Swine Disease Reporting System
Report # 77 (July 02, 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.

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.

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-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, 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 June 30, 2024.

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

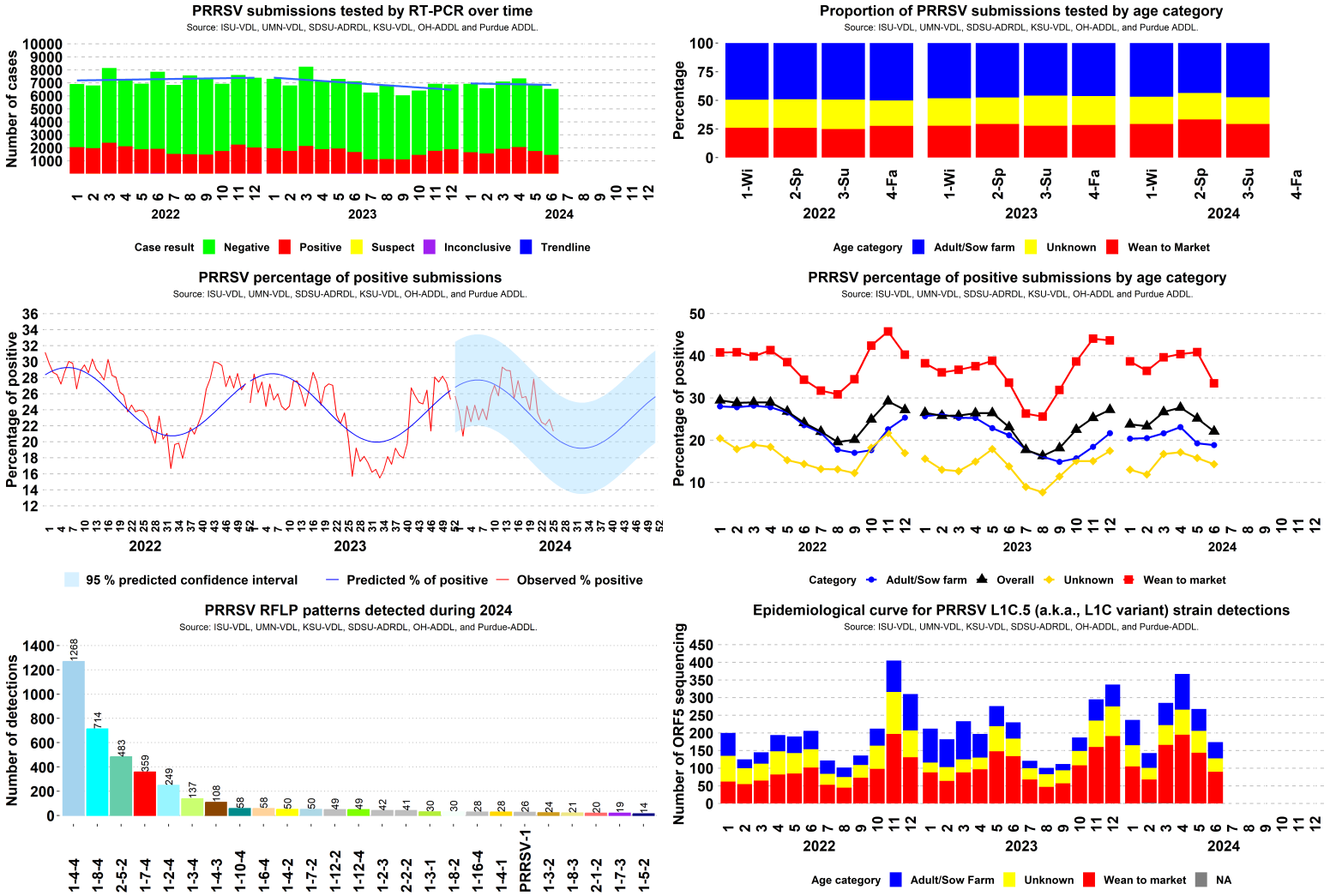


Figure 1. Top: *Left*: Results of PRRSV RT-PCR cases over time; *Right*: Proportion of accession ID cases tested for PRRSV by age group per year and season. **Middle**: *Left* Expected percentage of positive results for PRRSV RNA by RT-qPCR, with 95% confidence interval band for predicted results based 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, 22.09% of 6,537 cases tested PRRSV-positive in June, a moderate decrease from 25.16% of 6,900 in May;
  - Positivity in the adult/sow category in June was 18.85% (583 of 3,093), similar to 19.27% (589 of 3,056) in May;
  - Positivity in the wean-to-market category in June was 33.47% (643 of 1,921), a substantial decrease from 40.85% (880 of 2,154) in May;
- Overall PRRSV-percentage of positive cases was 3 standard deviations above state-specific baselines SD and IN;
- During June 2024, PRRSV L1C.5 (variant) strains were detected in IA (99), MN (31), MO (17), NE (15), SD (2), IL (2), IN (2) and OH (2).

Topic 2 – Enteric coronavirus RNA detection by RT-qPCR

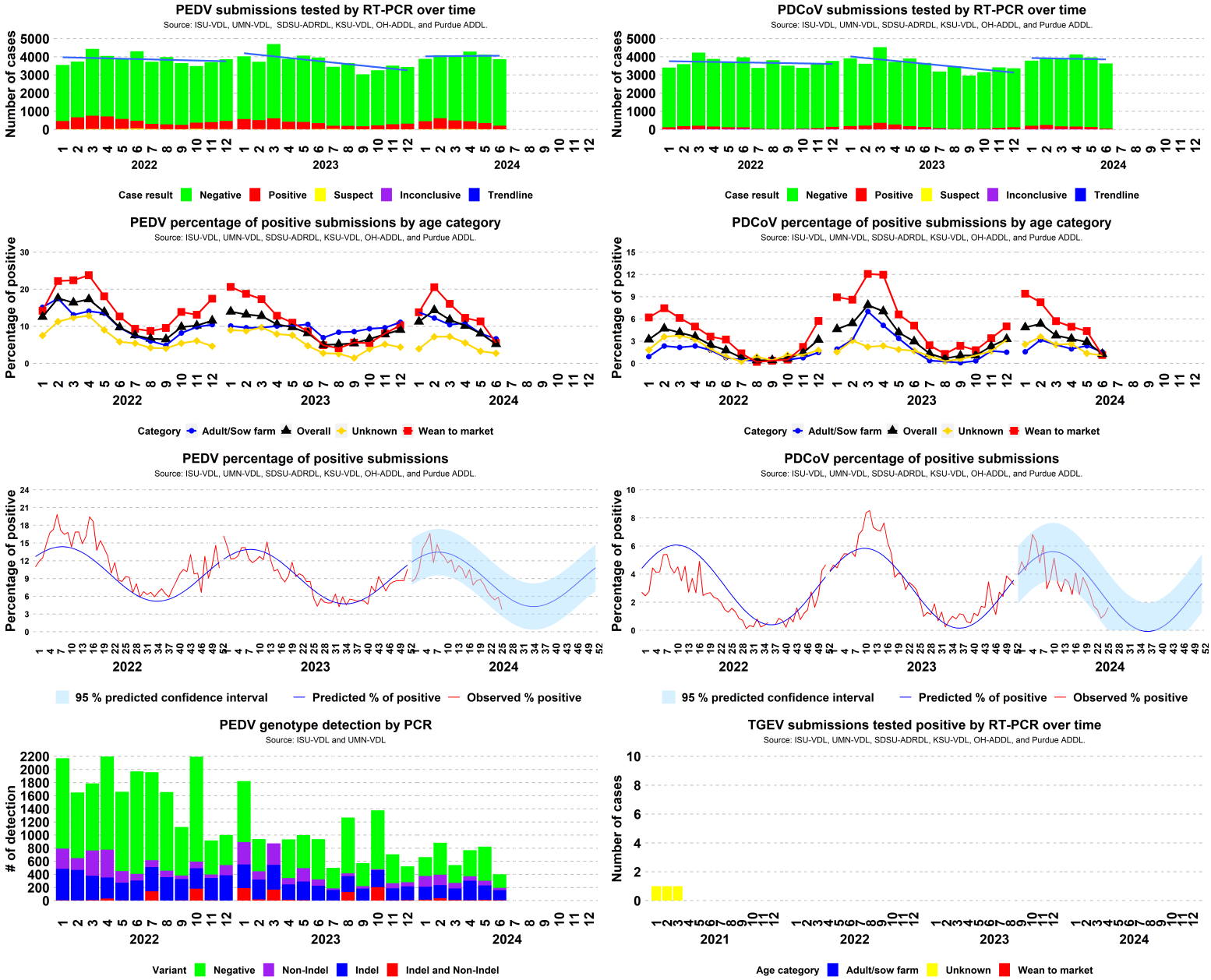


Figure 1. Top: *Left PEDV*; *Right PDCoV* cases tested by RT-PCR over time; **Second from top**: *Left PEDV*; *Right PDCoV* percentage of positive PCR positive results, by age category over time. **Third from top**: *Left PEDV*; *Right PDCoV* expected percentage of positive results for cases tested by RT-PCR and 95% confidence interval for 2024 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, 5.2% of 3,865 cases tested PEDV-positive in June, a moderate decrease from 8.08% of 4,120 in May;
  - Positivity in the adult/sow category in June was 6.65% (94 of 1,414), similar to 8.05% (118 of 1,466) in May;
  - Positivity in the wean-to-market category in June was 5.52% (79 of 1,430), a substantial decrease from 11.33% (180 of 1,589) in May;
  - Overall PEDV-percentage of positive cases was 3 standard deviations above state-specific baselines in KS and OH;
  - Overall, 1.75% of 401 samples had mixed PEDV genotype detection in June, similar to 1.46% of 823 in May;
- Overall, 1.27% of 3,631 cases tested PDCoV-positive in June, similar to 2.88% of 3,963 in May;
  - Positivity in the adult/sow category in June was 1.56% (21 of 1,350), similar to 2.37% (33 of 1,393) in May;
  - Positivity in the wean-to-market category in June was 1.12% (15 of 1,338), a moderate decrease from 4.35% (67 of 1,540) in May;
- Overall PDCoV-percentage of positive was within state-specific baselines in all 11 monitored states;
- There was 0 positive case for TGEV RNA-PCR in June, 2024 over a total of 3,515 cases tested. It has been 39 months (with a total of 136,791 cases tested) since the last TGEV PCR-positive result;
- **Check the advisory comments about PEDV genotype on the Bonus Page (page 8).**

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

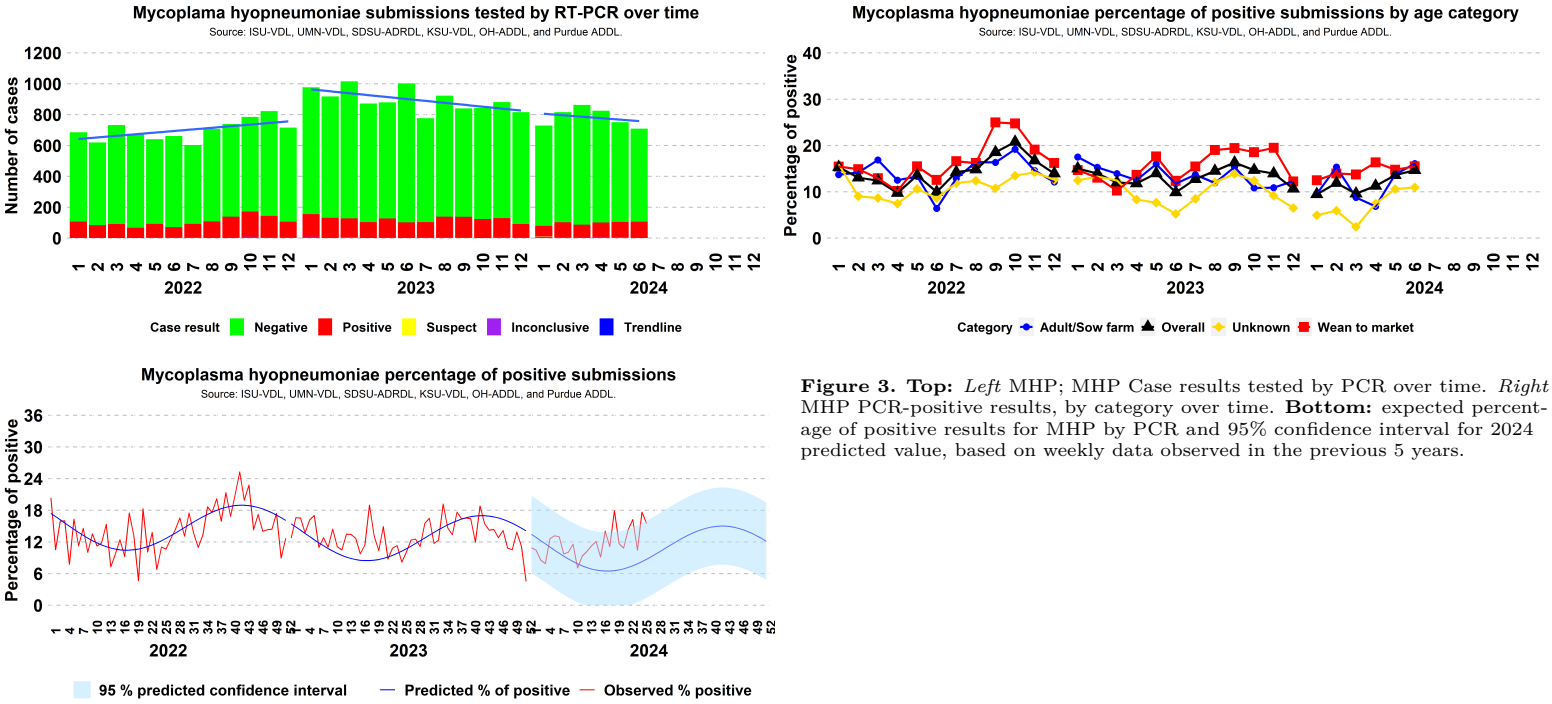
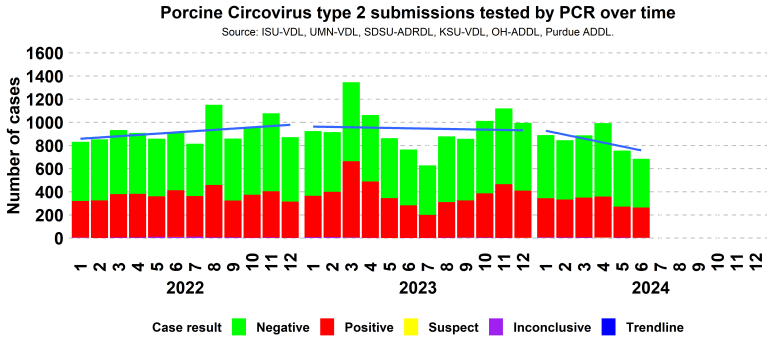


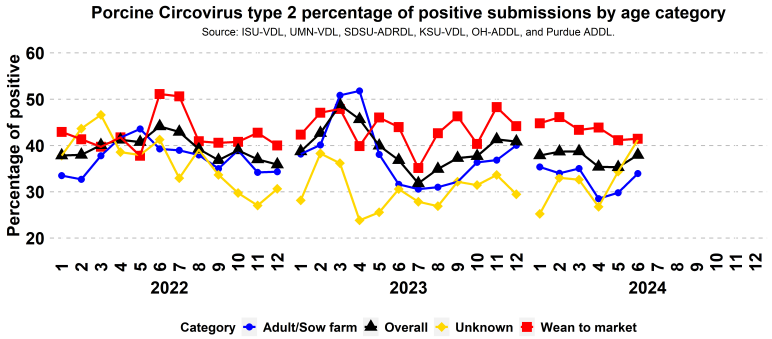
Figure 3. Top: *Left* MHP; MHP Case results tested by PCR over time. *Right* MHP PCR-positive results, by category over time. **Bottom:** expected percentage of positive results for MHP by PCR and 95% confidence interval for 2024 predicted value, based on weekly data observed in the previous 5 years.

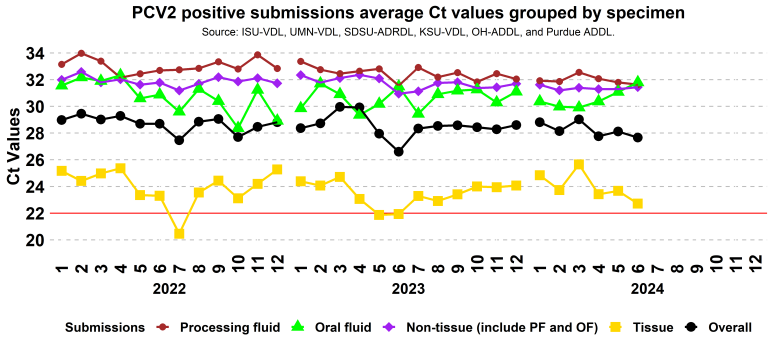
SDRS Advisory Group highlights:

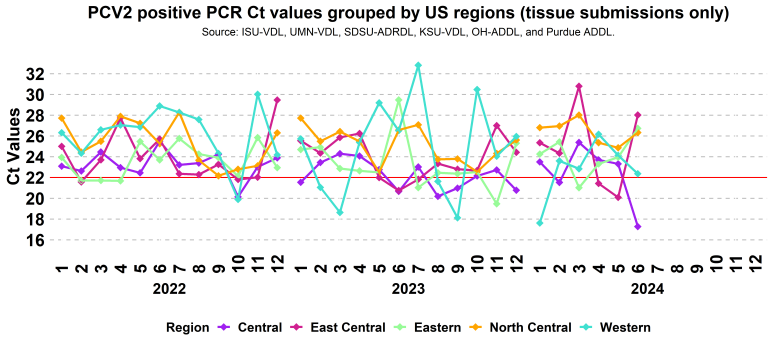
- Overall, 14.67% of 709 cases tested *M. hyopneumoniae*-positive cases in June, similar to 13.58% of 751 in May;
  - Positivity in the adult/sow category in June was 16.09% (42 of 261), a moderate increase from 13.73% (35 of 255) in May;
  - Positivity in the wean-to-market category in June was 15.49% (44 of 284), similar to 14.78% (51 of 345) in May;
- Overall MHP-percentage of positive cases was 3 standard deviations above state-specific baselines in SD;

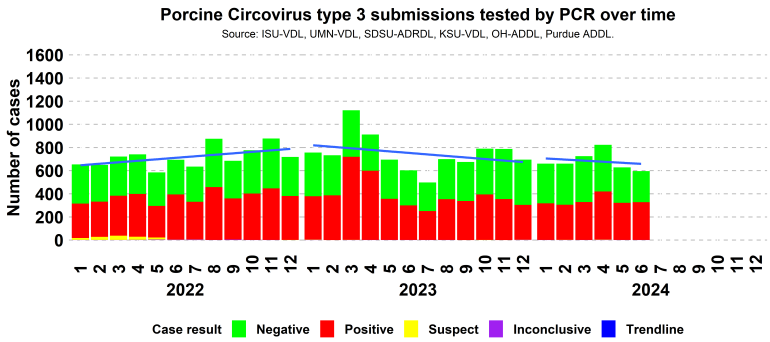
Topic 4 – Detection of Porcine Circoviruses type 2 and 3 DNA by PCR.











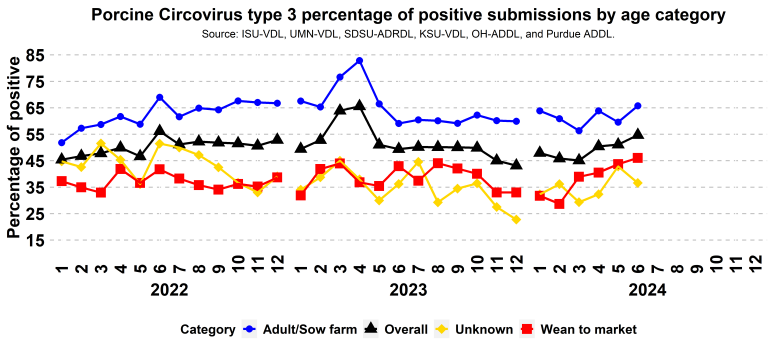


Figure 1. Top: *Left*: Results of PCV2 PCR cases over time; *Right*: PCV2 PCR-positive results, by category over time. **Middle**: *Left*: Average Ct values of PCV2 submissions by specimen; *Right*: Average Ct values of PCV2 tissue submissions by U.S. region; Central (IA), East Central (IL, IN, MO and 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, 37.96% of 685 cases tested PCV2-positive in June, a moderate increase from 35.32% of 756 in May;
  - Positivity in the adult/sow category in June was 33.96% (108 of 318), a moderate increase from 29.82% (99 of 332) in May;
  - Positivity in the wean-to-market category in June was 41.46% (119 of 287), similar to 41.16% (135 of 328) in May;
  - In the month of June, the regions with the lowest PCV2 average Ct values in tissue submissions was Central (29 submissions; average Ct 17.3), Western (21 submissions; average Ct 22.4), North Central (22 submissions; average Ct 26.3), Eastern (13 submissions; average Ct 26.7), and East Central (10 submissions; average Ct 28);
- Overall, 54.7% of 596 cases tested PCV3-positive in June, a moderate increase from 51.11% of 628 in May;
  - Positivity in the adult/sow category in June was 65.76% (194 of 295), a substantial increase from 59.6% (177 of 297) in May;
  - Positivity in the wean-to-market category in June was 46.09% (106 of 230), a moderate increase from 43.72% (108 of 247) in May.

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

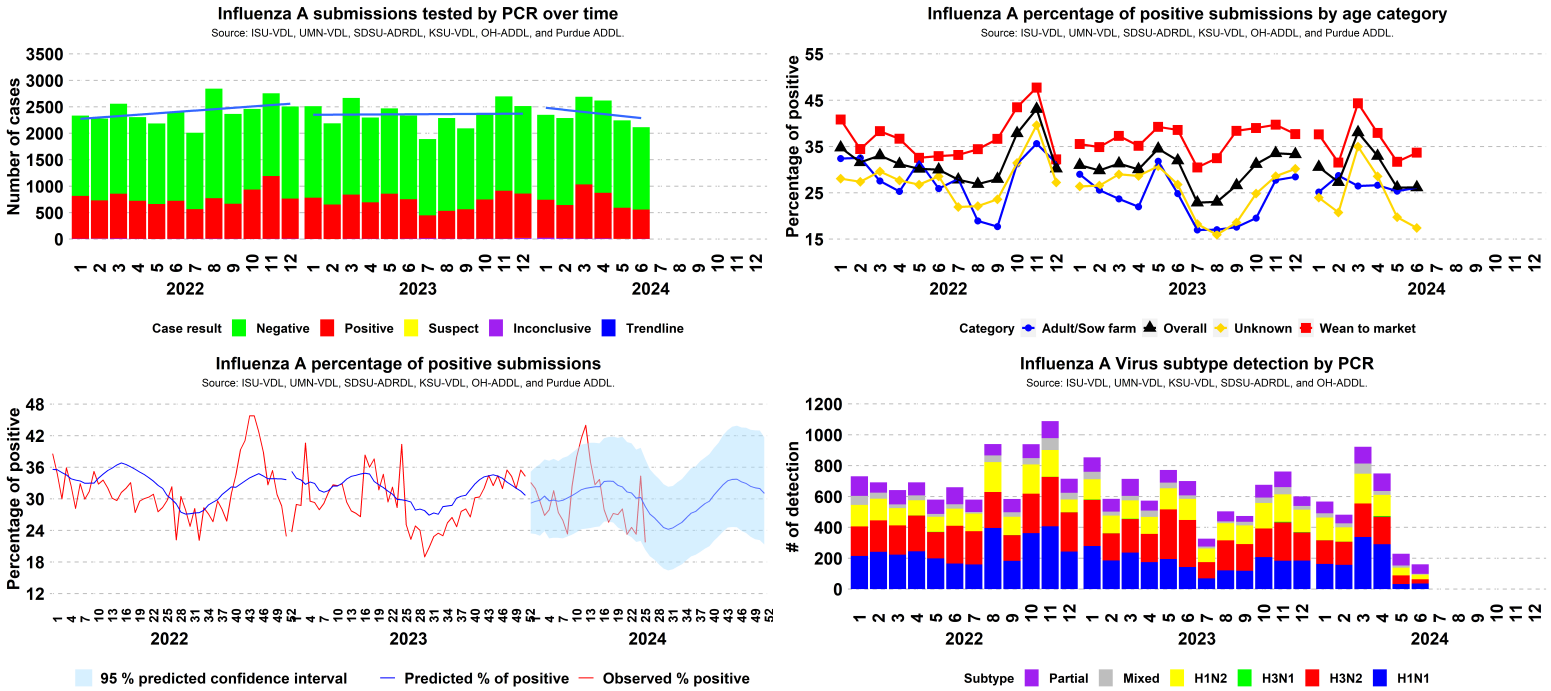


Figure 3. Top: *Left* Results of IAV PCR cases over time. *Right* Percentage of IAV PCR-positive results, by category over time. **Bottom:** *Left* expected percentage of positive results for IAV by PCR and 95% confidence interval for 2024 predicted value, based on weekly data observed in the previous 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, 26.18% of 2,116 cases tested IAV-positive cases in June, similar to 26.15% of 2,245 in May;
  - Positivity in the adult/sow category in June was 26.1% (125 of 479), similar to 25.37% (119 of 469) in May;
  - Positivity in the wean-to-market category in June was 33.67% (298 of 885), similar to 31.7% (311 of 981) in May.
- Overall IAV-percentage of positive was within state-specific baselines in all 11 monitored states;
- Overall, 3.11% of 161 samples had mixed subtype detection in June, a moderate decrease from 6.11% of 229 in May.

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

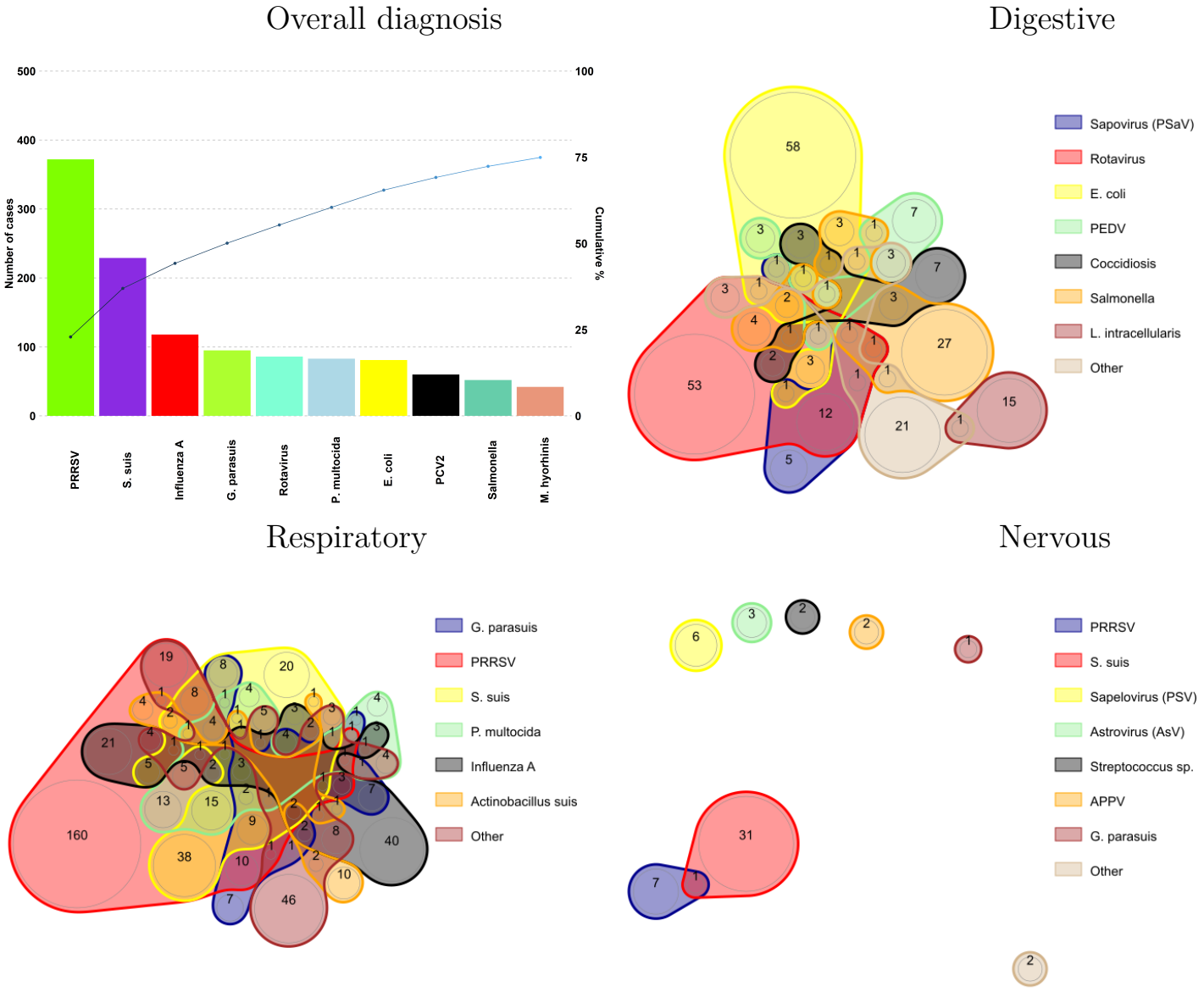


Figure 4. ISU-VDL most frequent overall confirmed tissue disease diagnosis. The presented system is described in the title of the chart. Colors represent one agent; line intersections present diagnosis of 2 or more agents within a submission. Only the most frequent etiology/disease are presented. Less 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 May. 1 to June. 24, 2024.

SDRS Advisory Group highlights:

• PRRSV (372) led cases with confirmed etiology, followed by *S. suis* (229), and Influenza A (118). PRRSV (339 of 911) led the number of confirmed respiratory diagnoses, Rotavirus (86 of 320) lead the number of confirmed digestive diagnoses, and *S. suis* (37 of 48) 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.*

PEDV genotype PCR data incorporated in the SDRS

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1 - Swine Disease Reporting System office, Ames, Iowa, USA.

The Swine Disease Reporting System (SDRS) aims to share information on 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 a request from our Advisory Board, the SDRS brings onboard information for PEDV genotype detection by PCR. Genotype information will provide PEDV variants that can be classified based on specific genetic characteristics, particularly in the spike (S) protein. There are two main types:

- S INDEL variants: Characterized by multiple deletions and insertions in the S1 subunit of the spike (S) protein (G1b genotype), these strains were associated with milder disease.

- Non-S INDEL variants: Lacking these specific deletions and insertions (G2b genotype), these strains were highly virulent and caused more severe disease.

These genetic differences can influence the PEDV pathogenicity and the immune response of the infected pigs. Also, the SDRS reports will highlight the number of mixed detections, which informs the number of multiple variants detected by a PCR in one sample. Historical data was fully incorporated, and a new chart under the enteric coronavirus report page will bring monthly updates about PEDV virus genotype detection.

Highlights from advisory group:

- Regardless the strain detected, a common approach adopted in the breeding herd is to move towards eliminating PEDV from the herd;
- The non-INDEL variants are more aggressive in the field, taking longer to eliminate from the farm;
- Some segments of the industry that had their herds in high-density areas prefer to expose the herd to the INDEL strain, which is much milder and causes fewer clinical signs compared with the non-INDEL variant in order to create herd immunity to avoid aggressive strains.

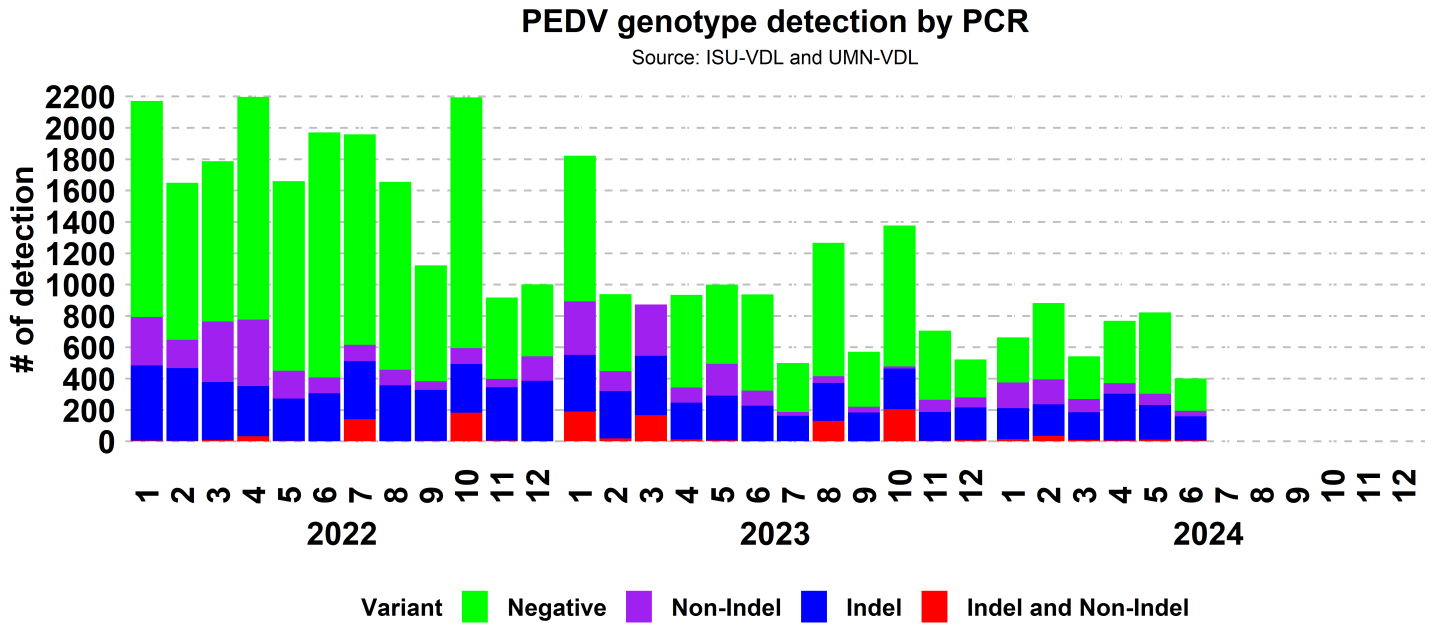

Figure 1: Detection of PEDV genotype by PCR. The colors represent each genotype Indel (blue), Non-Indel (purple), both variants detected in one sample (red), and none of the variants detected (green).