

Swine Disease Reporting System Report # 70 (December 5, 2023)

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. The SDRS projects are:

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 (web dashboards and monthly PDF report), 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.

Kansas State University: Rob McGaughey, Franco Matias-Ferreyra, Jamie Retallick, Jordan Gebhardt.

South Dakota State University: Jon Greseth, Darren Kersey, Travis Clement, Angela Pillatzki, Jane Christopher-Hennings.

Ohio Animal Disease and Diag. Lab.: Melanie Prarat, Ashley Johnson, Dennis Summers.

Purdue University: Craig Bowen, Kenitra Hendrix, Joseph Boyle.

The Ohio State University: Andreia Arruda.

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 and reports results, metadata, and sequences.

PRRS virus RFLP and Lineage report: Benchmarks patterns of PRRSV RFLP pattern and Lineages over time by specimen, age group, and US State.

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 report" and "video report" through Spotify, Apple Podcast, Google podcast, SwineCast, YouTube, LinkedIn, and the SDRS webpage.

Advisory Group: Reviews and discusses the data, providing their comments and perspectives monthly: Mark Schwartz, Paul Sundberg, Paul Yeske, Deborah Murray, Brigitte Mason, Peter Schneider, Sam Copeland, Luc Dufresne, Daniel Boykin, Corrine Fruge, William Hollis, Rebecca Robbins, Thomas Petznick and Kurt Kuecker.

In addition to this report, interactive dashboards and educational material are available at www.fieldepi.org/SDRS.



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 2023; Right: Epidemiological curve of detection for PRRSV Lineage 1C variant (L1C.5) strain.

SDRS Advisory Group highlights:

• Overall, 24.92% of 6,538 cases tested PRRSV-positive in November, a moderate increase from 22.5% of 6,408 in October;

• Positivity in the adult/sow category in November was 18.39% (534 of 2,903), a moderate increase from 15.72% (470 of 2,990) in October;

• Positivity in the wean-to-market category in November was 43.33% (851 of 1,964), a moderate increase from 38.65% (749 of 1,938) in October;

• Overall PRRS-percentage of positive cases was 3 standard deviations from state-specific baselines in IA, IL, and OH;

• During November 2023, PRRSV L1C variant (L1C.5) strains were detected in IA (50), NE (12), MO (12), MN (11) and OH (1);

• The wean-to-market category positivity is on a sharp rise, with three consecutive months of increase and a decrease in the average PCR average Ct values from 27.1 in August to 25 in November. The decreased average PCR Ct value trend for PRRSV has occurred year over year since 2017 in the wean-to-market category.;

• The advisory group highlighted that more clinical cases are expected during this period of the year, and then the Ct values tend to drop. Also, the advisory group emphasized that more prevalent PRRSV strains, such lineage L1C.5, had been recovering samples with lower PCR Ct values.



SDRS Advisory Group highlights:

• Overall, 7.64% of 3,349 cases tested PEDV-positive in November, similar to 6.58% of 3,254 in October;

• Positivity in the adult/sow category in November was 9.75% (121 of 1,241), similar to 9.35% (115 of 1,230) in October;

• Positivity in the wean-to-market category in November was 7.58% (92 of 1,214), a moderate increase from 5.48% (69 of 1,258) in October;

• Overall PEDV-percentage of positive cases was 3 standard deviations from state-specific baselines in SD, MO, and NC;

- Overall, 2.24% of 3,263 cases tested PDCoV-positive in November, similar to 1.08% of 3,157 in October;
 - Positivity in the adult/sow category in November was 1.77% (21 of 1,189), similar to 0.34% (4 of 1,176) in October;
 - Positivity in the wean-to-market category in November was 3.25% (39 of 1,201), similar to 1.78% (22 of 1,238) in October;
 - 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 November, 2023 over a total of 3,152 cases tested. It has been 33 months (with a total of 111,089 cases tested) since the last TGEV PCR-positive result;



95 % predicted confidence interval 🛛 — Predicted % of positive — Observed % positive

SDRS Advisory Group highlights:

- Overall, 13.87% of 829 cases tested *M. hyopneumoniae*-positive cases in November, similar to 14.69% of 844 in October;
 - Positivity in the adult/sow category in November was 11.55% (29 of 251), similar to 10.84% (27 of 249) in October;
 - Positivity in the wean-to-market category in November was 19.05% (64 of 336), similar to 18.57% (70 of 377) in October;
 - Overall MHP-percentage of positive was within state-specific baselines in all 11 monitored states.



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, 41.75% of 1,042 cases tested PCV2-positive in November, a moderate increase from 37.65% of 1,012 in October;
 - Positivity in the adult/sow category in November was 37.82% (194 of 513), similar to 36.23% (171 of 472) in October;
- Positivity in the wean-to-market category in November was 48.48% (208 of 429), a substantial increase from 40.35% (182 of 451) in October;
- In the month of November, the regions with the lowest PCV2 average Ct values was Central (74 submissions; average Ct 20.8), East Central (8 submissions; average Ct 24.4), Eastern (42 submissions; average Ct 25.3), North Central (28 submissions; average Ct 25.6), and Western (12 submissions; average Ct 26);
- Overall, 45.22% of 732 cases tested PCV3-positive in November, a moderate decrease from 49.94% of 789 in October;
- Positivity in the adult/sow category in November was 59.71% (206 of 345), a moderate decrease from 62.43% (226 of 362) in October;
- Positivity in the wean-to-market category in November was 33.79% (99 of 293), a substantial decrease from 40.06% (137 of 342) in October;



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: Number of IAV subtyping PCR detection over time; (Partial - only hemagglutinin or neuraminidase regions detected; Mixed - 3 or more haemagglutinin and neuroamnidase regions detected. i.e., "H1 H3 N1").

SDRS Advisory Group highlights:

• Overall, 33.53% of 2,517 cases tested IAV-positive cases in November, a moderate increase from 31.2% of 2,378 in October;

• Positivity in the adult/sow category in November was 27.83% (123 of 442), a substantial increase from 19.54% (94 of 481) in October;

• Positivity in the wean-to-market category in November was 39.84% (453 of 1,137), similar to 38.99% (487 of 1,249) in October.

• Overall, 6.48% of 679 samples had mixed subtype detection in November, similar to 4.95% of 667 in October;





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 October. 1 to November. 20, 2023.

SDRS Advisory Group highlights:

• PRRSV (427) led cases with confirmed etiology, followed by *S. suis* (303), and Influenza A (216). PRRSV (397 of 1315) led the number of confirmed respiratory diagnoses, *E. coli* (107 of 436) lead the number of confirmed digestive diagnoses, and *S. suis* (44 of 74) led the number of confirmed neurological diagnoses.

• From the week of October 30th until the week of November 20th, there were consecutive spikes in the number of systemic and nervous confirmed diagnosis. PRRSV, *Glaesserella parasuis*, *Streptococcus suis* had increased number of confirmed diagnosis in the same period.



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.

New PRRSV classification system: How the trends look over time?

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PRRSV sequencing is performed by targeting the open-reading frame-5 (ORF5) gene that is used to classify sequences according to restriction fragment length polymorphism (RFLP)[1] and Lineages [2,3]. A new PRRSV-2 classification system has been proposed to classify PRRSV-2 into eleven genetic lineages (L1-L11) and 21 sub-lineages (L1A-L1F, L1H-L1J, L5A-L5B, L8A-L8E, and L9A-L9E) covering PRRSV-2 wild-type and vaccine sequences recovered around the globe [4]. The L1C lineage has been further classified into more granular groups (L1C.1 – L1C.5)[4]. The L1C.5 group corresponds to the recently emerged L1C variant [4]. The advantage of the new classification is that lineages or sublineages can be expanded to include additional lineages, sublineages, or more granular classifications as needed.

SDRS has adopted the new PRRSV-2 classification system and reclassified its PRRSV ORF5 sequences to reflect the new lineage classification system. The changes will also be reflected in any sequence entering the database, monthly reports, and online dashboards (Figure 1). The trend in the last few years indicates the rise of lineage L1C.5, whereas there has been a decrease in the number of sequences in lineages L1A and L1H. These results are comparable to the previous lineage classification charts where there was an increase in detections for lineages L1C.5 and decrease in the number of sequences labeled L1H and L1A. The new classification system also reduced the number of sequences previously classified as unknown lineage from 10.12% to 1.92% for the sequences present in the SDRS database. In 2006 30.27% of the sequences were previously classified as unknown with the new system the unknown reduced to 5.59%. In 2023, 0.58% were classified as unknown in the new classification system compared to 11.18% in the previous classification system. Interactive online dashboards are available in the SDRS project website.



Figure 1: PRRSV ORF5 sequences classification over time. *Top*: distribution of ORF5 sequences according to lineages within a year. *Bottom*: number of PRRSV ORF5 sequences.



A tool to classify existing sequences using the new classification system and compare with the new lineage classification system has been made available to all veterinarians, producers, and stakeholders. The beta version of the tool can be found at the ORF5 Nextclade Classifier. A user can navigate to the ORF5 Nextclade Classifier and provide their own ORF5 sequences, and the tool creates a downloadable results page with reclassified sequences and, phylogenetic tree, across other functions.

Highlights:

- SDRS has adopted a new lineage classification system under which there are eleven lineages and 21 sublineages.;
- L1C-Variant has been re-classified to lineage L1C.5 and is currently the most detected wild-type strains.;

• Number of sequences determined as undetermined, in the SDRS database, have decreased from 10.12% in the previous classification system to 1.92% in the new classification system.