Swine Disease Reporting System
Report # 97 (March 3, 2026)

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 https://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:**
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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 and OH-ADDL.

PRRSView and FLUture and : Aggregates PRRSV and influenza A virus diagnostic data from the ISU-VDL. PRRSLoom-Variants: PRRSV-2 variant classification from UMN.

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

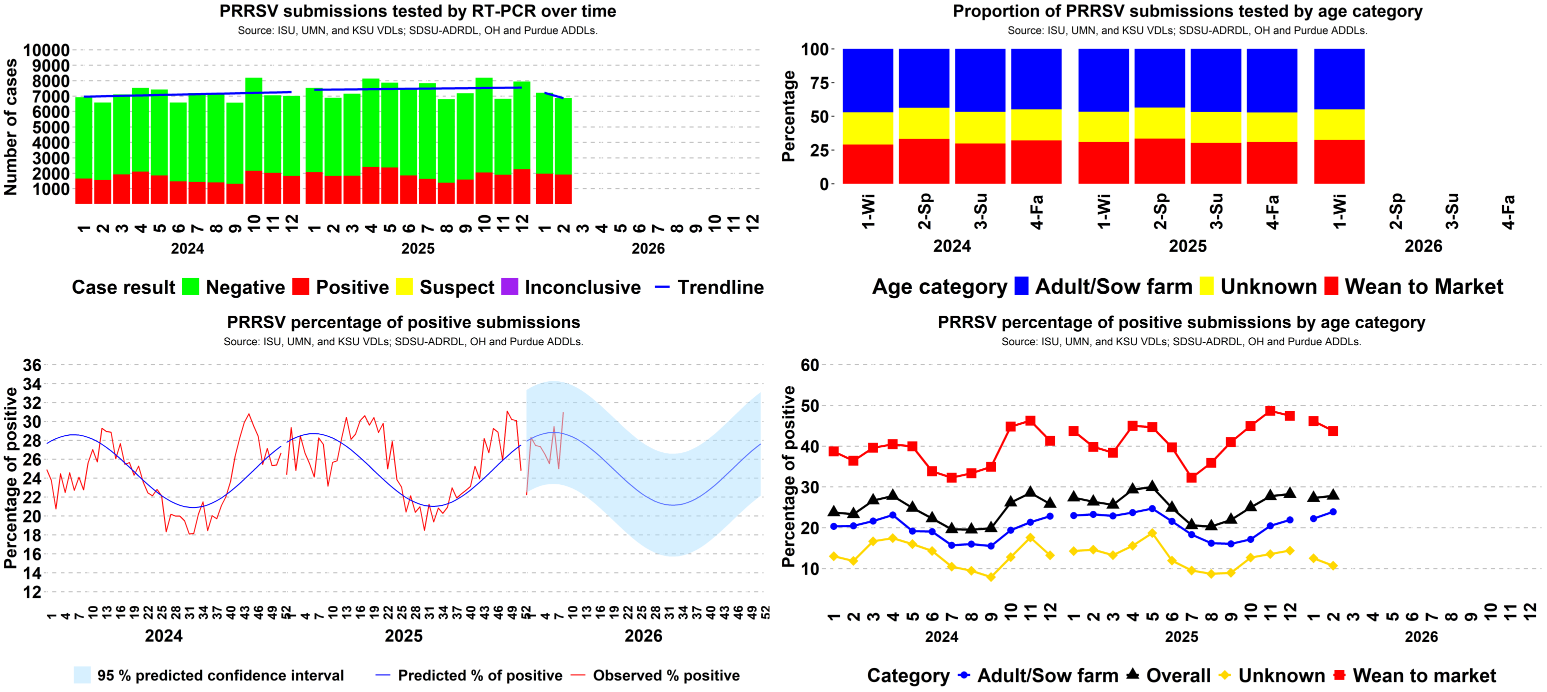
Audio and video reports: Key findings from SDRS projects are summarized monthly in a conversation between investigators and is available in the Spotify, Apple Podcast, YouTube, LinkedIn, and the SDRS webpage. In addition to this report, interactive dashboards and educational material are publicly available.

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

Note: This report contains data up to February 28, 2026.

Communications and information contained in this report are for general informational and educational purposes only and are not to be construed as recommending or advocating a specific course of action.

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


PRRSV submissions tested by RT-PCR over time

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

Proportion of PRRSV submissions tested by age category

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

PRRSV percentage of positive submissions

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

PRRSV percentage of positive submissions by age category

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

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, 27.84% of 6,871 cases tested PRRSV-positive in February, similar to 27.31% of 7,217 in January.
  - Positivity in the adult/sow category in February was 23.91% (738 of 3,086), similar to 22.26% (719 of 3,230) in January.
  - Positivity in the wean-to-market category in February was 43.73% (1,019 of 2,330), a moderate decrease from 46.16% (1,033 of 2,238) in January.
  - Overall PRRSV-percentage of positive cases was within state-specific baselines in all 11 monitored states.

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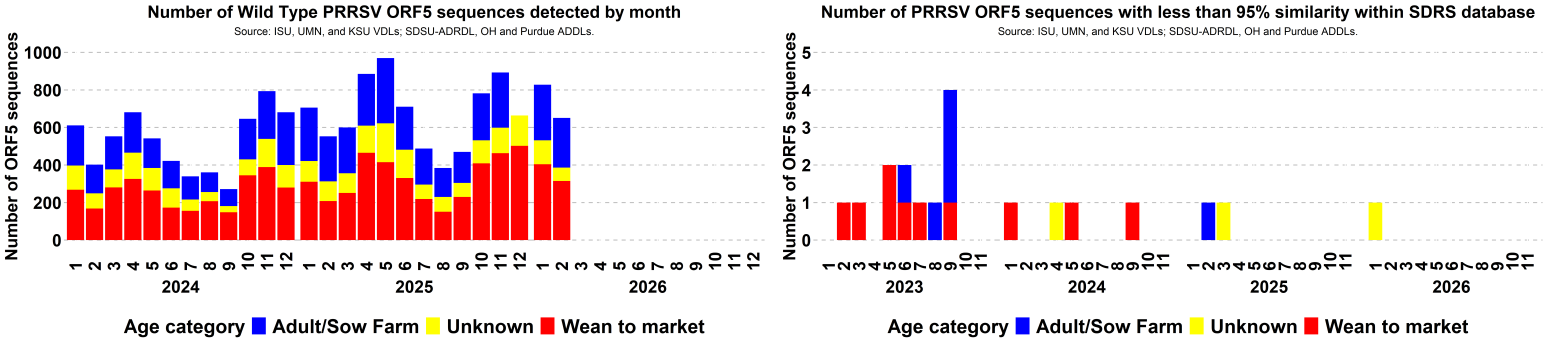
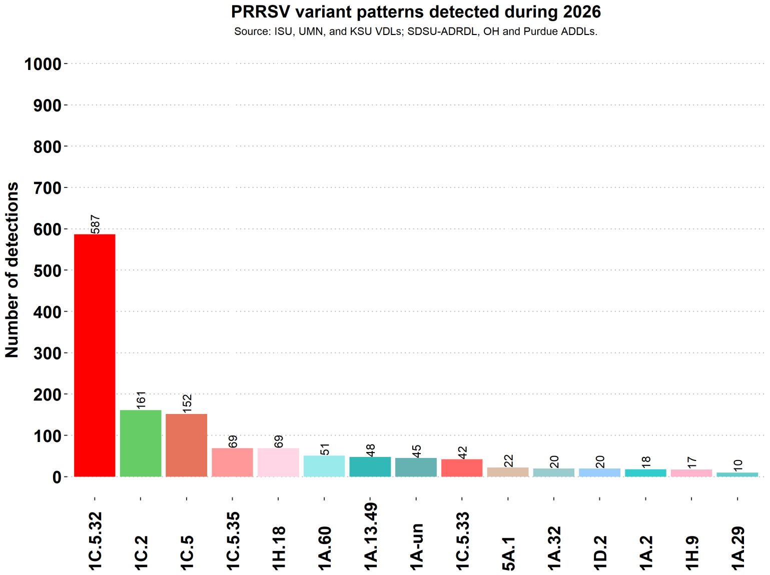
Topic 2 – PRRSV ORF5 sequences detection over time


Number of Wild Type PRRSV ORF5 sequences detected by month

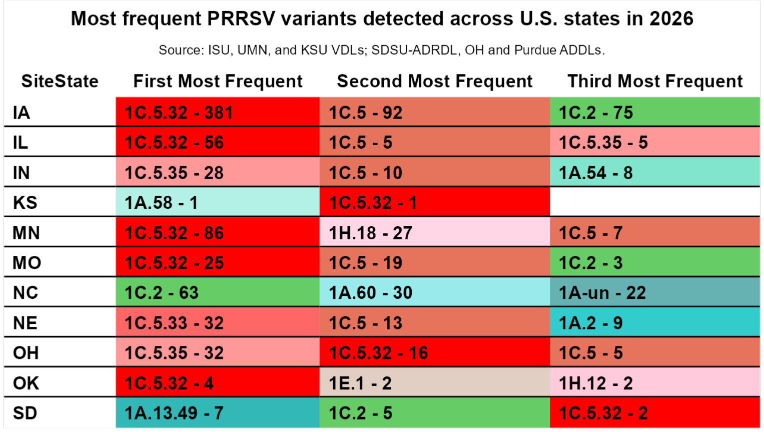
Source: ISU, UMN, and KSU VDLs; SDSU-ADRDL, OH and Purdue ADDLs.

Number of PRRSV ORF5 sequences with less than 95% similarity within SDRS database

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


PRRSV variant patterns detected during 2026

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


Most frequent PRRSV variants detected across U.S. states in 2026

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

SiteState	First Most Frequent	Second Most Frequent	Third Most Frequent
IA	1C.5.32 - 381	1C.5 - 92	1C.2 - 75
IL	1C.5.32 - 56	1C.5 - 5	1C.5.35 - 5
IN	1C.5.35 - 28	1C.5 - 10	1A.54 - 8
KS	1A.58 - 1	1C.5.32 - 1	
MN	1C.5.32 - 86	1H.18 - 27	1C.5 - 7
MO	1C.5.32 - 25	1C.5 - 19	1C.2 - 3
NC	1C.2 - 63	1A.60 - 30	1A-un - 22
NE	1C.5.33 - 32	1C.5 - 13	1A.2 - 9
OH	1C.5.35 - 32	1C.5.32 - 16	1C.5 - 5
OK	1C.5.32 - 4	1E.1 - 2	1H.12 - 2
SD	1A.13.49 - 7	1C.2 - 5	1C.5.32 - 2

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 variant; *Right*: Most frequently detected PRRSV ORF5 sequences in 2026, shown by variant at the U.S. state level along with their respective detection counts **Note: un indicates unclassified**.

SDRS Advisory Group highlights:

- During February, the states with higher number of PRRSV 1C.5.32 detections were detected IA, IL, MN, MO, NC, IN, OK, OH, NE, SD (respective number of sequences: 169, 31, 23, 10, 6, 3, 3, 2, 1, 1);
- In February 1C.5.32 (251) was the PRRSV variant most detected in the U.S., followed by 1C.2 (81), and 1C.5 (67);
- SDRS database identified first-time detection of PRRSV variants according to provided site state:
  - January 2026: 1H.18 (GA), 1K.1.5 (MO), 1K.4 (OH), 1C.5.32 (NC), and 1C.5.36 (PA).
  - February 2026: 1A.13.49 (KY), 1A.5 (MO), 1C.5.33 (ID), 1C.2.39 (MN), and 1C.5.32 (MI).
- Click on the links below to access the PRRSV genotype dashboard and the SDRS BLAST tool to compare your PRRSV ORF5 sequence with the SDRS database.

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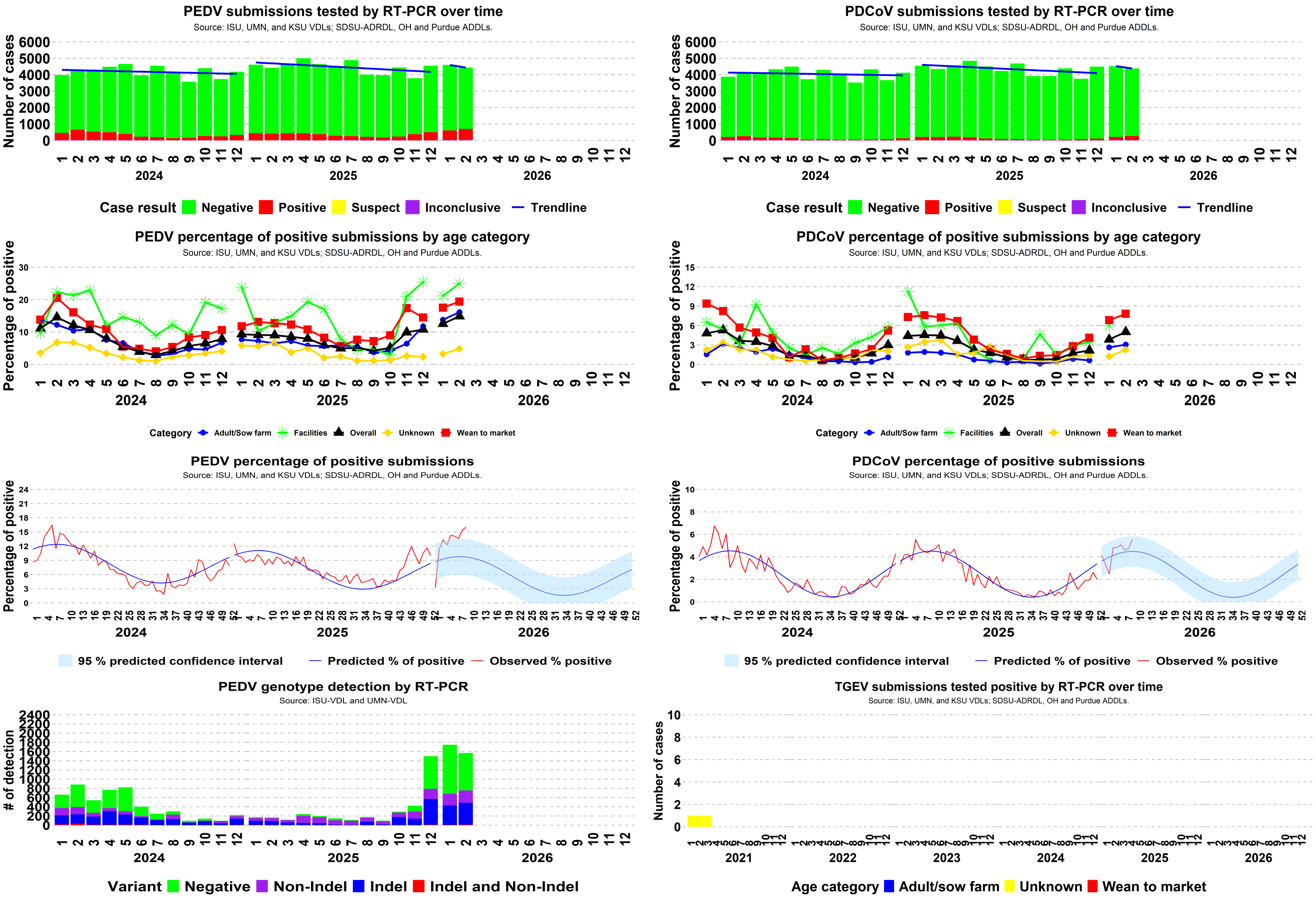
Topic 2 – Enteric coronavirus RNA detection by RT-qPCR



PEDV submissions tested by RT-PCR over time
Source: ISU, UMN, and KSU VDLs; SDSU-ADRDL, OH and Purdue ADDLs.

PDCoV submissions tested by RT-PCR over time
Source: ISU, UMN, and KSU VDLs; SDSU-ADRDL, OH and Purdue ADDLs.

PEDV percentage of positive submissions by age category
Source: ISU, UMN, and KSU VDLs; SDSU-ADRDL, OH and Purdue ADDLs.

PDCoV percentage of positive submissions by age category
Source: ISU, UMN, and KSU VDLs; SDSU-ADRDL, OH and Purdue ADDLs.

PEDV percentage of positive submissions
Source: ISU, UMN, and KSU VDLs; SDSU-ADRDL, OH and Purdue ADDLs.

PDCoV percentage of positive submissions
Source: ISU, UMN, and KSU VDLs; SDSU-ADRDL, OH and Purdue ADDLs.

PEDV genotype detection by RT-PCR
Source: ISU-VDL and UMN-VDL

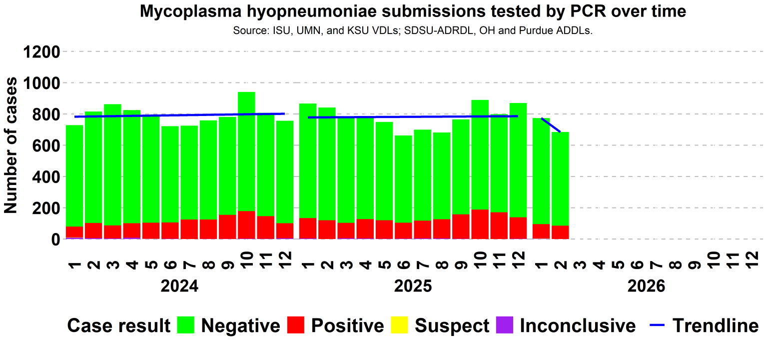
TGEV submissions tested positive by RT-PCR over time
Source: ISU, UMN, and KSU VDLs; SDSU-ADRDL, OH and Purdue ADDLs.

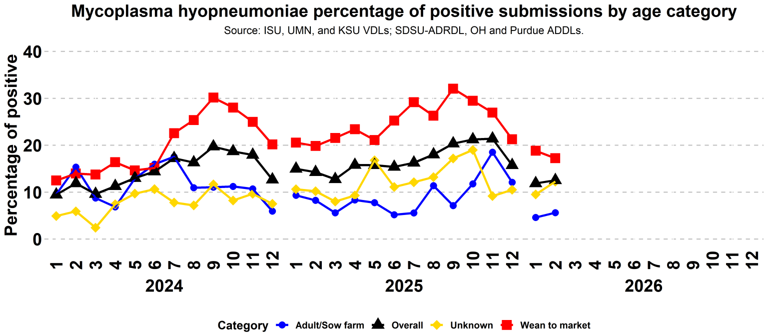
Figure 1. Top: Left PEDV; Right PDCoV cases tested by RT-PCR over time. Second from top: Left PEDV; Right PDCoV percentage of positive RT-PCR results by age category. Third from top: Left PEDV; Right PDCoV expected percentage of positives with 95% CI for 2026 prediction. Bottom: Left PEDV genotype detection over time; Right TGEV positive cases by age category.

SDRS Advisory Group highlights:

- Overall, 14.86% of 4,434 cases tested PEDV-positive in February, a moderate increase from 12.54% of 4,595 in January.
  - Positivity in the adult/sow category in February was 16.14% (268 of 1,660), a moderate increase from 13.78% (224 of 1,625) in January.
  - Positivity in the wean-to-market category in February was 19.41% (302 of 1,556), similar to 17.52% (280 of 1,598) in January.
  - Positivity in the facilities category in February was 25% (37 of 148), a moderate increase from 21.19% (32 of 151) in January.
  - Overall PEDV-percentage of positive cases was 3 standard deviations above state-specific baseline in IL.
  - Overall, 0.76% of 1,570 samples had mixed PEDV genotype detection in February, similar to 0.29% of 1,748 in January.
- Overall, 5.02% of 4,384 cases tested PDCoV-positive in February, similar to 3.85% of 4,522 in January.
  - Positivity in the adult/sow category in February was 3.07% (50 of 1,630), similar to 2.64% (42 of 1,588) in January.
  - Positivity in the wean-to-market category in February was 7.82% (121 of 1,547), similar to 6.83% (108 of 1,581) in January.
  - Positivity in the facilities category in February was 16.89% (25 of 148), a marked increase from 5.96% (9 of 151) in January.
  - 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 February, 2026 over a total of 4,263 cases tested. It has been 60 months (with a total of 224,986 cases tested) since the last TGEV PCR-positive result.

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





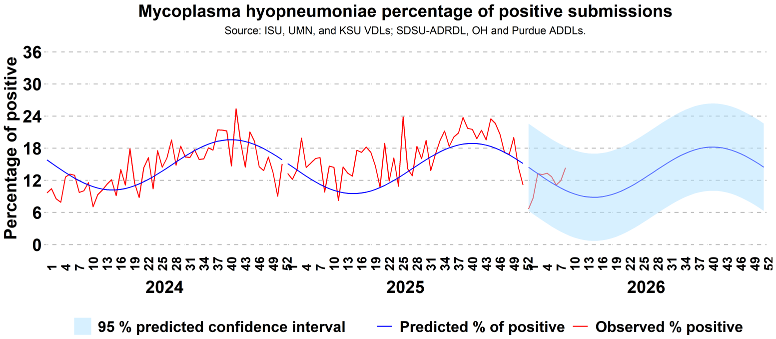


Figure 1. Top: *Left* MHP Case results tested by PCR over time. *Right* MHP PCR-positive results, by category over time. **Bottom:** expected percentage of positive results for MHP by PCR and 95% confidence interval for 2026 predicted value, based on weekly data observed in the previous 10 years.

SDRS Advisory Group highlights:

- Overall, 12.55% of 685 cases tested *M. hyopneumoniae*-positive in February, similar to 11.89% of 774 in January.
  - Positivity in the adult/sow category in February was 5.63% (13 of 231), similar to 4.61% (13 of 282) in January.
  - Positivity in the wean-to-market category in February was 17.24% (60 of 348), similar to 18.84% (65 of 345) in January.
  - Overall MHP-percentage of positive cases was within state-specific baselines in all 11 monitored states.

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

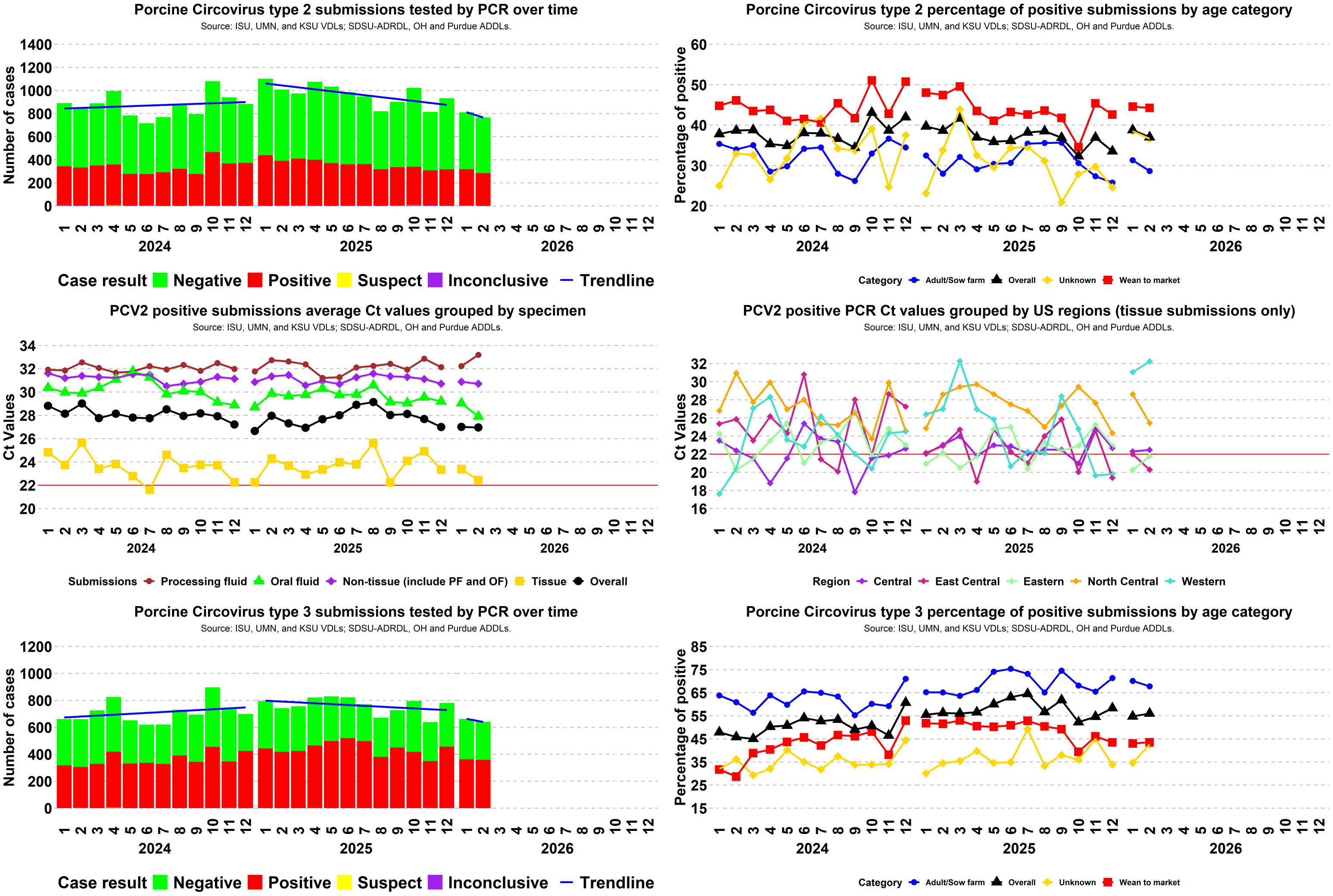
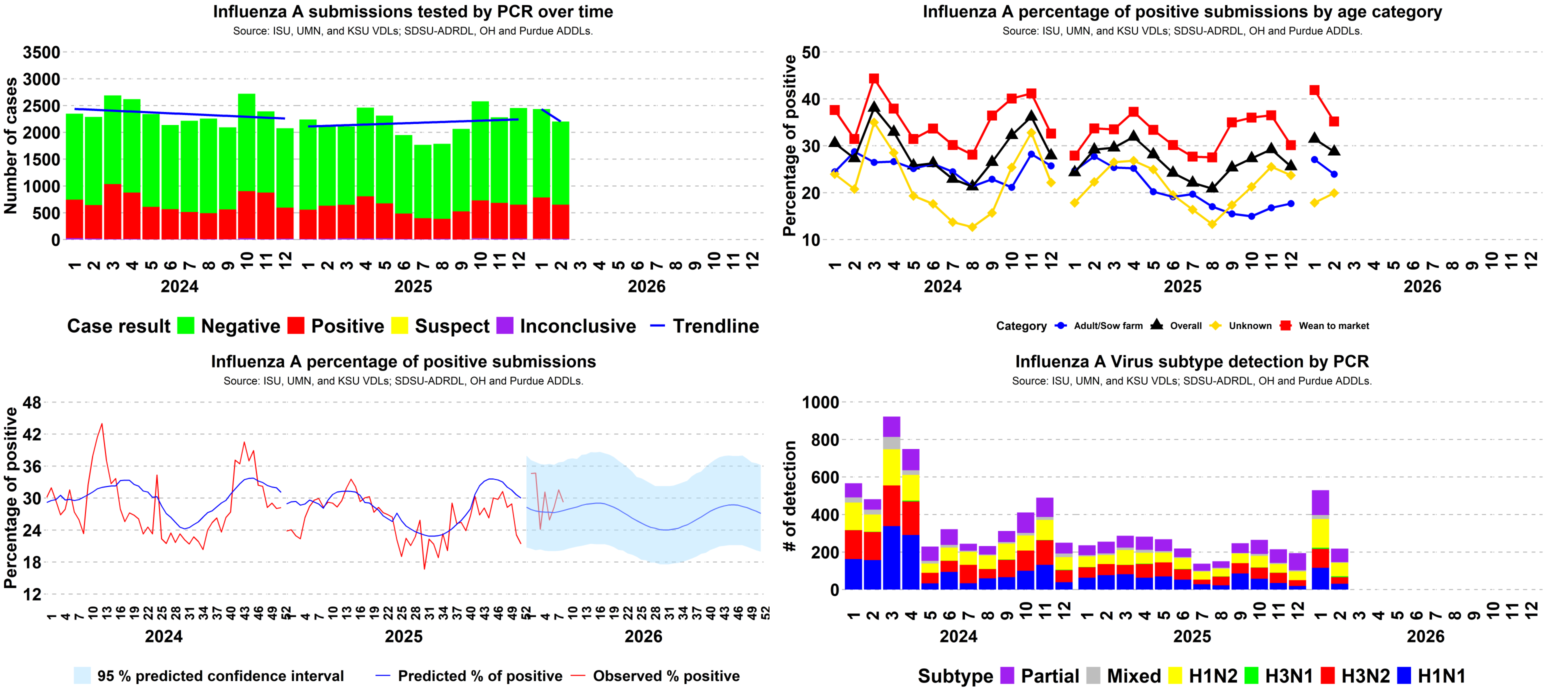


Figure 1. Top: *Left*: Results of PCV2 PCR cases over time; *Right*: PCV2 PCR-positive results, by category over time. **Middle**: *Left*: Average Ct values of PCV2 submissions by specimen; *Right*: Average Ct values of PCV2 tissue submissions by U.S. region; Central (IA), East Central (IL, IN, MO and 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, 37.03% of 767 cases tested PCV2-positive in February, similar to 38.79% of 812 in January.
  - Positivity in the adult/sow category in February was 28.66% (92 of 321), a moderate decrease from 31.33% (94 of 300) in January.
  - Positivity in the wean-to-market category in February was 44.27% (166 of 375), similar to 44.62% (174 of 390) in January.
  - In the month of February, the regions with the lowest PCV2 average Ct values in tissue submissions were East Central (22 submissions; average Ct 20.3), Eastern (35 submissions; average Ct 21.8), Central (41 submissions; average Ct 22.5), North Central (17 submissions; average Ct 25.5), and Western (2 submissions; average Ct 32.2).
- Overall, 56.01% of 641 cases tested PCV3-positive in February, similar to 54.75% of 663 in January.
  - Positivity in the adult/sow category in February was 67.77% (225 of 332), a moderate decrease from 70.13% (223 of 318) in January.
  - Positivity in the wean-to-market category in February was 43.57% (105 of 241), similar to 43.03% (105 of 244) in January.

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


Influenza A submissions tested by PCR over time

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

Influenza A percentage of positive submissions by age category

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

Influenza A percentage of positive submissions

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

Influenza A Virus subtype detection by PCR

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

Figure 1. 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 2026 predicted value, based on weekly data observed in the previous 4 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, 28.73% of 2,203 cases tested IAV-positive in February, a moderate decrease from 31.47% of 2,434 in January.
  - Positivity in the adult/sow category in February was 23.94% (118 of 493), a moderate decrease from 27.06% (141 of 521) in January.
  - Positivity in the wean-to-market category in February was 35.17% (402 of 1,143), a substantial decrease from 41.89% (493 of 1,177) in January.
  - Overall IAV-percentage of positive cases was 3 standard deviations above state-specific baseline in IA, OK and NC.
- Overall, 1.38% of 218 samples had mixed subtype detection in February, a moderate decrease from 3.96% of 530 in January.

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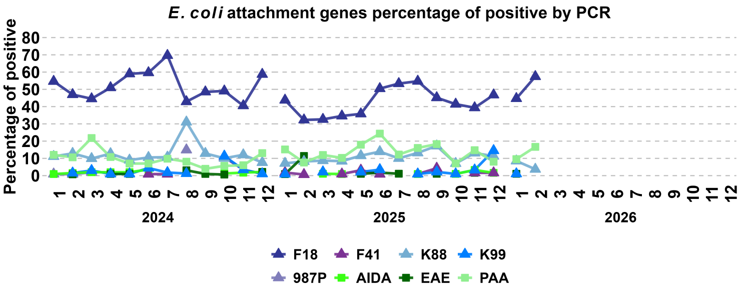
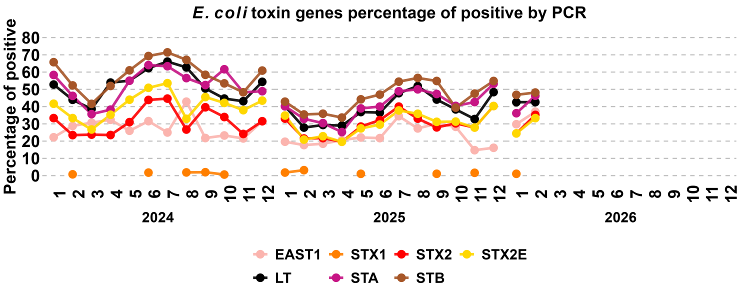
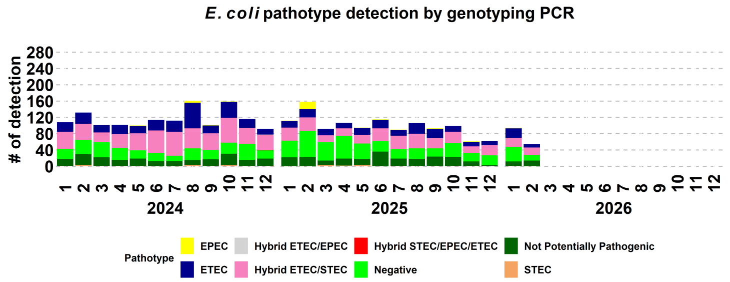
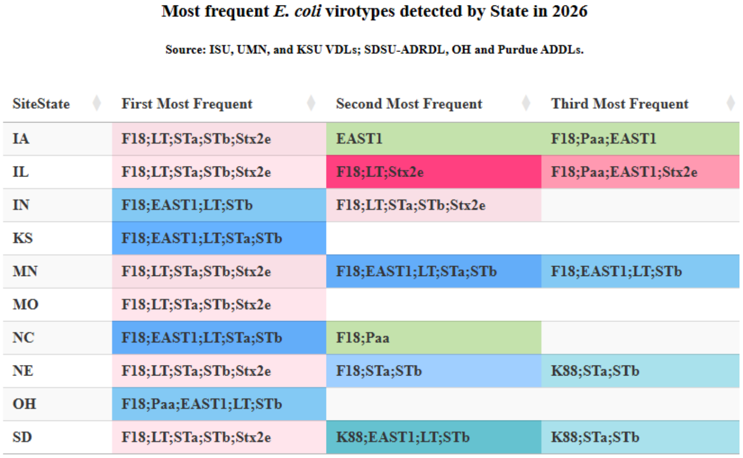
Topic 6 – Detection of *E. coli* DNA by Genotyping PCR.









Most frequent *E. coli* virotypes detected by State in 2026

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

SiteState	First Most Frequent	Second Most Frequent	Third Most Frequent
IA	F18;LT;STa;STb;Stx2e	EAST1	F18;Paa;EAST1
IL	F18;LT;STa;STb;Stx2e	F18;LT;Stx2e	F18;Paa;EAST1;Stx2e
IN	F18;EAST1;LT;STb	F18;LT;STa;STb;Stx2e	
KS	F18;EAST1;LT;STa;STb		
MN	F18;LT;STa;STb;Stx2e	F18;EAST1;LT;STa;STb	F18;EAST1;LT;STb
MO	F18;LT;STa;STb;Stx2e		
NC	F18;EAST1;LT;STa;STb	F18;Paa	
NE	F18;LT;STa;STb;Stx2e	F18;STa;STb	K88;STa;STb
OH	F18;Paa;EAST1;LT;STb		
SD	F18;LT;STa;STb;Stx2e	K88;EAST1;LT;STb	K88;STa;STb

Figure 1. Top: *Left E. coli* PCR-Positive results by attachment genes over time. *Right E. coli* PCR-Positive results by toxin genes over time. **Bottom:** *Left E. coli* number of samples tested by PCR genotype and their respective pathotype classification. *Right* Most frequent detected *E. coli* virotype by PCR in 2026 at U.S. state level (color code on table cells associated with the pathotype legend).

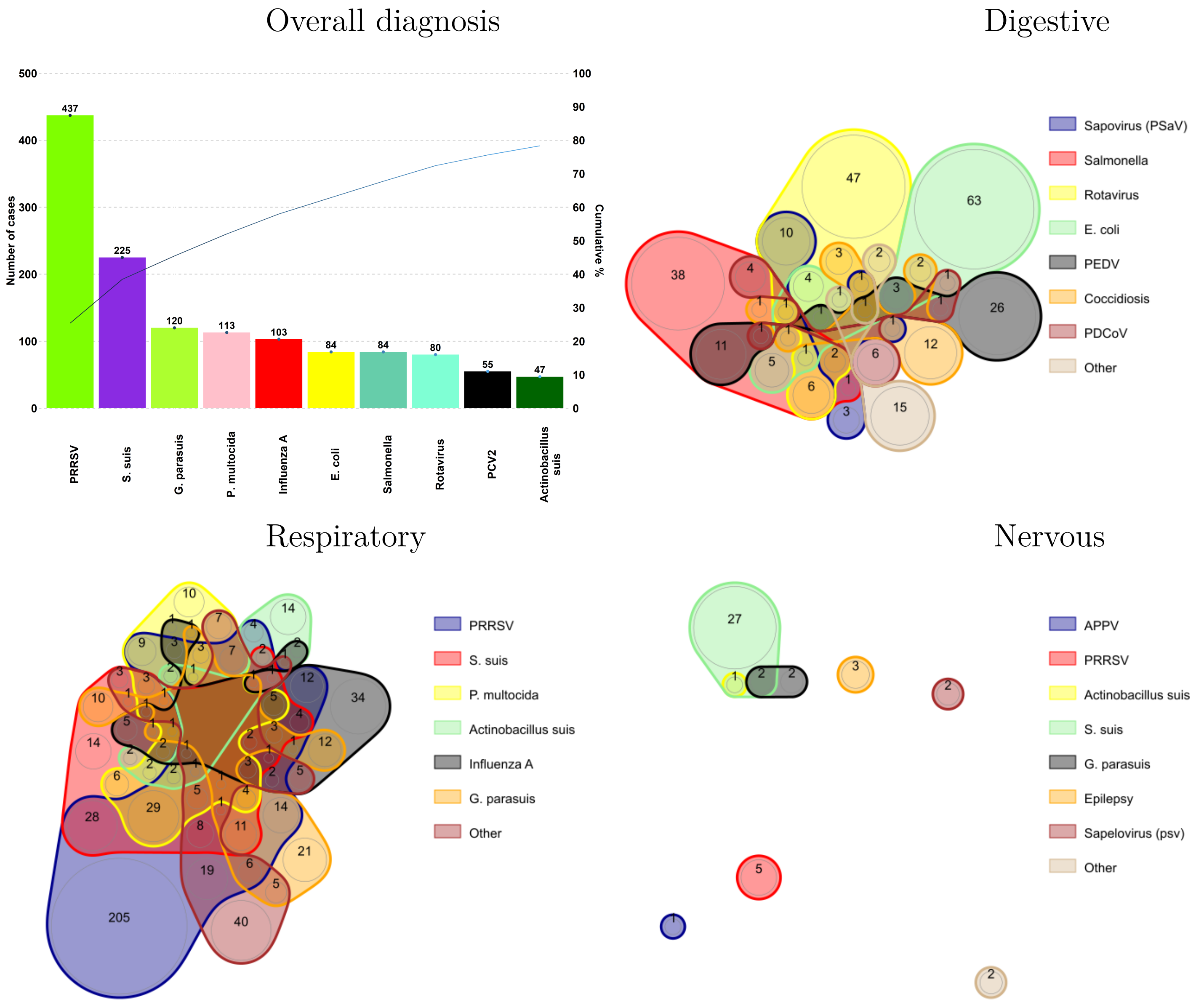
Education Material:

- Click on the links here to access the *E. coli* PCR Genotyping Interpretation Tool
- **Attachment genes: Fimbriae** – F18, K88(F4), K99(F5), 987P(F6), F41; **Adhesins** – EAE (Intimin), PAA, AIDA
- **Toxin genes: Heat-labile** – LT; **Heat-stable** – STa and STb; **Shiga toxins** – Stx1, Stx2 and Stx2e; and EAST1
- **Enterotoxigenic *E. coli* (ETEC):** Has fimbriae and toxin (not Stx2e) genes. Associated with neonatal and post-weaning diarrhea
- **Shiga toxin-producing *E. coli* (STEC):** Has fimbriae (F18) and toxin (must be Stx2e) gene. Associated with edema disease
- **Enteropathogenic *E. coli* (EPEC):** Presence of the EAE (Intimin) adhesin
- **Hybrids (ETEC/STEC, ETEC/EPEC, STEC/EPEC, ETEC/STEC/EPEC):** Combination of characteristics of more than one pathotype

SDRS Advisory Group highlights:

- Overall, 54 samples were tested for *E. coli* PCR in February.
  - In February, the *E. coli* pathotypes with higher number of sample detections were Hybrid ETEC/STEC (18 detections), Not Potentially Pathogenic (14 detections), and ETEC (8 detections).
  - In February, the *E. coli* attachment genes with higher detection rate were F18 (57.41%), PAA (16.67%), and K88 (3.70%).
  - In February, the *E. coli* toxin genes with higher detection rate were STB (48.15%), STA (46.30%), and LT (42.59%).

Topic 7 – Confirmed tissue cases etiologic/disease diagnosis at the ISU-VDL and OH-ADDL


Overall diagnosis

Digestive

Respiratory

Nervous

Figure 4. ISU-VDL and OH-ADDL 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, Yanez 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 January 01, 2026 to February 24, 2026

SDRS Advisory Group highlights:

- PRRSV (437) led cases with confirmed etiology, followed by *S. suis* (225), and *G. parasuis* (120). PRRSV (401 of 1054) led the number of confirmed respiratory diagnoses, *E. coli* (83 of 352) lead the number of confirmed digestive diagnoses, and *S. suis* (30 of 48) led the number of confirmed neurological diagnoses.

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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 SDRS Story: Eight Years of Monitoring, Learning, and Supporting U.S. Swine Health

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The SDRS's goal is to share information on the activity of endemic and emerging pathogens affecting the swine population in the U.S., assisting veterinarians and producers in making informed decisions on disease prevention, detection, and management. Currently, SDRS is the only publicly available source of swine health information from U.S. veterinary diagnostic laboratories (VDLs). The SDRS has provided science-based spatiotemporal information on pathogen activity in all age categories, from boar studs to breeding herds to finishing with great representativeness of the U.S. swine industry.

I. Major project developments (2018–2025)

Since its launch in 2018, SDRS has steadily expanded its diagnostic scope and genomic resolution. The system began with RT-PCR monitoring for PRRSV from ISU-VDL, and rapidly expanded to other pathogens like PEDV, PDCoV, and TGEV, and other laboratories UMN, KSU, SDSU, OH, Purdue VDLs. Today, SDRS houses a database containing information for ten endemic porcine pathogens, PRRSV ORF5 sequences, IAV and PEDV PCR genotyping information from all participant laboratories and confirmed tissue diagnosis from ISU and OH VDLs, across more than 1.7 million cases. SDRS is one of the largest U.S. and international databases for veterinary diagnostic information, and planned enhancements in 2026 will further improve access to real time, standardized swine health data (Figure 1).

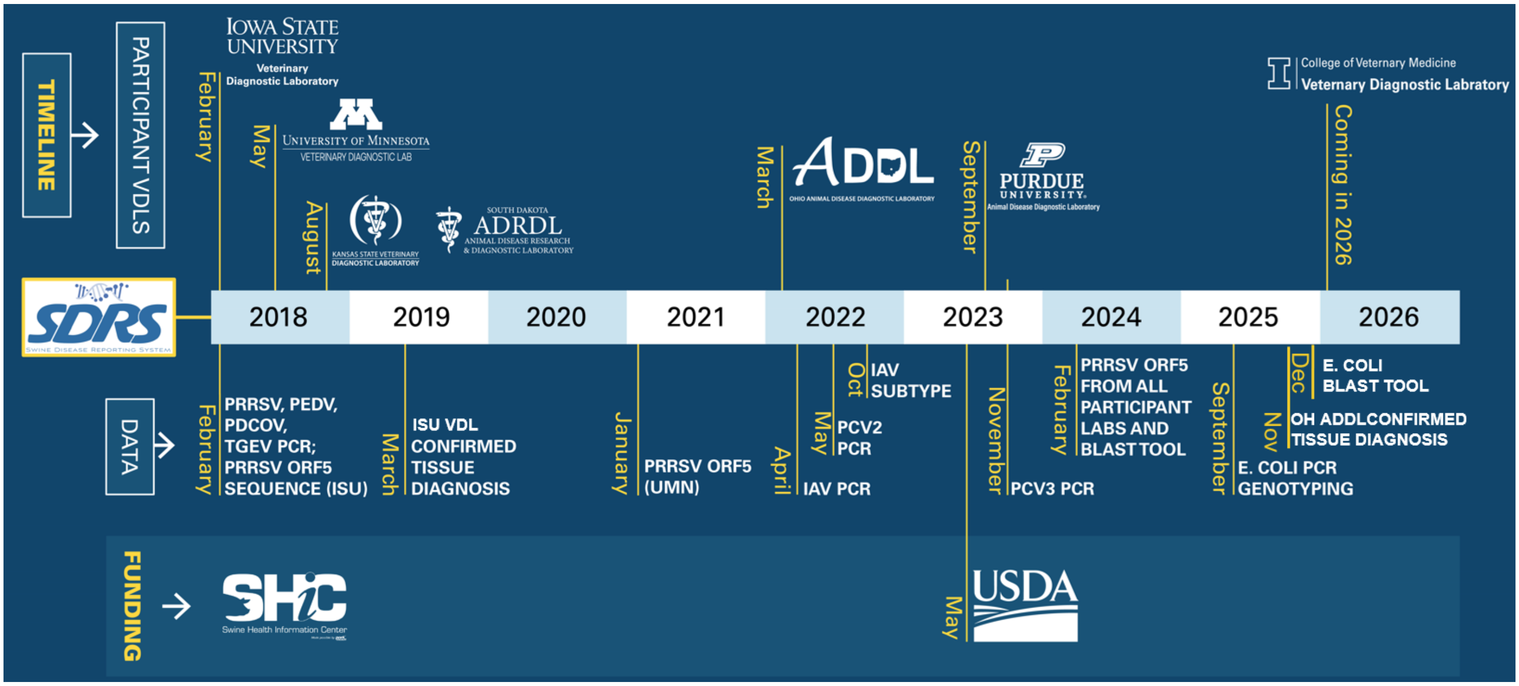

Figure 1. The development of SDRS over time

The system's expansion has been matched by rapid growth in its audience. SDRS report subscribers increased from 43 in 2018 to over 700 as of February 2026, representing veterinarians, producers, diagnosticians, and industry partners across multiple countries. This growth underscores the industry's increasing reliance on SDRS as a central communication platform for disease intelligence.

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II. Key Contributions to U.S. Swine Health and Disease Management

SDRS delivers high value, actionable insights that directly support disease control efforts, pathogen monitoring, and herd-level decision making, revealing key macro-epidemiological trends of pathogen activity in the U.S. swine herd:

- The grow-finish herd is a hotspot for pathogen activity, variant emergence, and amplification, thereby increasing regional infection pressure and the risk of outbreaks in breeding herds.
- Recurrent preceding increase in pathogen activity in grow-finish farms compared to sow farms during the second half of the year.
- Absence of detection of TGEV since 2021.
- SDRS tracks temporal and geographic patterns of pathogen emergence and spread across the U.S. swine population.
- Decline in *Mycoplasma hyopneumoniae (MHP)* activity in the field by reducing the number of confirmed tissue diagnoses and PCR detection in sow farms.
- New surveillance categories, such as the PEDV facility category, reveal off-farm transmission pathways.
- Real-time detection and tracking of emerging PRRSV variants, including first-ever introductions and rapid expansion of aggressive strains.
- Sequence-based tools, such as the PRRSV ORF5 BLAST feature.
- Multi-pathogen trend analysis identifies the agents that consistently drive disease pressure, especially PRRSV and *Streptococcus suis (S. suis)*.
- Co-infection insights, such as recurring PRRSV–IAV overlap.
- Developed and launched the only *E. coli* genotyping classification and benchmarking tool at overall and state levels.
- Maintained ongoing discussion of veterinary diagnostic data standardization and multi-institutional exchange.

Support national elimination and control programs

SDRS data has been instrumental for national initiatives such as the AASV PEDV Elimination Task Force. In 2024, a new PEDV "facility" category was added to capture data from truck washes, packing plants, and vehicles, providing visibility into off-farm transmission pathways. In 2025, this category showed elevated PEDV positivity during the weeks of November 2 and November 16, reaching 25.15% in December, the highest level since 2023, demonstrating how this new category helps the industry detect emerging risks earlier and strengthen biosecurity at critical interfaces. SDRS has also documented the success of MHP elimination efforts, with sow farm detections by PCR reaching a historic low positivity by late 2025, and a reduction in confirmed tissue disease diagnosis cases declining from 496 in 2020 to 249 in 2025, alongside a shift in specimen selection for MHP PCR testing toward deep tracheal swabs.

Evidence of continued decline in detection

SDRS has documented a sustained absence of TGEV detections in U.S. herds. As of February 2026, no TGEV-positive RT-PCR cases have been detected for 60 consecutive months across more than 224,986 cases tested. This sustained monitoring helps the industry verify ongoing control progress, document the absence of detection at a national scale, and ensure that diagnostic laboratories identify and flag any re-introduction early.

Enhanced pathogen surveillance and early warning signals

The SDRS PRRSV ORF5 sequencing detection monitoring, coupled with the PRRSV BLAST tool, introduced in 2024, strengthens early-warning capacity by allowing veterinarians and producers to rapidly compare their PRRSV ORF5 sequences against the SDRS database and identify when, where similar viruses have occurred, i.e., state, along with their genetic signatures of lineage, variant, and RFLP patterns. This capability directly supports outbreak investigations by helping users determine whether a sequence is related to known regional strains or represents a new introduction. SDRS also provides real time first-ever detections as the introduction of PRRSV variant 1C.2 in North Carolina and North Dakota in 2025. The system also tracks the rapid expansion of aggressive PRRSV variants, including the 1C.5 and 1C.5.32 strains, which became dominant wild-type strain across multiple states. This real-time variant tracking strengthens outbreak response and helps producers prepare for shifts in PRRSV behavior.

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Prioritization of health risks through multi pathogen trend analysis

SDRS provides a comprehensive, multi-pathogen view of swine health, helping the industry identify which agents consistently drive disease pressure and how long-term trends inform surveillance and control priorities. PRRSV continues to be the most influential pathogen in growing pigs, reaching its highest proportion of PCR positive submissions in the wean to market category in December 2025, accounting for 48.5% of all positive cases since 2018. Disease index trends from 2020–2025 reinforce this pattern, highlighting PRRSV, along with S. suis, as the most impactful contributors to disease pressure. The addition of *E. coli* PCR genotyping in 2025 offers real time visibility into one of the a economically important enteric pathogens, while 20 years of IAV data revealed seasonal patterns, age group risk differences, and mixed subtype infections that guide vaccination timing and biosecurity planning. Multi pathogen analyses also identify important co infection dynamics, such as the recurring overlap of PRRSV and IAV activity, which intensifies respiratory disease severity. Together, these insights clarify where disease pressure originates and how it shifts over time, enabling more strategic and proactive herd health planning.

III. Research, training, and industry engagement

SDRS also contributes to scientific advancement and workforce development within the swine industry.

Peer-reviewed research and macroepidemiological insights

SDRS has also contributed to eleven peer-reviewed publications that advance swine health surveillance, including studies on the macroepidemiology of PRRSV, PEDV, PDCoV, TGEV, PCV2 and PCV3, long-term IAV detection trends, PRRSV sequencing for tracking genetic evolution, the use of diagnostic codes for population-level health management, PRRSV2 RFLP-defined genetic diversity, prediction of seasonal PRRSV RNA patterns, the relationship of PRRSV RNA detection between adult/sow farm and wean-to-market age categories, *E.coli* systematic review and meta-analysis, disease diagnosis trends and confirmed tissue diagnosis integration from two diagnostic laboratories.

Training the next generation of swine health professionals

SDRS has supported the completion of 2 MS, 2 PhD, and 1 MBA degrees, and is currently engaged with 3 MS and 2 PhD students focused on swine health data analytics, strengthening the industry's capacity for data-driven decision-making.

Industry engagement and preparedness initiatives

The project organizes annual Winter Preparedness discussions and AASV–SDRS Advisory Group meetings to gather expert feedback, interpret emerging trends, and identify research priorities that directly support producers and veterinarians.

Educational media and data literacy tools

SDRS has expanded its communication platforms to include PDF monthly report, podcasts (Spotify, Apple Podcast, and Amazon Music), and educational video tutorials. These resources train users to interpret diagnostic charts, understand pathogen seasonality, and apply data-driven insights to herd health management. To broaden accessibility, SDRS also produces YouTube videos with English and Spanish subtitles, supporting a more diverse workforce across the U.S. pork industry.

IV. Acknowledgments and continued commitment

The developments summarized in this retrospective reflect steady, collaborative work across laboratories, veterinarians, producers, and researchers. SDRS operates with the efforts of six VDL partners, the SDRS Advisory Board, and numerous collaborators continue to share data, expertise, and guidance with a shared commitment to improving swine health. We extend our sincere appreciation for their ongoing partnership, which enables SDRS to remain a reliable, science-based resource for the U.S. swine industry. As the system continues to evolve, ongoing support from the industry will remain essential to sustaining SDRS and expanding access to timely, data-driven swine health information. The SDRS was established and has been maintained through competitive grants awarded to the project by the Swine Health Information Center, and funding for additional research has also been awarded by Iowa Pork Producers and by the Agriculture and Food Research Initiative Competitive Grant no. 2023–67015-39883 from the USDA's National Institute of Food and Agriculture.

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