

# Swine Disease Reporting System

## Report # 84 (February 04, 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](http://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](#); Project coordinator: [Guilherme Cezar](#)

*Iowa State University:* Edison Magalhães, Gustavo Silva, Marcelo Almeida, Bret Crim, Kinath Rupasinghe, Srijita Chandra, Eric Burrough, Phillip Gauger, Joseph Thomas, Darin Madson, Michael Zeller, Rodger Main.

*University of Minnesota:* Mary Thurn, Paulo Lages, Cesar Corzo, Stephanie Rossow, Matt Sturos, Hemant Naikare.

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

*South Dakota State University* and *South Dakota AIB:* Jon Greseth, Darren Kersey, Travis Clement, Angela Pillatzki, Jane Christopher-Hennings, Beth Thompson.

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

*Purdue University* 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.

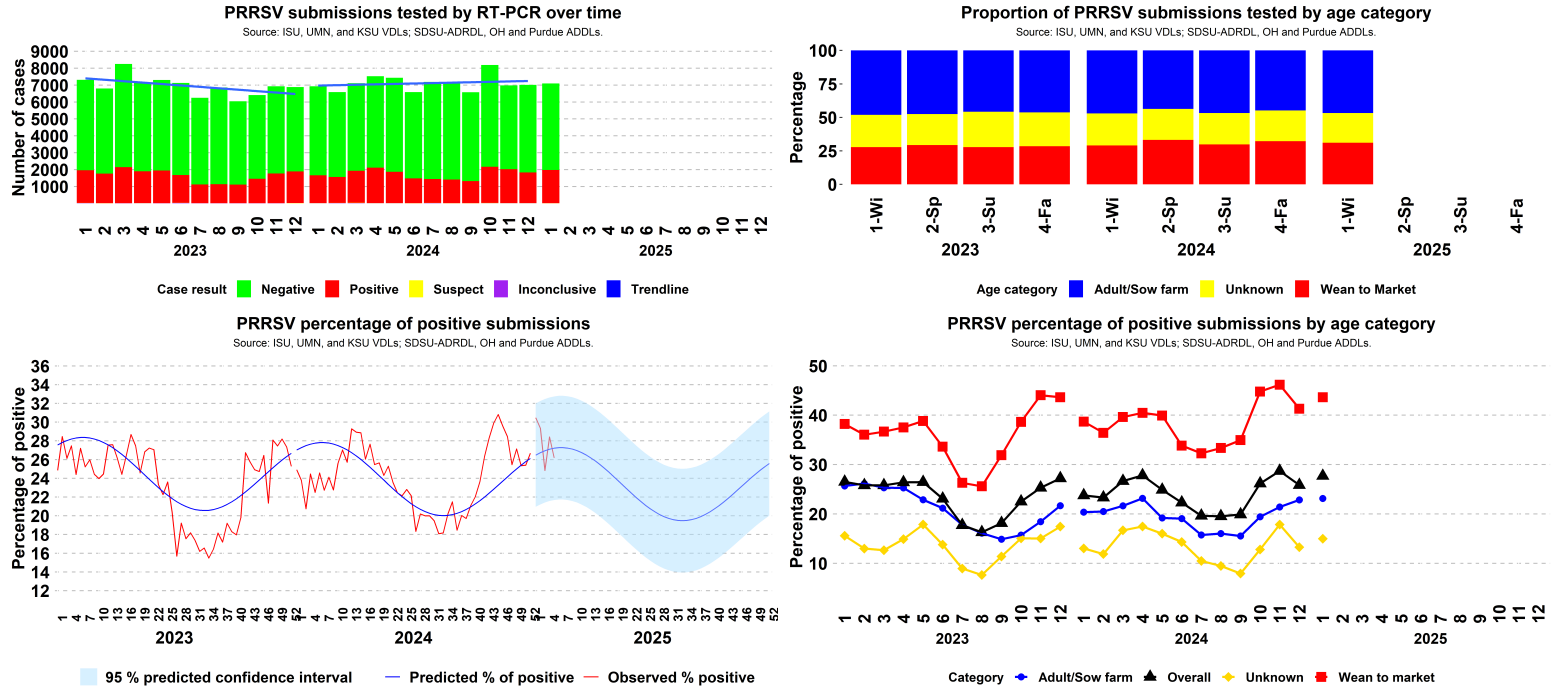
**PRRS virus RFLP/Lineage report** and **BLAST tool:** Benchmark PRRSV ORF5 sequences and compare your PRRSV sequence with what have been detected in the U.S.

**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, and Lauren Glowzinski.

**Note:** This report contains data up to January 31, 2025.

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

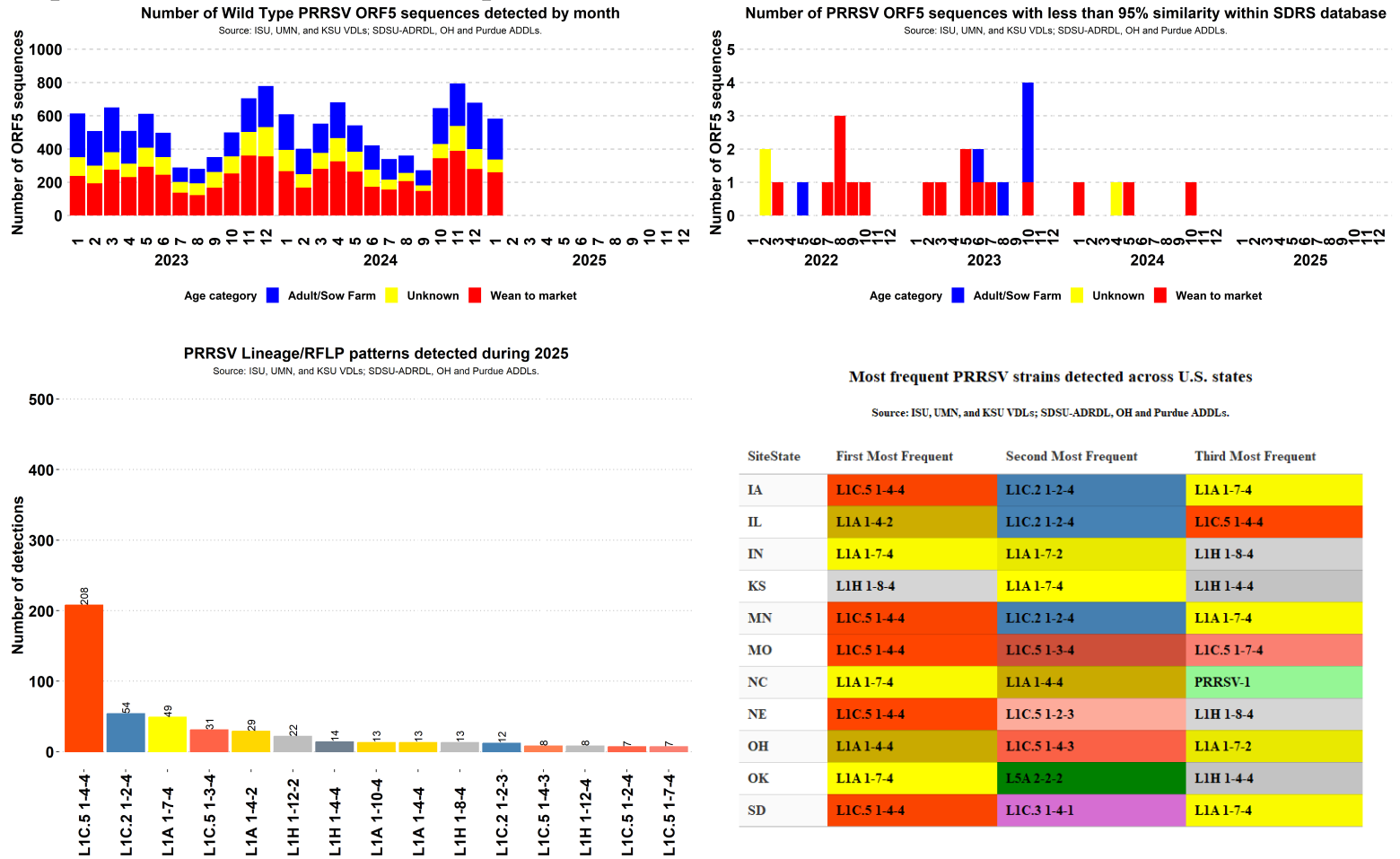


**Figure 1. Top:** *Left:* Results of PRRSV RT-PCR cases over time; *Right:* Proportion of accession ID cases tested for PRRSV by age group per year and season. **Bottom:** *Left:* Expected percentage of positive results for PRRSV RNA by RT-qPCR, with 95% confidence interval band for predicted results 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, 27.69% of 7,099 cases tested PRRSV-positive in January, similar to 25.85% of 7,011 in December;
  - Positivity in the adult/sow category in January was 23.12% (767 of 3,317), similar to 22.85% (759 of 3,321) in December;
  - Positivity in the wean-to-market category in January was 43.63% (963 of 2,207), a moderate increase from 41.31% (830 of 2,009) in December;
- Overall PRRSV-percentage of positive cases was within state-specific baselines in all 11 monitored states;

## Topic 2 – PRRSV ORF5 sequences detection over time

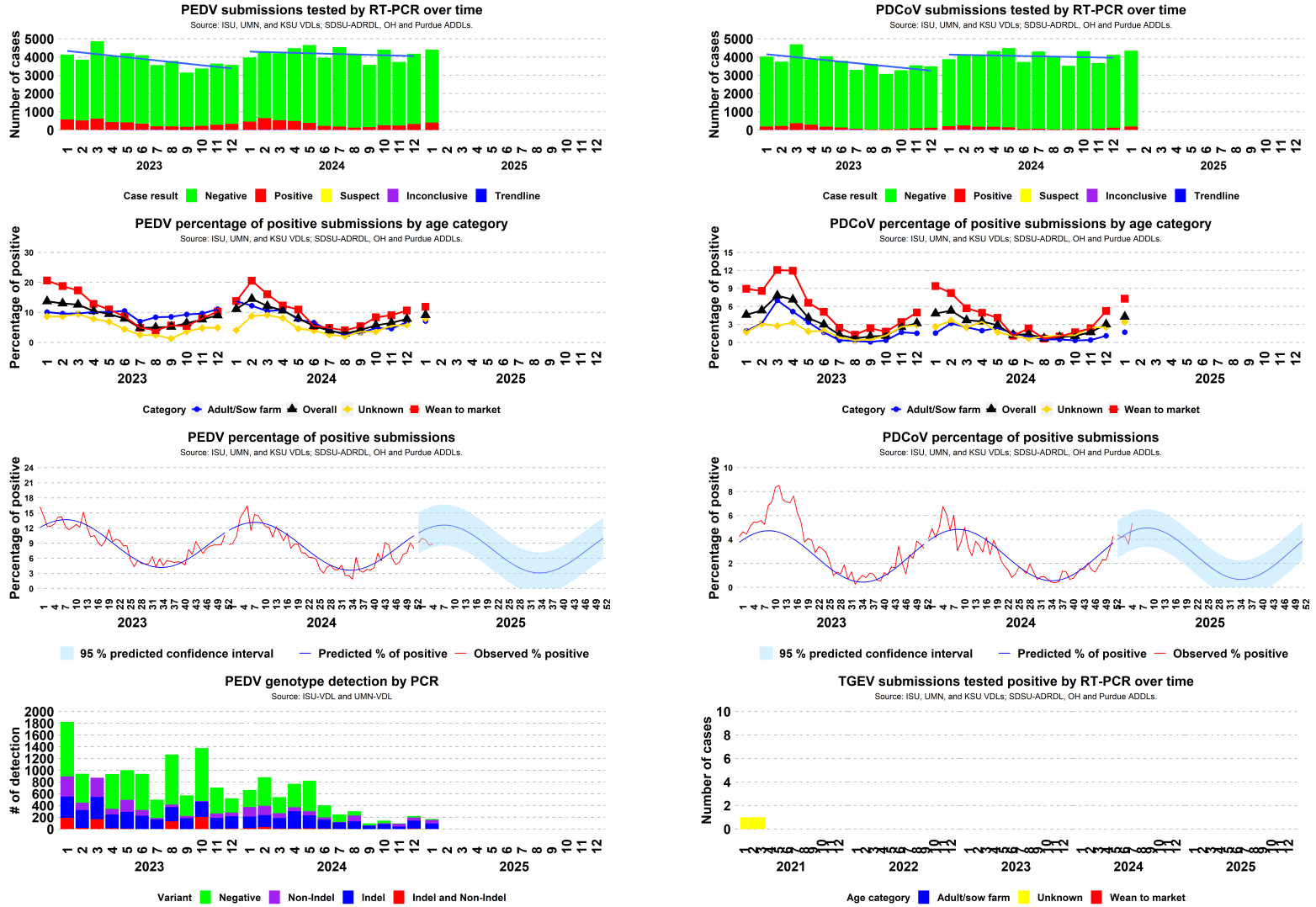


**Figure 1. Top: Left:** Number of PRRSV ORF5 sequences detected by age category; **Right:** Number of PRRSV ORF5 sequences with less than 95% similarity after BLAST analysis with the sequences in the SDRS database (Sequences with more than 6 ambiguities, sequences with less than 597 nucleotides or higher 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 by lineage and RFLP at U.S. state level.

### SDRS Advisory Group highlights:

- During January 2025, The states with higher number of PRRSV L1C.5 (variant) detections were detected IA, MO, MN, NE, IL, SD, IN, OH, OK (respective number of sequences: 156, 41, 36, 20, 9, 6, 3, 2, 1).
- In January L1C.5 1-4-4 (208) was the PRRSV sequence most detected in the U.S., followed by L1C.2 1-2-4 (54), and L1A 1-7-4 (49);
- 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.
- The advisory group highlighted that the PRRSV Lineage 1C.2 (mainly RFLP 1-2-4) caused significant clinical issues, leading to the depopulation of sow farms and poor production records. Some mentioned that it is severely affecting wean-to-finish sites in 2025 with high mortality rates and minimal response to treatments. The bonus page (end of this report) brings a deep dive into the L1C.2 activity in the U.S. swine herds.

## 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. **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.

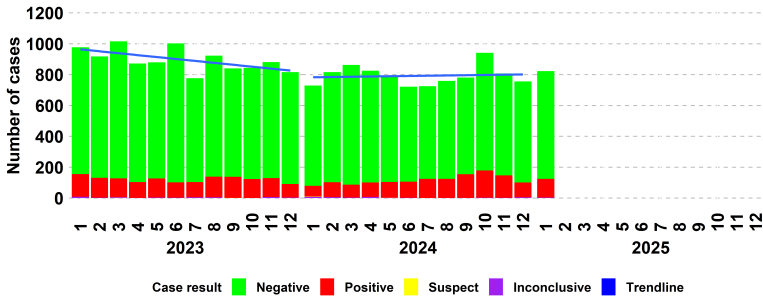
### SDRS Advisory Group highlights:

- Overall, 9.13% of 4,402 cases tested PEDV-positive in January, similar to 7.87% of 4,180 in December;
  - Positivity in the adult/sow category in January was 7.12% (111 of 1,558), similar to 6.75% (101 of 1,497) in December;
  - Positivity in the wean-to-market category in January was 11.88% (197 of 1,658), similar to 10.62% (159 of 1,497) in December;
  - Overall PEDV-percentage of positive cases was 3 standard deviations above state-specific baseline in IN;
  - Overall, 1.18% of 170 samples had mixed PEDV genotype detection in January, similar to 2.7% of 222 in December;
- Overall, 4.28% of 4,348 cases tested PDCoV-positive in January, similar to 3.01% of 4,118 in December;
  - Positivity in the adult/sow category in January was 1.71% (26 of 1,523), similar to 1.1% (16 of 1,452) in December;
  - Positivity in the wean-to-market category in January was 7.28% (120 of 1,648), a moderate increase from 5.23% (78 of 1,492) in December;
- Overall PDCoV-percentage of positive cases was within state-specific baselines in all 11 monitored states;
- There was 0 positive case for TGEV RNA-PCR in January, 2025 over a total of 4,245 cases tested. It has been 47 months (with a total of 169,736 cases tested) since the last TGEV PCR-positive result;
- Some advisory members mentioned that clean-ups are proceeding as expected, with some production systems reporting failure to eliminate PEDV within the typical time frame (less than 4-6 months). Wean-to-finish activity is present but not as severe as in previous years. Over the years, the decrease in PEDV positivity might be attributed to ongoing efforts to improve wean-to-finish biosecurity to reduce PEDV incidence.

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

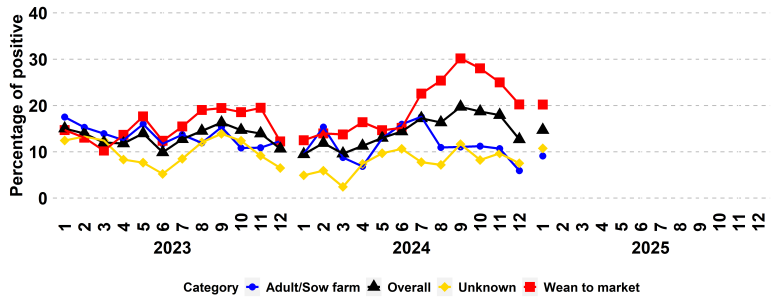
**Mycoplasma hyopneumoniae submissions tested by PCR over time**

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



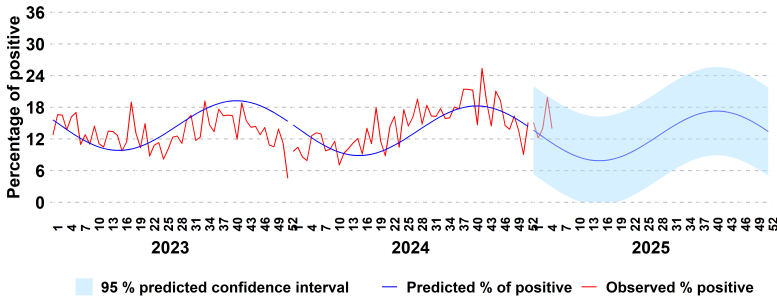
**Mycoplasma hyopneumoniae percentage of positive submissions by age category**

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



**Mycoplasma hyopneumoniae percentage of positive submissions**

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



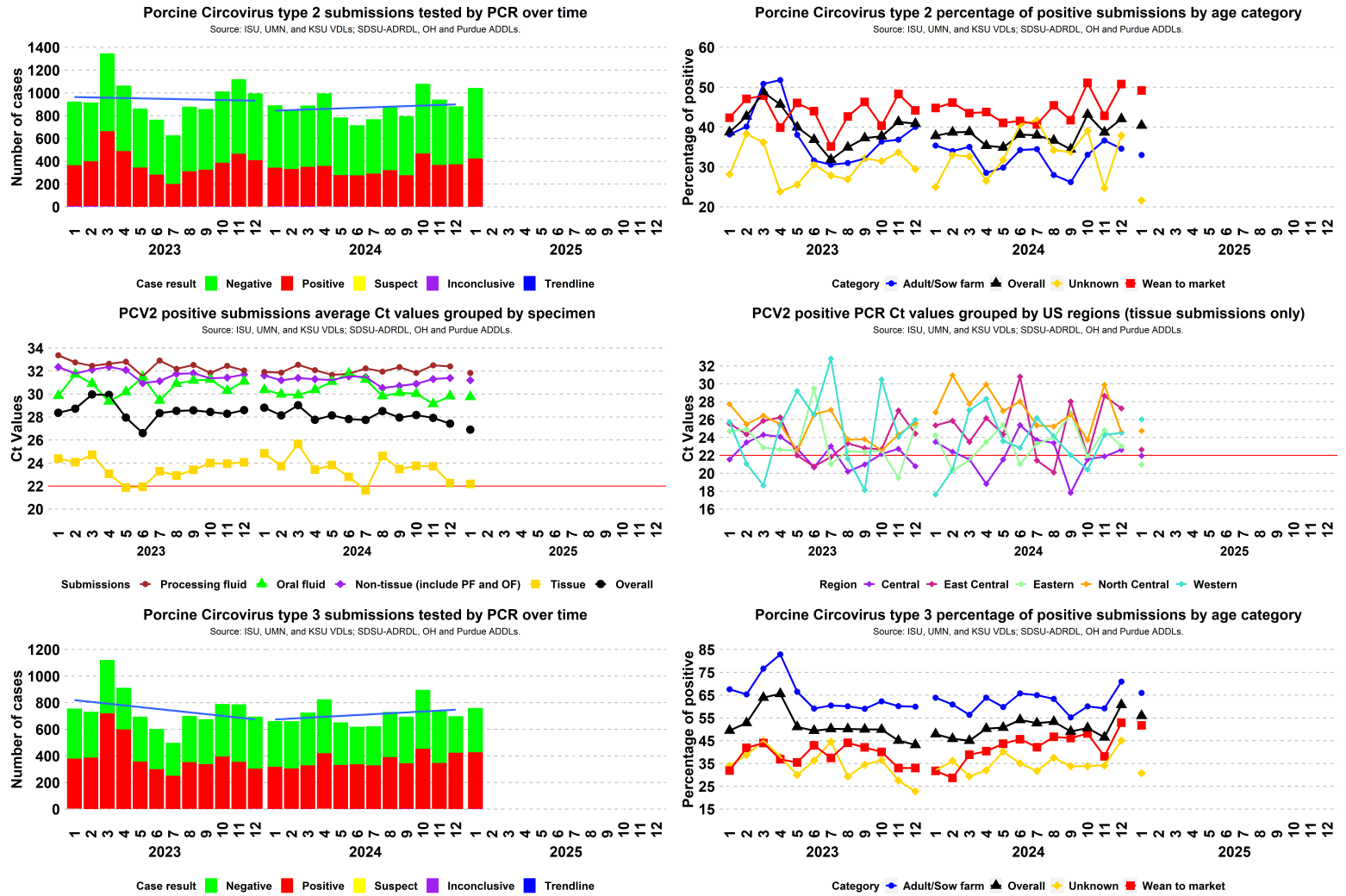
**Figure 3. Top:** *Left* MHP; MHP Case results tested by PCR over time. *Right* MHP PCR-positive results, by category over time. **Bottom:** expected percentage of positive results for MHP by PCR and 95% confidence interval for 2025 predicted value, based on weekly data observed in the previous 5 years.

#### SDRS Advisory Group highlights:

- Overall, 14.7% of 823 cases tested *M. hyopneumoniae*-positive cases in January, a moderate increase from 12.7% of 756 in December;
  - Positivity in the adult/sow category in January was 9.12% (25 of 274), a moderate increase from 5.95% (16 of 269) in December;
  - Positivity in the wean-to-market category in January was 20.2% (79 of 391), similar to 20.23% (69 of 341) in December;
- 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.

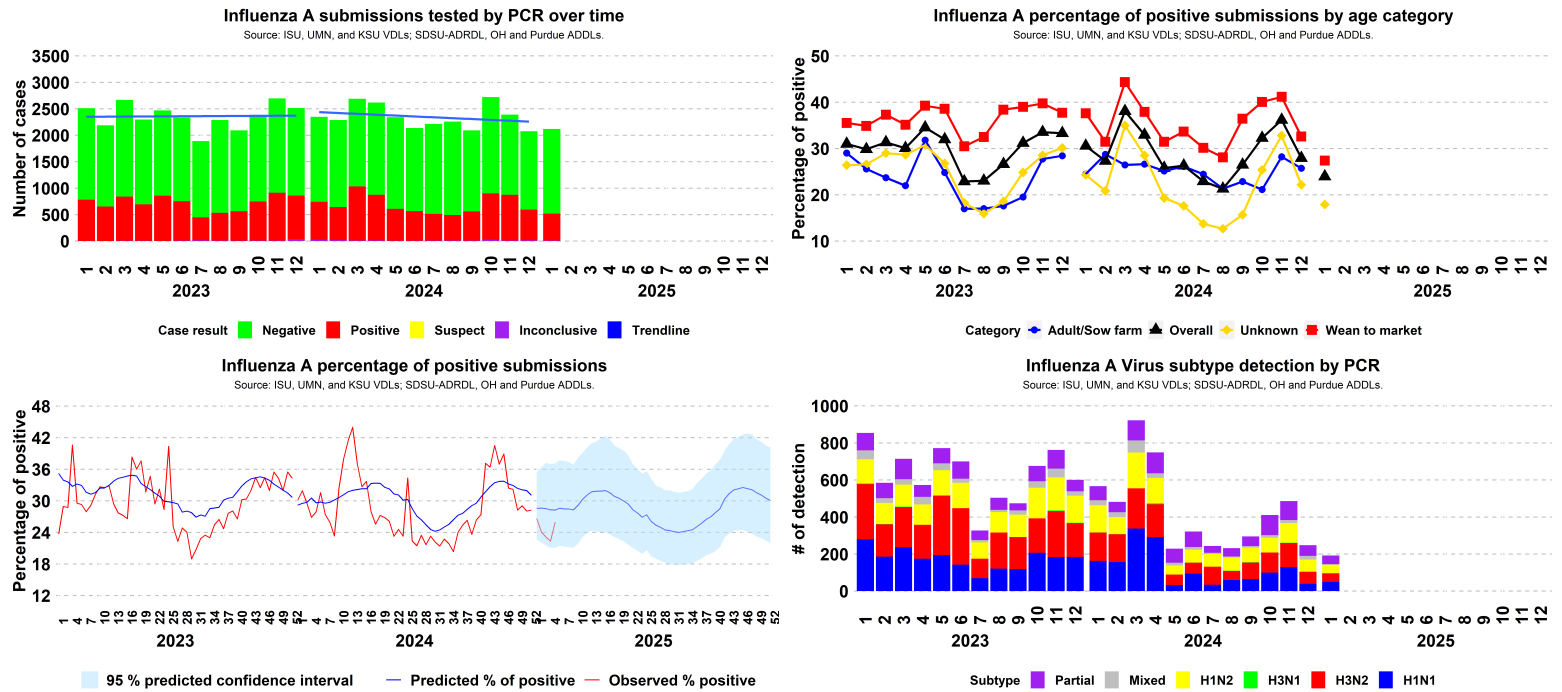


**Figure 1. Top:** *Left:* Results of PCV2 PCR cases over time; *Right:* PCV2 PCR-positive results, by category over time. **Middle:** *Left:* Average Ct values of PCV2 submissions by specimen; *Right:* Average Ct values of PCV2 tissue submissions by U.S. region; Central (IA), East Central (IL, IN, MO 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, 40.42% of 1,044 cases tested PCV2-positive in January, similar to 42.06% of 882 in December;
- Positivity in the adult/sow category in January was 33.01% (137 of 415), similar to 34.59% (138 of 399) in December;
- Positivity in the wean-to-market category in January was 49.17% (266 of 541), similar to 50.77% (197 of 388) in December;
- In the month of January, the regions with the lowest PCV2 average Ct values in tissue submissions was Eastern (32 submissions; average Ct 20.9), Central (102 submissions; average Ct 22), East Central (17 submissions; average Ct 22.6), North Central (21 submissions; average Ct 24.7), and Western (14 submissions; average Ct 26);
- Overall, 55.92% of 760 cases tested PCV3-positive in January, a moderate decrease from 60.74% of 698 in December;
  - Positivity in the adult/sow category in January was 65.98% (223 of 338), a moderate decrease from 70.96% (237 of 334) in December;
  - Positivity in the wean-to-market category in January was 51.74% (178 of 344), similar to 52.9% (155 of 293) in December.
- The advisory group highlighted a concern that PCV2 has increased due to vaccine administration compliance issues, affecting wean-to-finish sites. Some advisory members also mentioned an uptick in PCV2 cases, was observed during severe PRRS outbreaks, enhancing the number of PCV2 cases due to co-infections.

## 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, 23.96% of 2,120 cases tested IAV-positive cases in January, a moderate decrease from 27.92% of 2,077 in December;
  - Positivity in the adult/sow category in January was 24.17% (117 of 484), similar to 25.74% (122 of 474) in December;
  - Positivity in the wean-to-market category in January was 27.4% (283 of 1,033), a substantial decrease from 32.59% (321 of 985) in December.
- Overall IAV-percentage of positive cases was within state-specific baselines in all 11 monitored states;
- Overall, 2.08% of 192 samples had mixed subtype detection in January, a substantial decrease from 7.66% of 248 in December.





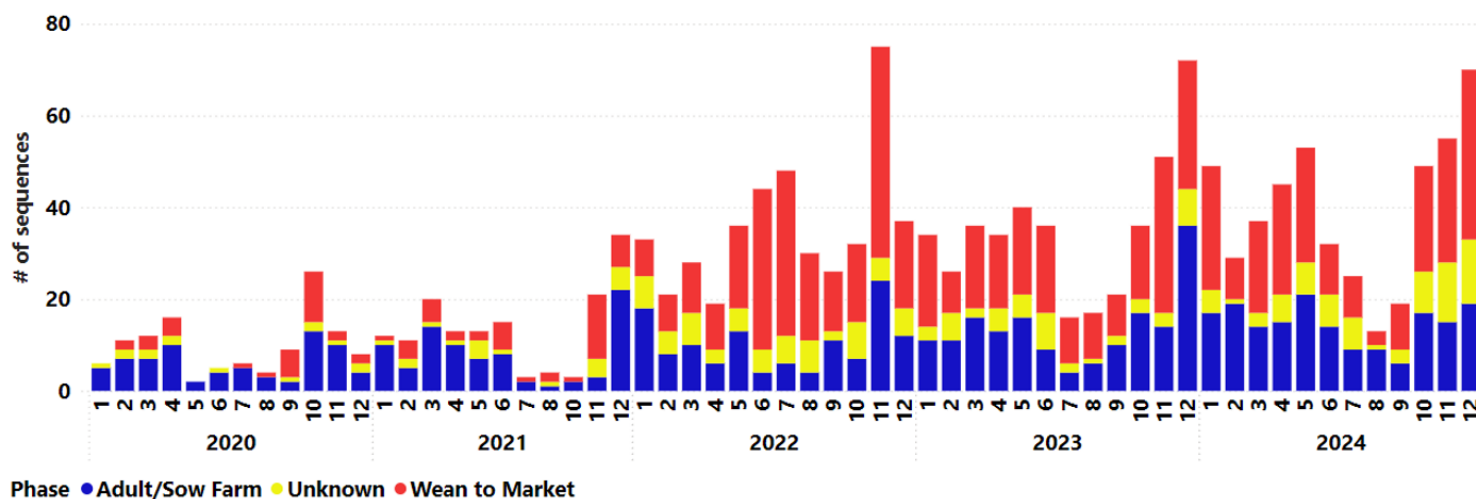
**Note:** The SDRS is a collaborative project among multiple VDLs in the US swine industry. The VDL collaborators and industry partners are all invited to submit content to share on this bonus page related to disease prevention, control, and management. Stay tuned for more content in future editions.

## The U.S. scenario of the PRRSV L1C.2 detection

Guilherme Cezar<sup>1</sup>, Kinath Rupasinghe<sup>1</sup>, Daniel Linhares<sup>1</sup>, Giovanni Trevisan<sup>1</sup>

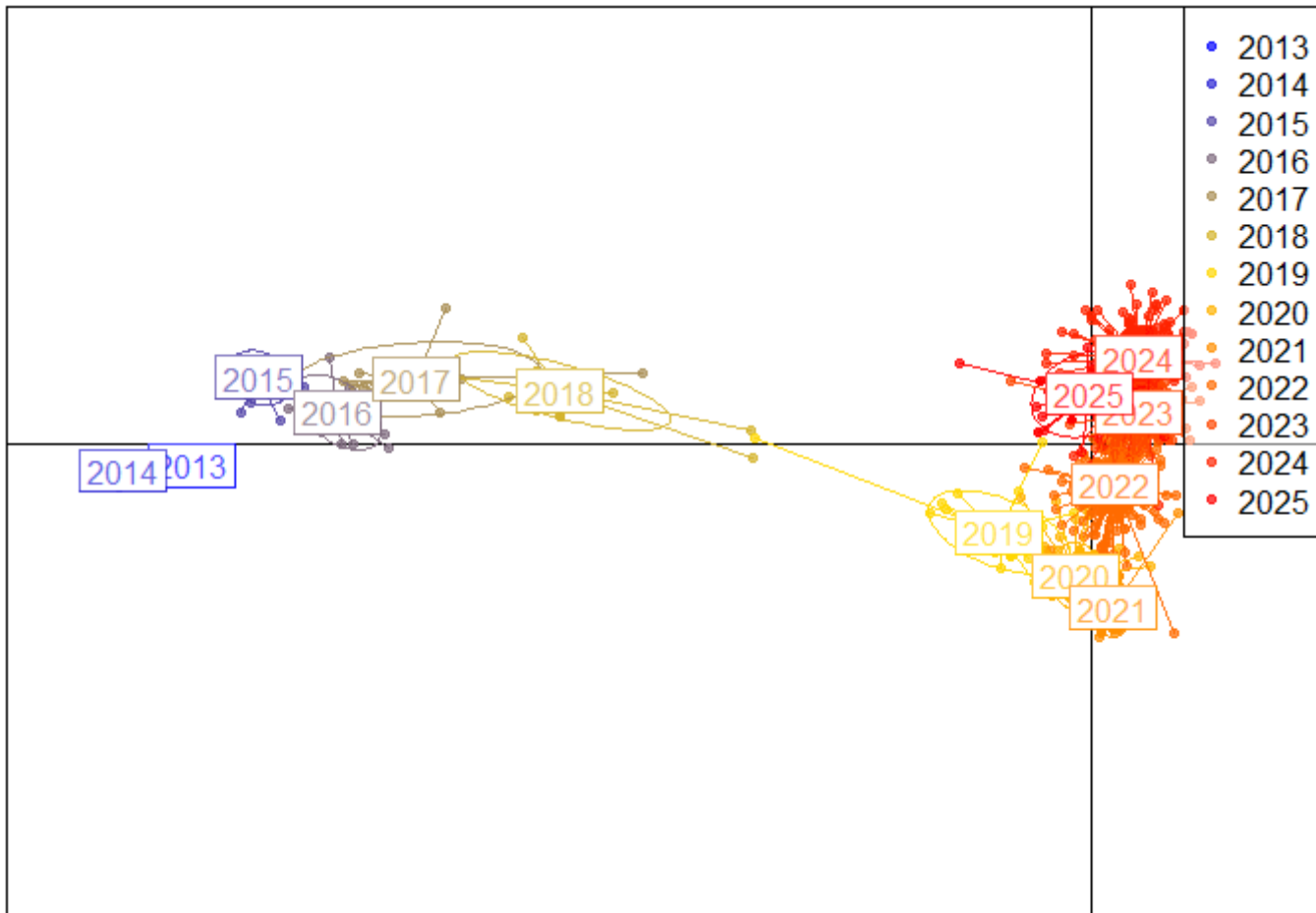
<sup>1</sup> - Iowa State University, Ames, IA, USA.

The Swine Disease Reporting System (SDRS) provides valuable insights into both endemic and emerging diseases impacting the swine population in the USA. SDRS has been closely monitoring the epidemiological curve of the lineage 1C.2 (L1C.2) sequences (figure 1). The first L1C.2 sequences were detected in 2013, and since then, L1C.2 has been detected across many states. Since 2022, the L1C.2 has been more frequently detected, and from October to December of 2024, the number of L1C.2 has been consistently above 50 sequences per month, with many recovered RT-qPCR on the tens.



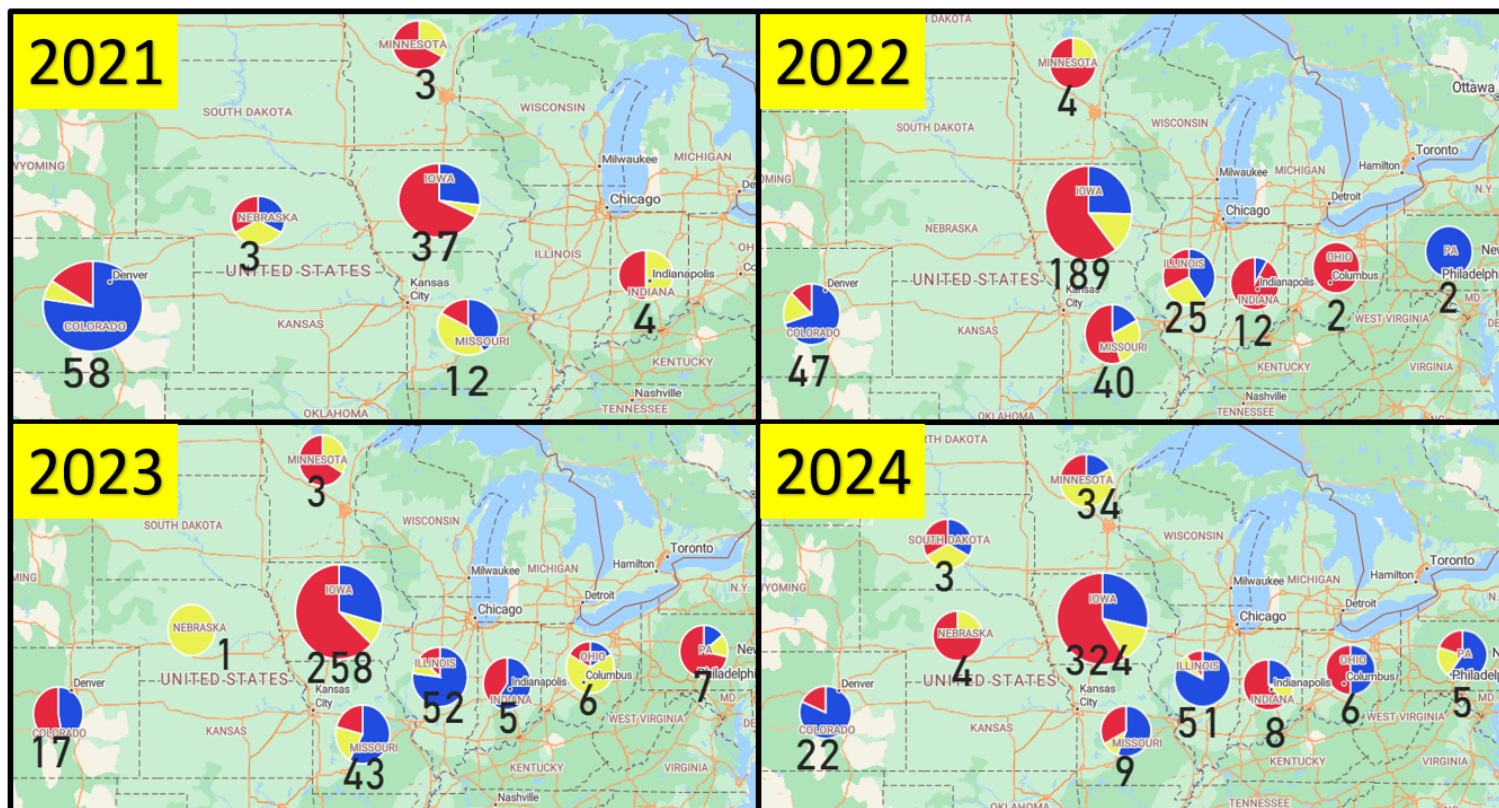
**Figure 1.** Detection of PRRSV L1C.2 detection over time.

The increased detection of L1C.2 coincided with a genetic change in the virus, based on ORF5 sequence data. There are three major clusters of L1C sequences. One group detected up to 2018 that is no longer detected (figure 2). A distinct group was detected in 2019, showing a significant accumulation of genetic changes from previous years. It kept evolving until 2021 and is represented by the unidirectionality of overlapping clusters from 2019 to 2021 (figure 2). In 2022, a change in the direction of overlapping clusters provided evidence of expanding the genetic diversity of PRRSV strains classified within L1C.2 during recent years coinciding with the period of time, whereas the L1C.2 becomes more frequently detected.



**Figure 2.** Discriminant analysis of principal components for porcine reproductive and respiratory syndrome virus open reading frame 5 (ORF5) sequences classified as L1C.2 for 2013–2025. Ellipses represent groups sharing genetic similarities; each year is represented by a different color, and each dot represents an ORF5 sequence.

The cumulative L1C.2 detection by state from 2021 to 2024 are provided in Figure 3. Most of the L1C.2 have been detected from wean-to-market samples in Iowa, whereas the L1C.2 was the second most frequently detected, only behind the L1C.5. The L1C.2 was the primary wild-type virus detected in Illinois. L1C.2 became more commonly detected in Minnesota in May 2024 and ended 2024 as the third most frequent wild-type strain detected in this state. The increased frequency of detection of L1C.2 shows regional spread, and L1C.2 could become an imminent animal health threat. The SDRS provides a [search tool](#) where users can provide a given ORF5 sequence and see if a similar sequence has been seen before and where and what the level of nucleotide identity and associated genetic characteristics of sequences present in the SDRS database.



Phase ● Adult/Sow Farm ● Unknown ● Wean to Market

Figure 3. Cumulative detection of L1C.2 over time by U.S. states.

**Highlights:**

- L1C.2 became the lineage predominantly detected in Illinois and the second most detected in Iowa during 2024;
- L1C.2 has been detected in 11 U.S. states in 2024 demonstrating a large distribution of cases throughout the Midwest;
- L1C.2 had multiple cases with qRT-PCR Ct values around 10, demonstrating a high viral load;
- Increased detection of L1C.2 coincided with genetic changes in the virus, showing three major clusters of L1C sequences: One group detected up to 2018, no longer detected; a distinct group from 2019 evolved until 2021, showing significant genetic changes; overlapping clusters indicated expanding genetic diversity of PRRSV strains within L1C.2, coinciding with more frequent detection in 2022.