

# Swine Disease Reporting System

## Report # 76 (June 04, 2024)

**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 Animal Disease and Diagnostic Laboratory (ADDL), and Purdue ADDL.

### Collaborators:

*Swine Disease Reporting System office:* Principal investigators: [Daniel Linhares](#) & [Giovani Trevisan](#); Project coordinator: [Guilherme Cezar](#), Communications: [Edison Magalhães](#), Data analyst: Srijita Chandra.

*Iowa State University:* Gustavo Silva, Marcelo Almeida, Bret Crim, Kinath Rupasinghe, Eric Burrough, Phillip Gauger, Christopher Siepker, Marta Mainenti, Michael Zeller, Rodger Main.

*University of Minnesota:* Mary Thurn, Paulo Lages, Cesar Corzo, Albert Rovira, Hemant Naikare.

*Kansas State University* and *Kansas Dept. of Agr.:* Rob McGaughey, Franco Matias-Ferreira, 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, Ashley Johnson, Dennis Summers, Andréia Arruda.

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

**Disease Diagnosis System:** A pilot program with the ISU-VDL consisting of reporting disease detection (not just pathogen detection by PCR), based on diagnostic codes assigned by veterinary diagnosticians.

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

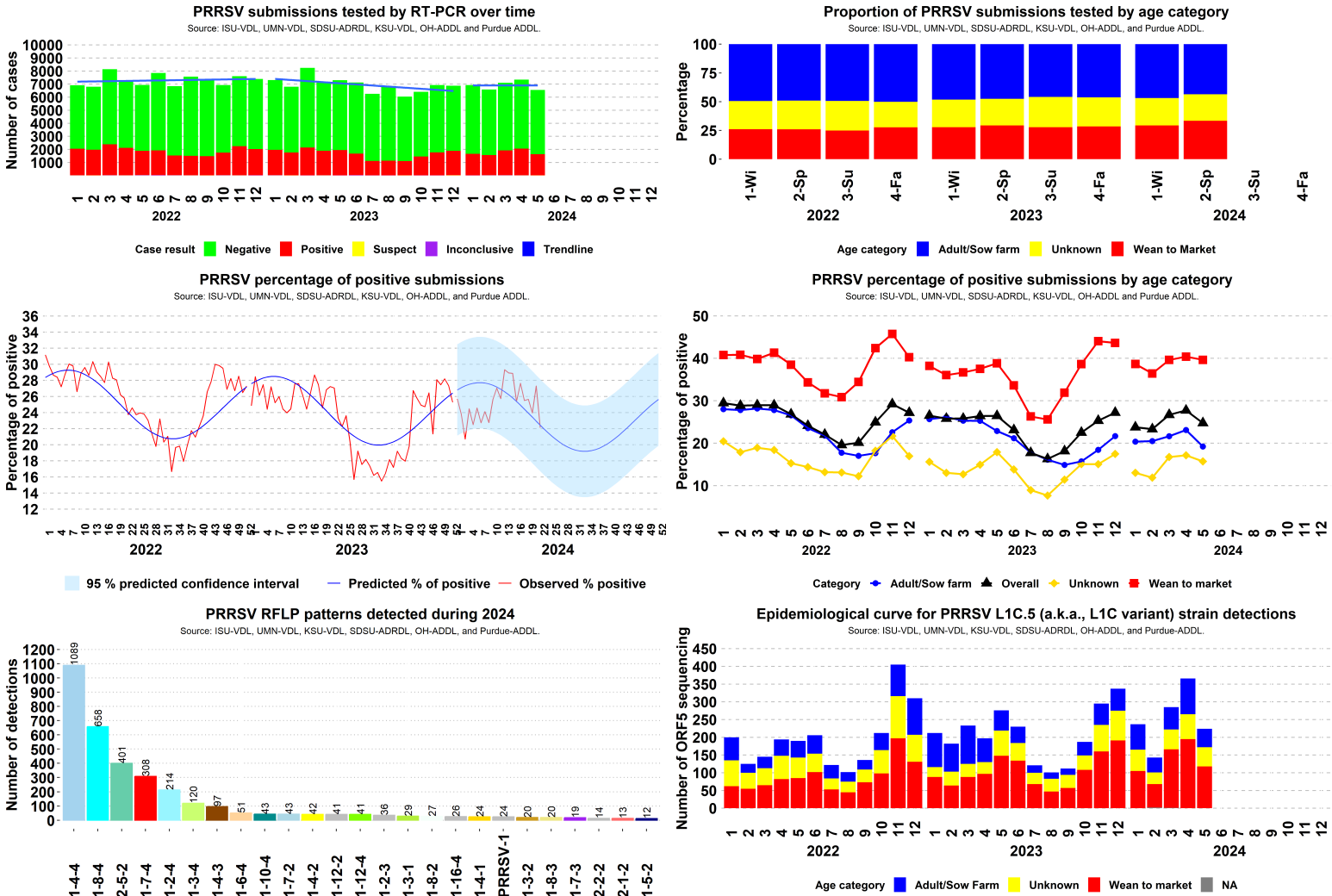
**PRRS virus RFLP/Lineage report** and **BLAST tool:** Benchmark PRRSV ORF5 sequences and compare your PRRSV sequence with what have been detected in the U.S.

**Audio and video reports:** Key findings from SDRS projects are summarized monthly in a conversation between investigators and available in the form of an “audio/video report” through [Spotify](#), [Apple Podcast](#), [Google podcast](#), [SwineCast](#), [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 Glowzenski.

**Note:** This report contains data up to May 31, 2024.

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

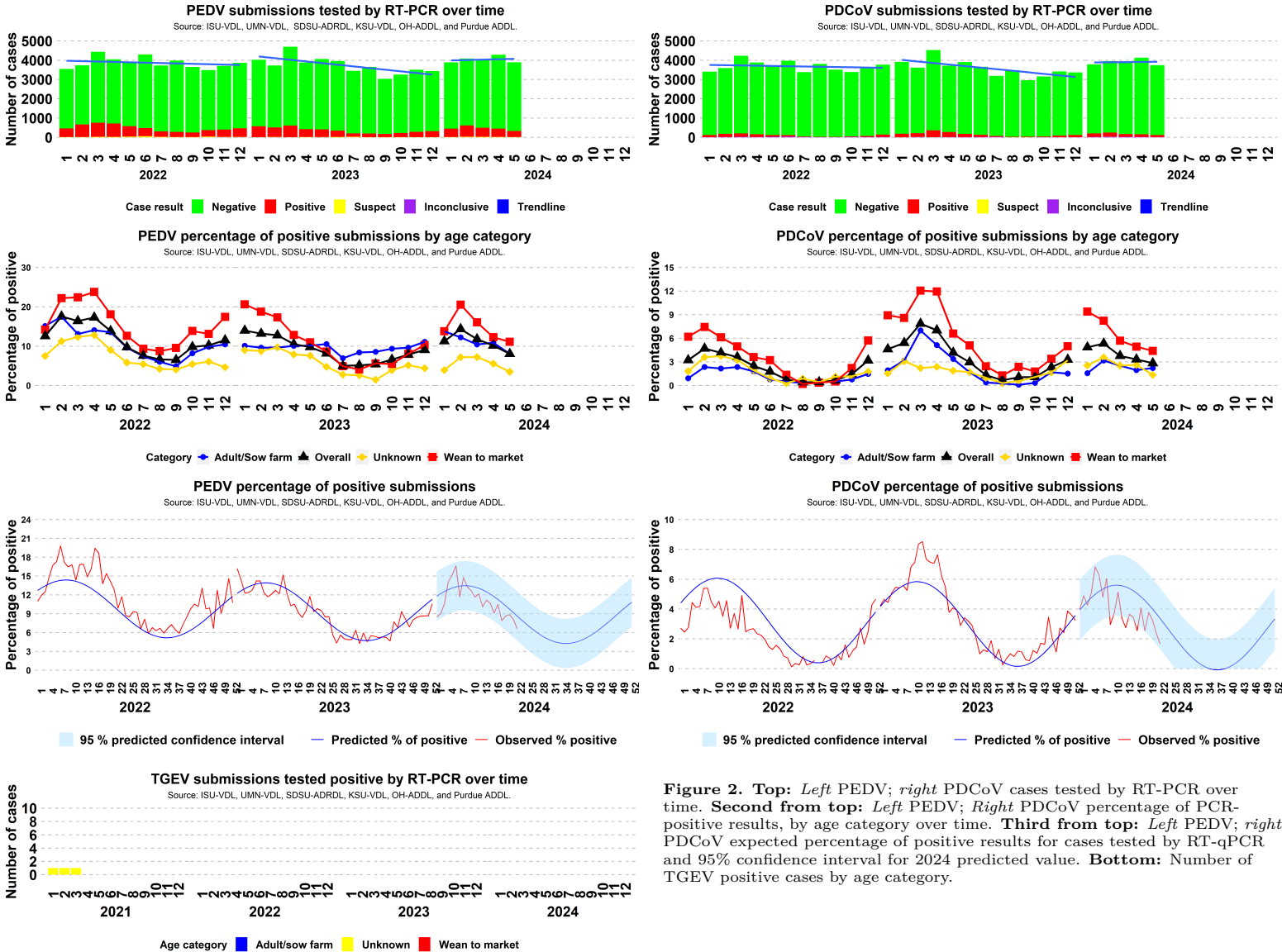


**Figure 1.** *Top: Left:* Results of PRRSV RT-PCR cases over time; *Right:* Proportion of accession ID cases tested for PRRSV by age group per year and season. *Middle: Left* Expected percentage of positive results for PRRSV RNA by RT-qPCR, with 95% confidence interval band for predicted results based on weekly data observed in the previous 3 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. *Bottom Left:* The 25 most frequently detected RFLP patterns during 2024; *Right:* Epidemiological curve of detection for PRRSV Lineage 1C variant (L1C.5) strain.

## SDRS Advisory Group highlights:

- Overall, 24.76% of 6,552 cases tested PRRSV-positive in May, a moderate decrease from 27.72% of 7,345 in April;
  - Positivity in the adult/sow category in May was 19.22% (558 of 2,903), a moderate decrease from 23.12% (734 of 3,175) in April;
  - Positivity in the wean-to-market category in May was 39.64% (813 of 2,051), similar to 40.4% (1,020 of 2,525) in April;
- Overall PRRSV-percentage of positive cases was 3 standard deviations above state-specific baselines in IA, SD, and IN;
- During May 2024, PRRSV L1C.5 (variant) strains were detected in IA (136), MN (35), MO (25), NE (11), IN (5), IL (3), SD (2) and OH (2).
- The advisory group highlighted the increased number of L1C.5 detections, hitting hard mainly the state of Iowa. The advisory group highlighted that other lineages, such as L1A and L1H, are also causing issues in the field.

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

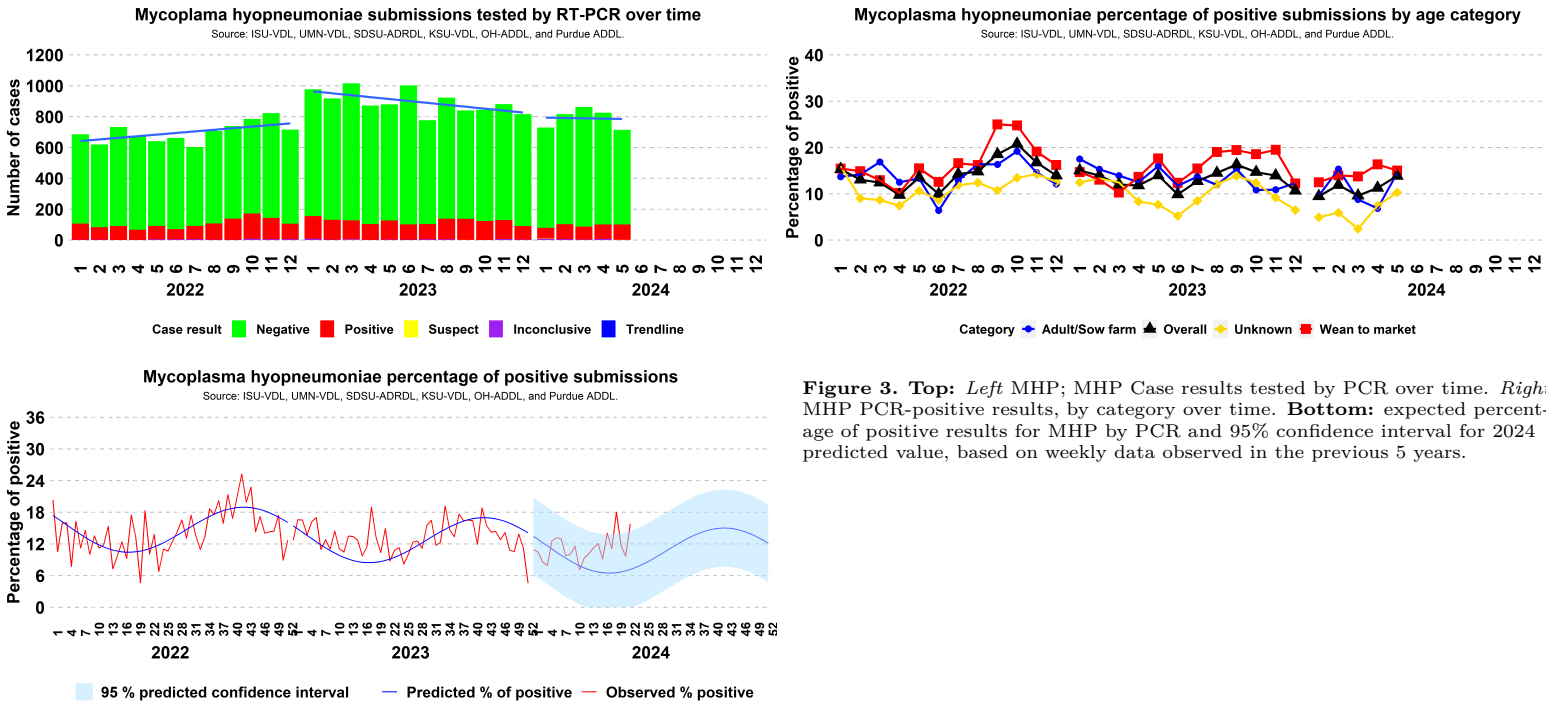


**Figure 2. Top: Left** PEDV; **right** PDCoV cases tested by RT-PCR over time. **Second from top: Left** PEDV; **Right** PDCoV percentage of PCR-positive results, by age category over time. **Third from top: Left** PEDV; **right** PDCoV expected percentage of positive results for cases tested by RT-qPCR and 95% confidence interval for 2024 predicted value. **Bottom:** Number of TGEV positive cases by age category.

## SDRS Advisory Group highlights:

- Overall, 8.04% of 3,892 cases tested PEDV-positive in May, a moderate decrease from 10.16% of 4,283 in April;
- Positivity in the adult/sow category in May was 8.03% (111 of 1,383), a moderate decrease from 10.89% (170 of 1,561) in April;
- Positivity in the wean-to-market category in May was 11.11% (167 of 1,503), similar to 12.28% (208 of 1,694) in April;
- Overall PEDV-percentage of positive cases was 3 standard deviations above state-specific baselines in KS;
- Overall, 2.83% of 3,743 cases tested PDCoV-positive in May, similar to 3.32% of 4,131 in April;
- Positivity in the adult/sow category in May was 2.21% (29 of 1,314), similar to 1.96% (29 of 1,481) in April;
- Positivity in the wean-to-market category in May was 4.4% (64 of 1,456), similar to 4.94% (82 of 1,661) in April;
- Overall PDCoV-percentage of positive cases was 3 standard deviations above state-specific baselines in MN;
- There was 0 positive case for TGEV RNA-PCR in May, 2024 over a total of 3,564 cases tested. It has been 39 months (with a total of 133,230 cases tested) since the last TGEV PCR-positive result;

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



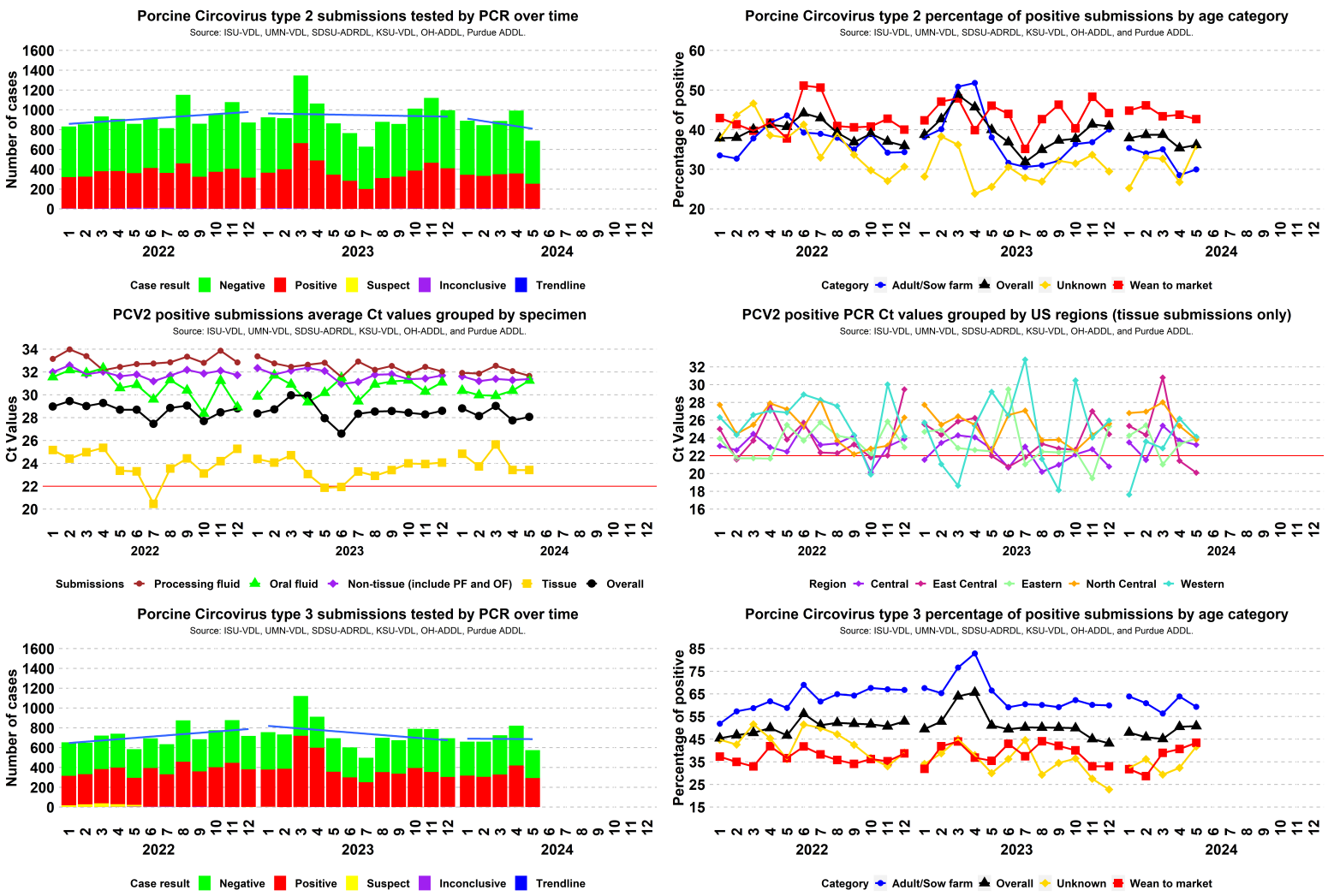
**Figure 3. Top: Left** MHP; MHP Case results tested by PCR over time. **Right** MHP PCR-positive results, by category over time. **Bottom:** expected percentage of positive results for MHP by PCR and 95% confidence interval for 2024 predicted value, based on weekly data observed in the previous 5 years.

#### SDRS Advisory Group highlights:

- Overall, 13.87% of 714 cases tested *M. hyopneumoniae*-positive cases in May, a moderate increase from 11.27% of 825 in April;
  - Positivity in the adult/sow category in May was 14.46% (35 of 242), a substantial increase from 6.86% (19 of 277) in April;
  - Positivity in the wean-to-market category in May was 15.03% (49 of 326), similar to 16.35% (61 of 373) in April;
- Overall MHP-percentage of positive cases was 3 standard deviations above state-specific baselines in SD;
- The advisory group highlighted that there is not an unusual increased number of *Mycoplasma hyopneumoniae* outbreaks in the field. Still, according to them, it is a concern to have increased positivity “out of season,” they emphasize the importance of keeping biosecurity.



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

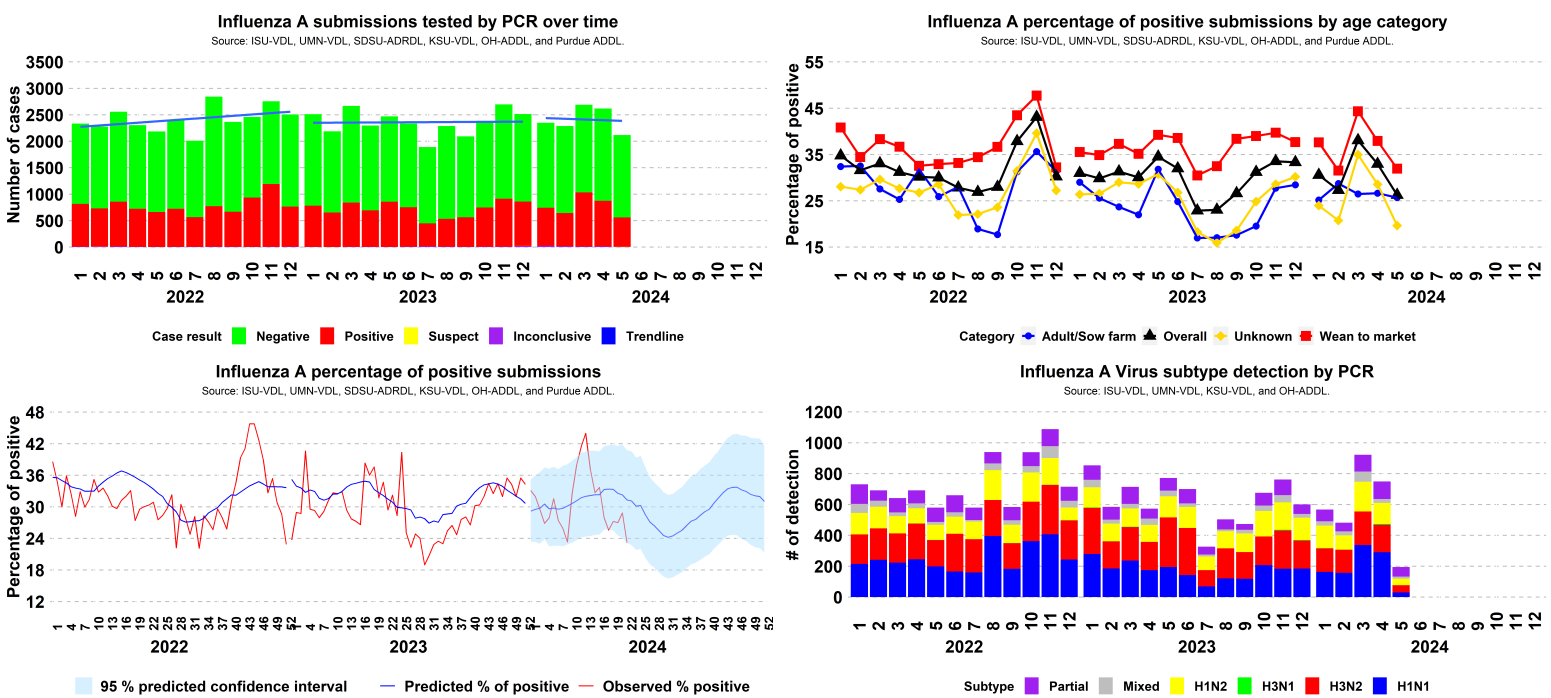


**Figure 1. Top:** *Left:* Results of PCV2 PCR cases over time; *Right:* PCV2 PCR-positive results, by category over time. **Middle:** *Left:* Average Ct values of PCV2 submissions by specimen; *Right:* Average Ct values of PCV2 tissue submissions by U.S. region; Central (IA), East Central (IL, IN, MO 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). **Bottom Left:** Results of PCV3 PCR cases over time; *Right:* PCV3 PCR-positive results, by category over time.

## SDRS Advisory Group highlights:

- Overall, 36.14% of 689 cases tested PCV2-positive in May, similar to 35.35% of 993 in April;
  - Positivity in the adult/sow category in May was 29.97% (92 of 307), similar to 28.54% (121 of 424) in April;
  - Positivity in the wean-to-market category in May was 42.66% (125 of 293), similar to 43.76% (200 of 457) in April;
- In the month of May, the regions with the lowest PCV2 average Ct values in tissue submissions was East Central (7 submissions; average Ct 20.1), Central (43 submissions; average Ct 23.2), North Central (25 submissions; average Ct 23.8), Eastern (11 submissions; average Ct 24), and Western (9 submissions; average Ct 24.1);
- Overall, 50.78% of 575 cases tested PCV3-positive in May, similar to 50.49% of 822 in April;
  - Positivity in the adult/sow category in May was 59.27% (163 of 275), a moderate decrease from 63.9% (246 of 385) in April;
  - Positivity in the wean-to-market category in May was 43.44% (96 of 221), a moderate increase from 40.66% (135 of 332) in April.

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



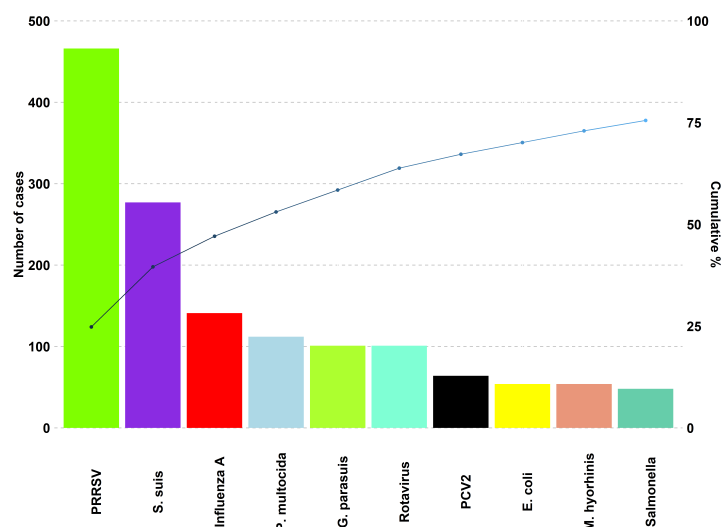
**Figure 3. Top:** *Left* Results of IAV PCR cases over time. *Right* Percentage of IAV PCR-positive results, by category over time. **Bottom:** *Left* expected percentage of positive results for IAV by PCR and 95% confidence interval for 2024 predicted value, based on weekly data observed in the previous 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:

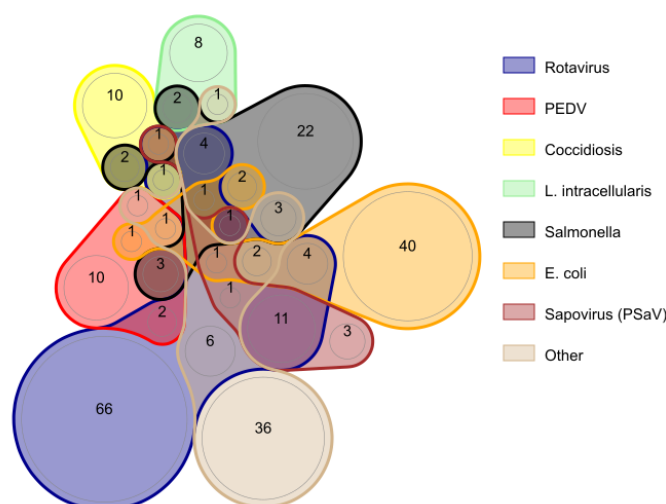
- Overall, 26.25% of 2,118 cases tested IAV-positive cases in May, a substantial decrease from 32.95% of 2,619 in April;
  - Positivity in the adult/sow category in May was 25.69% (111 of 432), similar to 26.64% (130 of 488) in April;
  - Positivity in the wean-to-market category in May was 31.96% (295 of 923), a substantial decrease from 37.92% (504 of 1,329) in April.
- Overall IAV-percentage of positive was within state-specific baselines in all 11 monitored states;
- Overall, 6.67% of 195 samples had mixed subtype detection in May, a moderate increase from 3.34% of 749 in April.

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

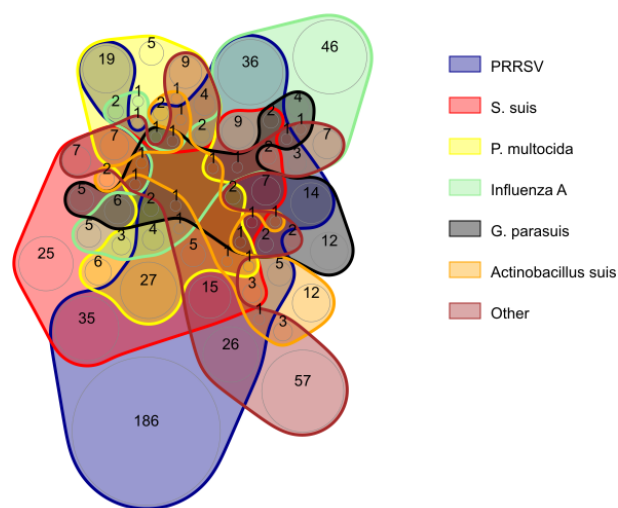
### Overall diagnosis



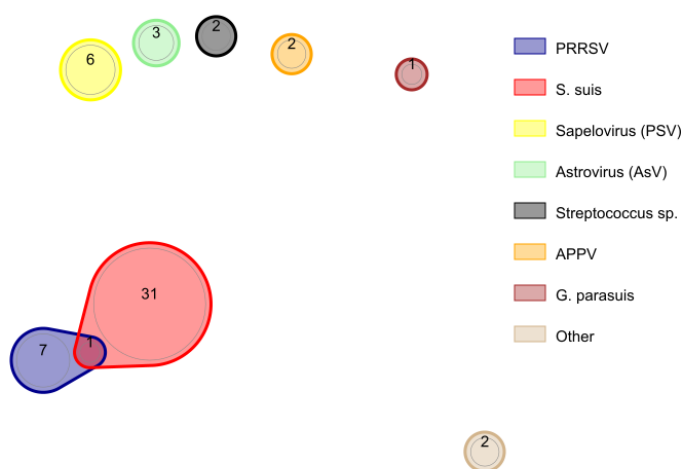
### Digestive



### 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, Mainenti, Michael, Piñeyro, Siepker, Madson, Thomas 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 April. 1 to May. 20, 2024.

### SDRS Advisory Group highlights:

- PRRSV (466) led cases with confirmed etiology, followed by *S. suis* (277), and Influenza A (141). PRRSV (428 of 1156) led the number of confirmed respiratory diagnoses, Rotavirus (101 of 307) lead the number of confirmed digestive diagnoses, and *S. suis* (32 of 56) led the number of confirmed neurological diagnoses.
- The advisory group highlighted that they have seen more bacterial co-infections such as *Pasteurella multocida*, *Glaesserella parasuis* and *Streptococcus suis* associated with PRRSV in the field. PRRSV, *Streptococcus suis*, Influenza A virus, *Pasteurella multocida*, and *Glaesserella parasuis* are the top 5 most diagnosed disease at ISU-VDL from April to May 2024.

**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.

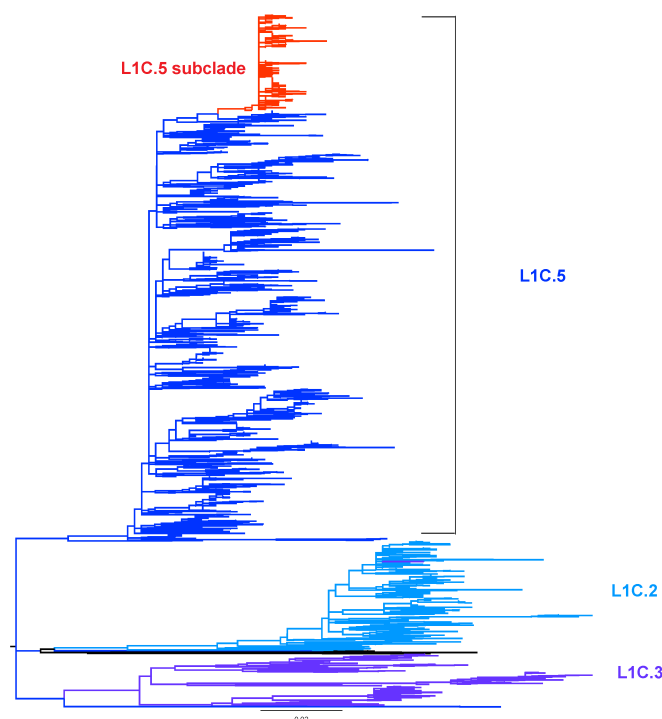
## Detection of an emergent PRRSV Lineage 1C.5 Subclade

Rabsa Naseer<sup>1</sup>, Michael Zeller<sup>1</sup>, Phill Gauger<sup>1</sup>

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

Since its emergence in 2020, the Iowa State University Veterinary Diagnostic Laboratory (ISU VDL) has detected nearly 5,000 unique PRRSV-2 Lineage 1C.5 cases, accounting for approximately 56% of the total Lineage 1C cases sequenced at the ISU VDL from February 2020 to May 2024. The ISU VDL regularly tracks the diversity of circulating PRRSV strains using phylogenetic and epidemiological methods, which led to the recent discovery of a new divergent Lineage 1C.5 subclade. A total of 306 cases were identified as members of this subclade, sampled from July 2023 to May 2024. The sequences of this subclade show high genetic similarity of over 97%, with an average nucleotide difference of approximately four nucleotide bases. This close genetic similarity within a window of around ten months suggests a clonal expansion is in progress. The index case was identified from an Iowa production system on July 20th, 2023. Much of these Lineage 1C.5 clonal expansion cases have been derived from Iowa swine farms, highlighting a regional outbreak. There have been sporadic detections in Minnesota (4), Illinois (3), and Nebraska (2). This lineage has been detected primarily in grow-finisher farms (277), with several cases at nurseries (26). The typical presentation is interstitial pneumonia, common in PRRS related cases.

The prevalence of cases related to this strain of Lineage 1C.5 has increased over time. Initially, cases were slightly increased during November and December of 2023. This was followed by a significant rise in 2024, with cases jumping from 12 in February to 49 in March and the most substantial increase occurring in April, with 110 detections. In May, 52 cases were detected, the most recent detection reported on May 17th, 2024. The genetic diversity of the L1C.5 was assessed using Bayesian phylodynamic methods. The overall genetic diversity of the entire Lineage 1C.5 peaked in February of 2023, after which it started to decline, with a sharp decrease occurring in November of the same year. This is typical when a genetic strain is being selected for and can occur if one strain has an advantage in spreading between pigs. The cycle threshold (Ct) is a diagnostic value used to determine if a sample is positive for a pathogen and is inversely related to how much virus is present in the sample. The median cycle threshold values for Lineage 1C.5 are dependent on sample type, approximately 16 in lung specimens and 28 to 30 in oral fluid specimens. This subclade of Lineage 1C.5 follows the same pattern with similar Ct values. The average Ct values for lung and oral fluid specimens across the Lineage 1C.5 subclade are generally lower than those of Lineage 1A. The median Ct values for Lineage 1A are recorded at 18.4 for lung specimens and 31.4 for oral fluid specimens. This indicates a higher viral load in Lineage 1C.5 compared to Lineage 1A. The effective reproduction number, a measure used to indicate how many subsequent infections occur from a primary infected pig, was estimated using phylogenetic methods. The estimated values ranged between 1.2 and 3.2 since the start of the year, suggesting a fast spread among the swine population.



**Figure 1.** Clonal expansion demonstrated in red color in the phylogenetic tree with PRRSV lineages.

Continued monitoring of PRRSV diversity, including Lineage 1C.5, is crucial for effective management. The emergence of a new divergent Lineage 1C.5 subclade in Iowa highlights a regional outbreak warranting attention, especially regarding its potential dominance as transmission spreads. Analysis revealing clonal expansion within Lineage 1C.5 suggests heightened transmissibility, while lower median Ct values and a higher effective reproduction number emphasize potentially increased virulence and spread. These findings underscore the importance of continued surveillance to mitigate the impact of PRRSV outbreaks on swine health.

### Highlights:

- There have been approximately 300 sequences detected since June 2023 of genetically related Lineage 1C.5 subclade;
- Most detections are currently in Iowa, primarily sequenced from grow-finisher farms;
- Clinical significance is undetermined, but the situation is being monitored.