a monthly basis, color coded by lineage.
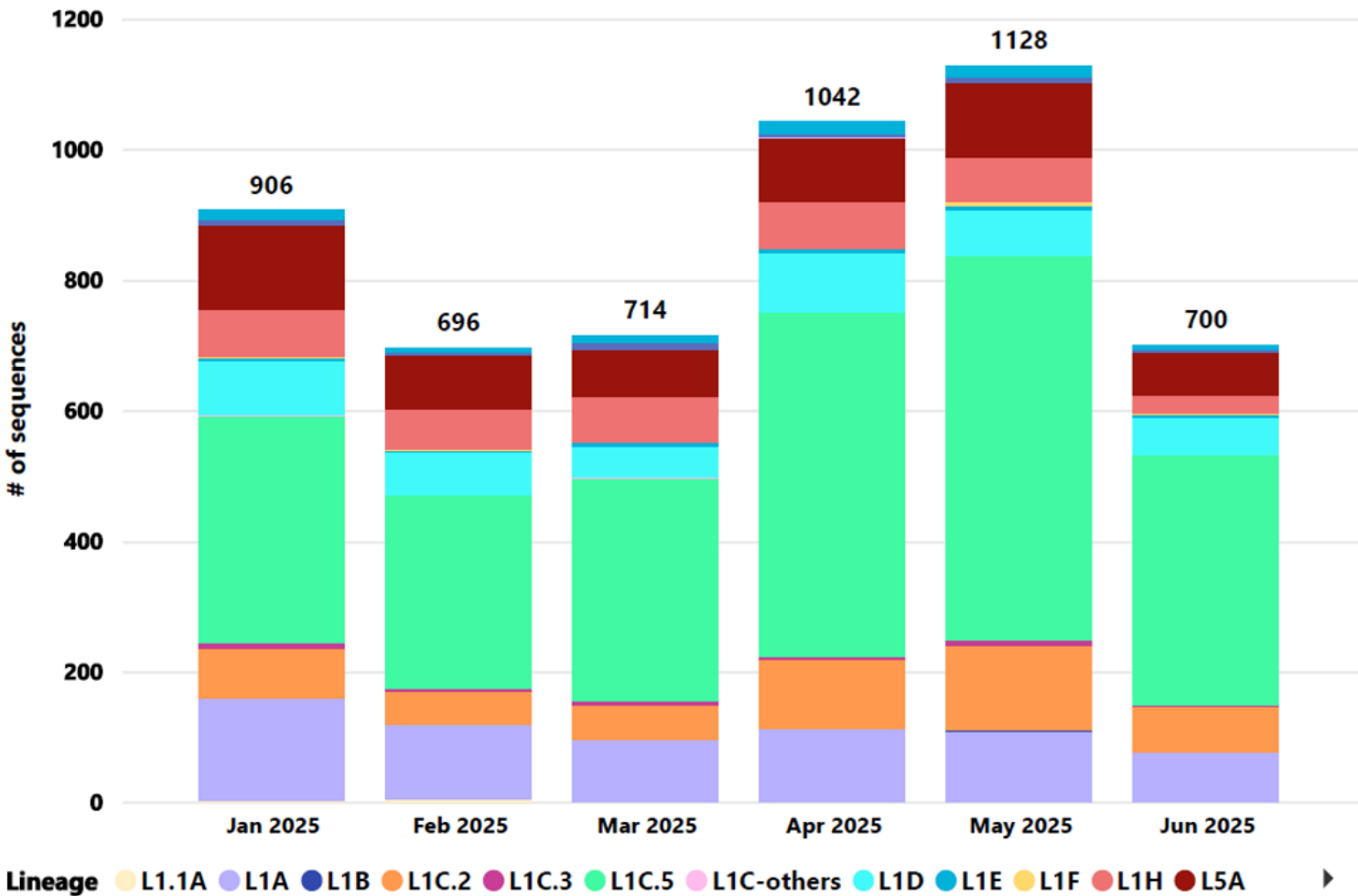
The variant 1C.5.32 has shown a significant increase in detections in IA and MN since April and May. In IA, there were 162 reported sequences in April, which represents a 47.3% increase compared to March. The number rose further to 213 sequences in May, marking a 31.5% increase from April. Similarly, MN reported the highest numbers of this variant, with 75 sequences in April and 103 in May. The variant 1C.5.32 remains the most detected variant in IA and MN until the end of June 2025. In addition to these established hotspots, the SDRS database recorded the first-time detection of variant 1C.5.32 in OK, OH, TX, CO and PA (Figure 2a).

Variant 1C.2 has shown a significant increase since March 2025, with a total of 438 sequences, predominantly occurring in IA with 302 sequences, followed by MN with 252 sequences. The SDRS database also recorded the first-time detection of variant 1C.2 in ND and NC (Figure 2b).

Figure 2. Dynamics of detection of PRRSV variants - map showing the scenario of the PRRSV variant 1C.5.32 (a) and variant 1C.2 (b) demonstrating the states that had the first detection of the variant in 2025 (c)

2a. Distribution of 1C.5.32

2b. Distribution of 1C.2

Detection color label ● First-time detected ● Previously detected

2c. States first-time detected variants 1C.2 & 1C.5.32

Variant	State	Phase	Detected date
1C.2	NC	Adult/Sow	5/28/2025
1C.2	ND	Adult/Sow	1/9/2025
1C.5.32	CO	Adult/Sow	4/3/2025
1C.5.32	OH	Wean to Market	1/22/2025
1C.5.32	OK	Adult/Sow	1/6/2025
1C.5.32	PA	Wean to Market	6/23/2025
1C.5.32	TX	Adult/Sow	1/31/2025

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