Swine Disease Reporting System
Report # 57 (November 1, 2022)

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 (USA), and reports the major findings to the swine industry. Our goal is 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 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 University VDL, and Ohio Animal Disease and Diagnostic Lab.

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, Eric Burrough, Phillip Gauger, Christopher Siepker, Alyona Michael, Panchan Sitthicharoenchai, Rodger Main.

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

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

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

Ohio Animal Disease and Diag. Lab.: Melanie Prarat, William Hennessy, Ashley Sawyer, Dennis Summers.

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.

FLUture: Aggregates influenza A virus (IAV) 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 detected at the ISU-VDL, UMN-VDL, KSU-VDL, and OH-ADDL over time by specimen, age group, and US State.

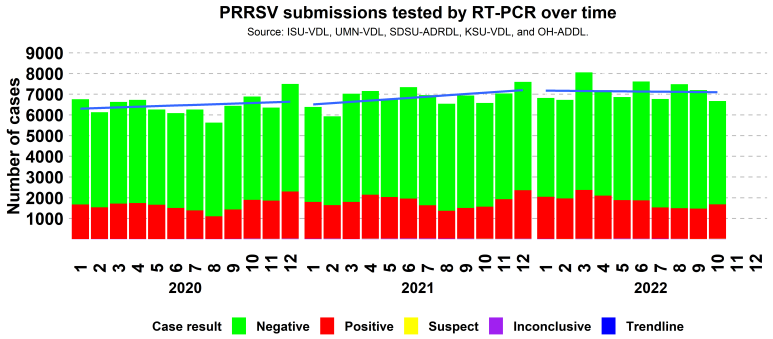
Audio and video reports: Key findings from SDRS projects are summarized monthly in a conversation between investigators and available in the form of an "audio report" and "video report" through Spotify, SwineCast, YouTube, LinkedIn, and the SDRS webpage.

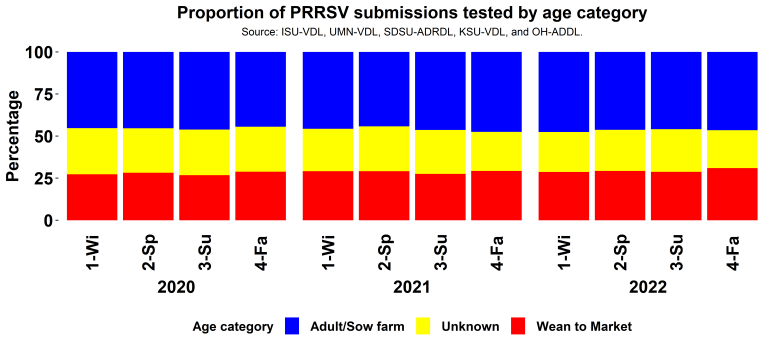
Advisory Group: Reviews and discusses the data, providing their comments and perspectives monthly: Mark Schwartz, Paul Sundberg, Paul Yeske, Tara Donovan, Deborah Murray, Scott Dee, Brigitte Mason, Peter Schneider, Sam Copeland, Luc Dufresne, Daniel Boykin, Corrine Fruge, and William Hollis.

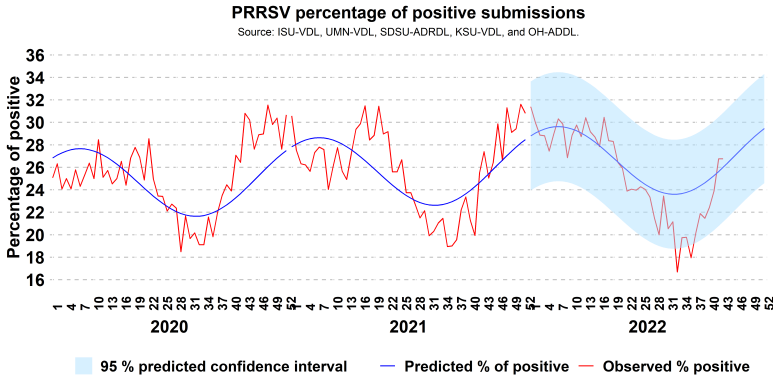
In addition to this report, interactive dashboards with aggregated test results are available at www.fieldepi.org/SDRS.

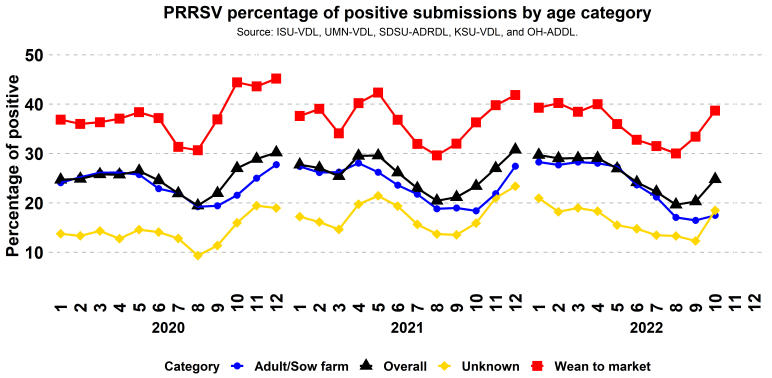
Note: This report contains data up to October 31, 2022.

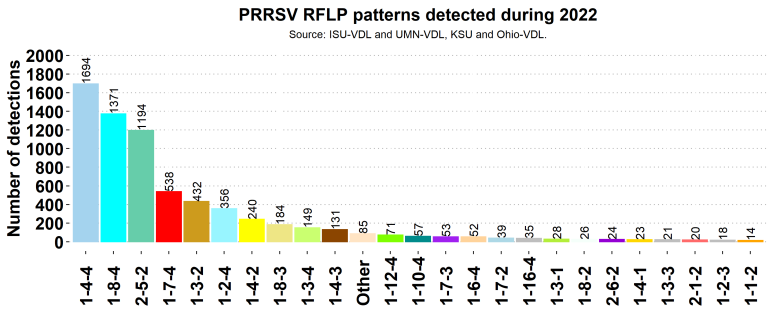
Topic 1 – Detection of PRRSV RNA over time by RT-qPCR.











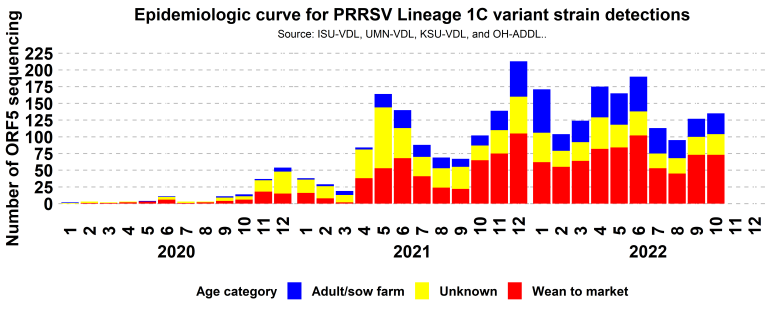


Figure 1. Top: *Left*: Results of PRRSV RT-PCR cases over time; *Right*: Proportion of accession ID cases tested for PRRSV by age group per year and season. **Middle**: *Left* Expected percentage of positive results for PRRSV RNA by RT-qPCR, with 95% confidence interval band for predicted results based 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 2022; *Right*: Epidemiological curve of detection for PRRSV Lineage 1C variant strain.

SDRS Advisory Group highlights:

- Overall, 24.8% of 6,669 cases tested PRRSV-positive in October, a moderate increase from 20.3% of 7,198 in September;
  - Positivity in the adult/sow category in October was 17.49% (539 of 3,082), similar to 16.46% (554 of 3,366) in September;
  - Positivity in the wean-to-market category in October was 38.7% (865 of 2,235), a substantial increase from 33.41% (689 of 2,062) in September;
- Overall PRRSV-percentage of positive cases was 3 standard deviations from state-specific baselines in NE and MO;
- The advisory group highlighted that it is important to reinforce biosecurity and biocontainment measures to prevent breaks in sow farms since an increased detection in grow-finish sites is occurring. Limiting the number of caretakers flowing in different grow-finish sites was suggested by the advisory group in this period to avoid spreading the virus;
- The sharp increase in PRRSV RNA detection was driven by grow-finish cases. Sow farms are therefore at increased risk of PRRSV exposure;
- January 2021 to September 2021, the VDLs performed 5,033 PRRSV ORF5 sequences. Comparing the same period in 2022, it had a 26.54% (1,366) increase in the number of sequences performed for PRRSV (6,369);
- The advisory group highlighted that the increased number of sequences performed might be associated with instability in sow farms, lateral breaks in grow-finish sites, and increased farm surveillance targeting lineage 1C variant RFLP 1-4-4. Also, the severity of outbreaks and longer time to achieve stability led production systems to request more PRRSV sequencing to better understand the virus dynamics.

Topic 2 – Enteric coronavirus RNA detection by RT-qPCR

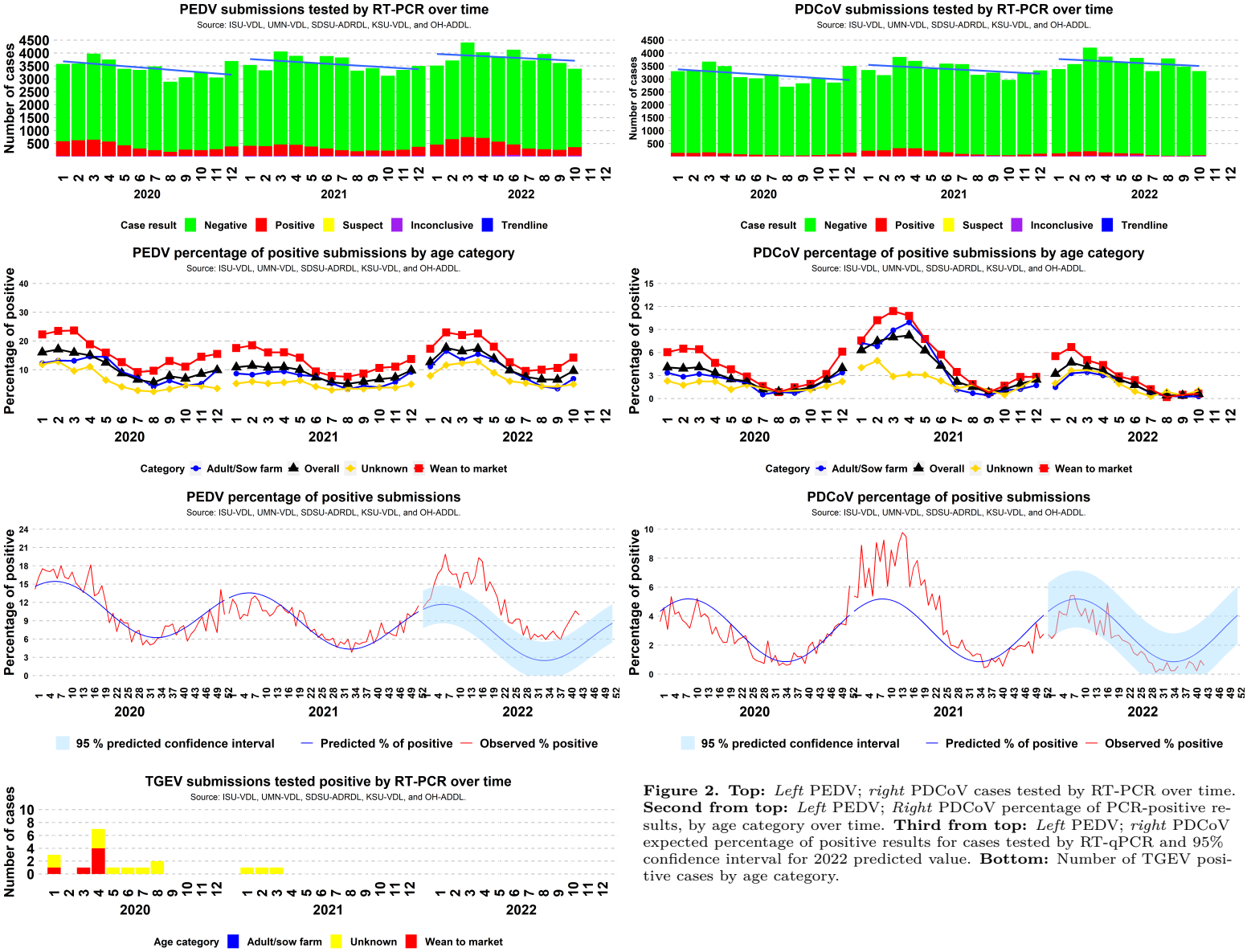


Figure 2. Top: *Left* PEDV; *right* PDCoV cases tested by RT-PCR over time. **Second from top:** *Left* PEDV; *Right* PDCoV percentage of PCR-positive results, by age category over time. **Third from top:** *Left* PEDV; *right* PDCoV expected percentage of positive results for cases tested by RT-qPCR and 95% confidence interval for 2022 predicted value. **Bottom:** Number of TGEV positive cases by age category.

SDRS Advisory Group highlights:

- Overall, 9.62% of 3,388 cases tested PEDV-positive in October, a moderate increase from 6.58% of 3,615 in September;
  - Positivity in the adult/sow category in October was 6.89% (77 of 1,118), a moderate increase from 3.45% (40 of 1,158) in September;
  - Positivity in the wean-to-market category in October was 14.23% (209 of 1,469), a moderate increase from 10.64% (158 of 1,485) in September;
  - The overall PEDV-percentage of positive cases was 3 standard deviations from state-specific baselines in IA, KS, MO and NC;
- Overall, 0.61% of 3,303 cases tested PDCoV-positive in October, similar to 0.4% of 3,478 in September;
  - Positivity in the adult/sow category in October was 0.28% (3 of 1,084), similar to 0.27% (3 of 1,128) in September;
  - Positivity in the wean-to-market category in October was 0.62% (9 of 1,448), similar to 0.49% (7 of 1,419) in September;
  - Overall PDCoV-percentage of positive cases was within state-specific baselines in all 11 monitored states;
- There was 0 positive case for TGEV RNA in October, 2022 over a total of 3,173 cases tested;
- The advisory group highlighted that it is an atypical year for PEDV, and the increased activity in grow-finish sites this month is related to farms monitoring positive flows derived from sow farms breaks in the first semester. Also, re-breaks are occurring due to biosecurity failures in grow-finish sites. Additionally, the moderate increase (4.92%) in PEDV detection during September 18 to October 23 (weeks 39 to 42) raises concern for the potential abnormal activity of PEDV detection in the upcoming months

Topic 3 – Detection of *M. hyopneumoniae* and Porcine Circovirus-2 DNA by PCR.

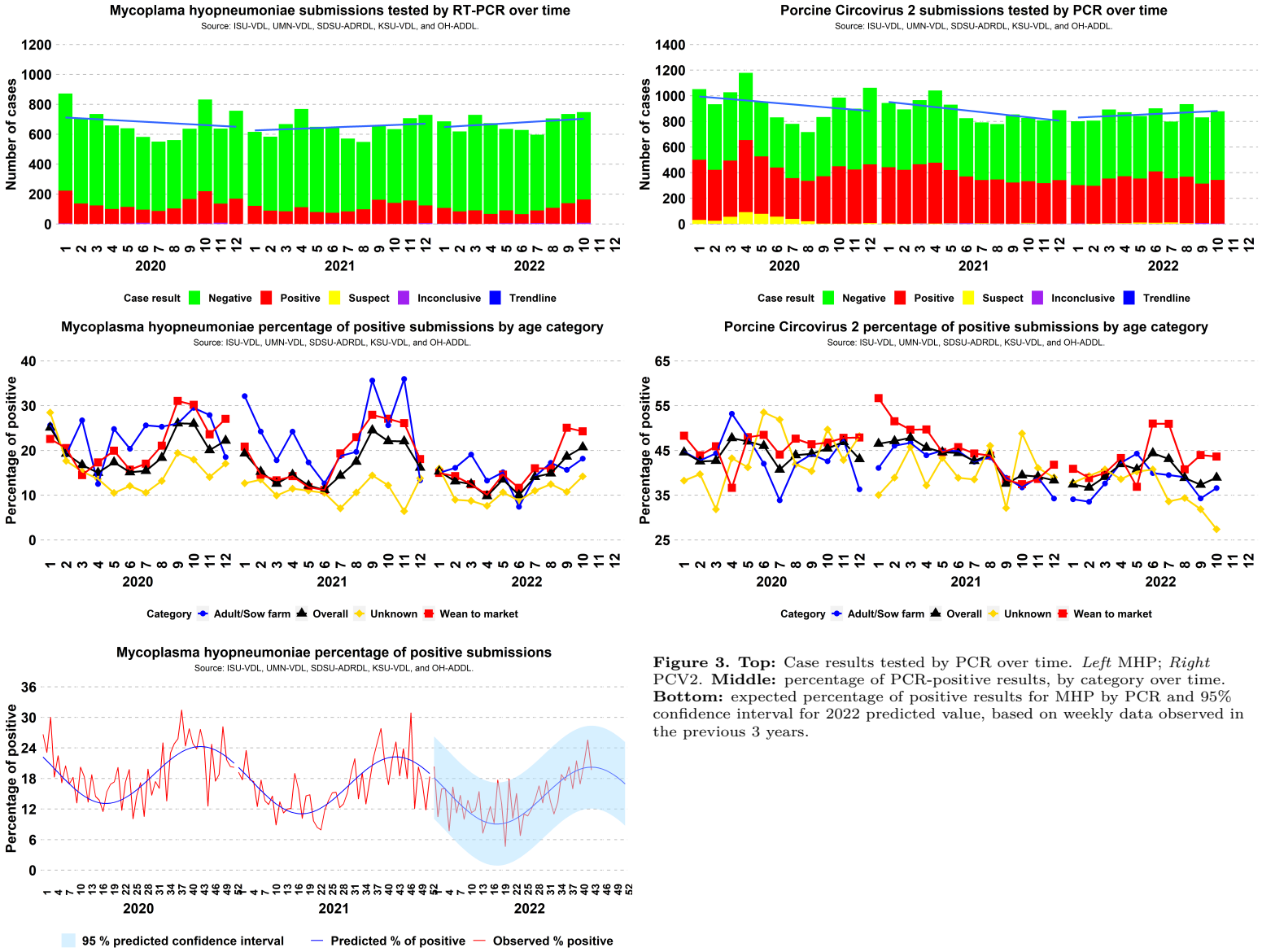
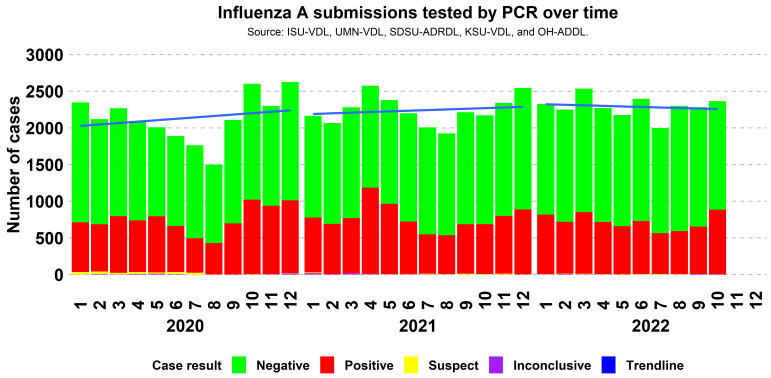


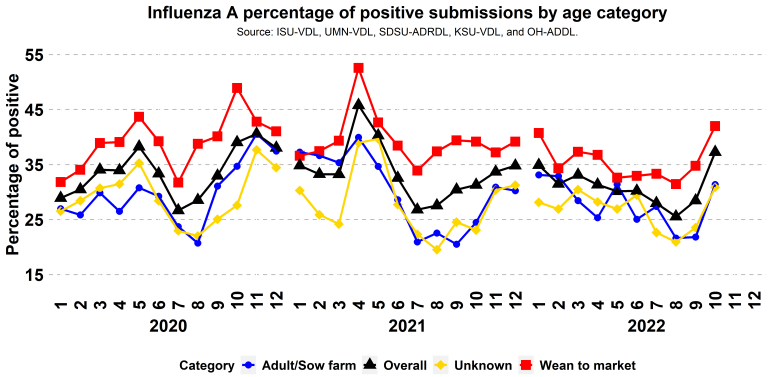
Figure 3. Top: Case results tested by PCR over time. *Left* MHP; *Right* PCV2. **Middle:** percentage of PCR-positive results, by category over time. **Bottom:** expected percentage of positive results for MHP by PCR and 95% confidence interval for 2022 predicted value, based on weekly data observed in the previous 3 years.

SDRS Advisory Group highlights:

- Overall, 20.72% of 748 cases tested *M. hyopneumoniae*-positive cases in October, a moderate increase from 18.64% of 735 in September;
  - Positivity in the adult/sow category in October was 18.18% (22 of 121), a moderate increase from 15.67% (21 of 134) in September;
  - Positivity in the wean-to-market category in October was 24.26% (106 of 437), similar to 25.07% (90 of 359) in September;
  - Overall MHP-percentage of positive was within state-specific baselines in all 11 monitored states;
- Overall, 38.93% of 876 cases tested PCV2-positive in October, similar to 37.33% of 825 in September;
  - Positivity in the adult/sow category in October was 36.6% (153 of 418),a moderate increase from 34.29% (155 of 452) in September;
  - Positivity in the wean-to-market category in October was 43.64% (168 of 385), similar to 43.97% (124 of 282) in September;
- The advisory group highlighted the importance of establishing control and elimination protocols for *Mycoplasma hyopneumoniae* before the fall season to avoid multiple respiratory pathogens circulating in the farm, increasing the losses in the production systems.

Topic 4 – Detection of Swine Influenza A Virus (IAV) RNA by RT-PCR.





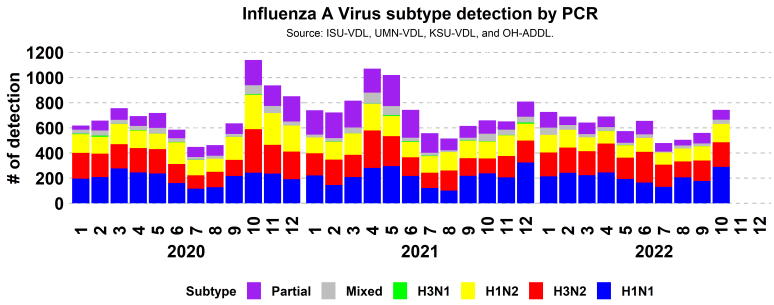
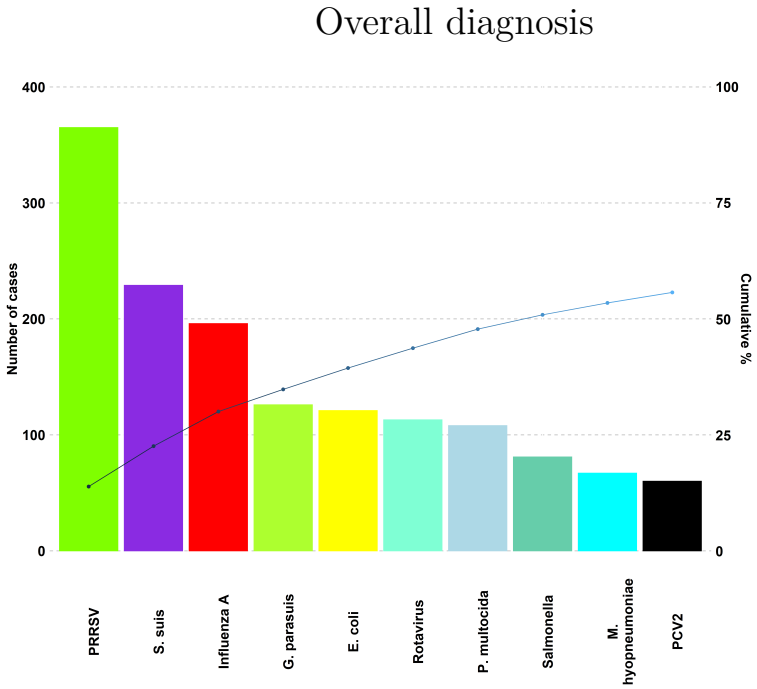


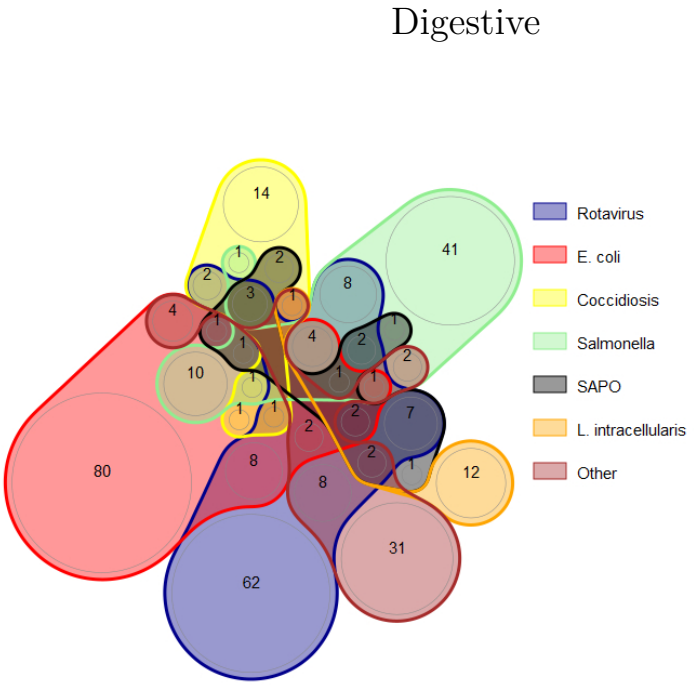
Figure 3. Top: *Left* Results of IAV PCR cases over time. *Right* Percentage of IAV PCR-positive results, by category over time. **Bottom:** Number of IAV subtyping PCR detection over time; (Partial - only hemagglutinin or neuraminidase region detected; Mixed - 3 or more haemagglutinin and neuroaminidase regions detected. i.e., "H1 H3 N1").

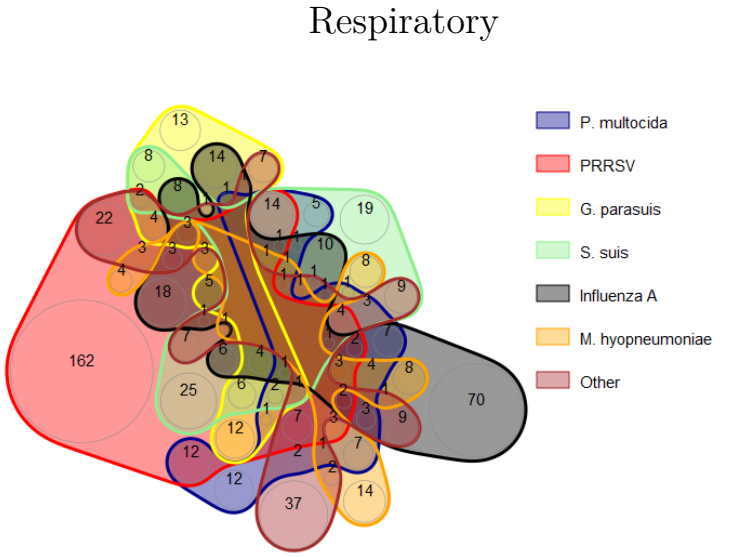
SDRS Advisory Group highlights:

- Overall, 37.26% of 2,362 cases tested IAV-positive cases in October, a substantial increase from 28.46% of 2,277 in September;
- Positivity in the adult/sow category in October was 31.38% (139 of 443), a substantial increase from 21.82% (84 of 385) in September;
- Positivity in the wean-to-market category in October was 42.01% (557 of 1,326), a substantial increase from 34.77% (363 of 1,044) in September.
- Overall, 3.78% of 503 samples were mixed subtype detection in September, similar to 4.82% of 498 in August;
- The advisory group highlighted that whole herd vaccination of Influenza before the colder months (October, November, December) is important to prevent interactions of this virus with other pathogens (PRRSV, *Mycoplasma hyopneumoniae*, *Streptococcus suis*, and *Pasteurella multocida*) that enhances losses in the production systems. Also, the pumping manure season, dust derived from the crop harvesting, and abrupt temperature shifts are occurring in this period, increasing the challenges in farms, making the animals more predisposed to respiratory pathogens.

Topic 5 – Confirmed tissue cases etiologic/disease diagnosis at the ISU-VDL.







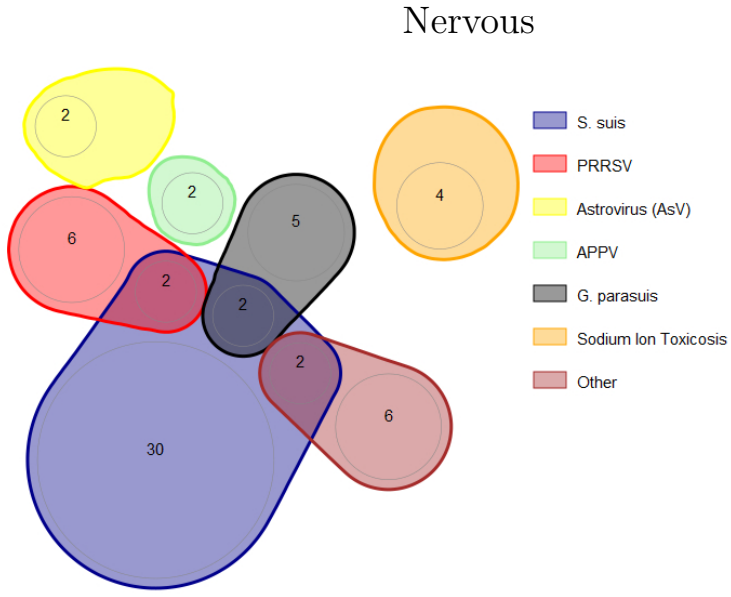


Figure 4. ISU-VDL most frequent overall confirmed tissue disease diagnosis. The presented system is described in the title of the chart. Colors represent one agent; line intersections present diagnosis of 2 or more agents within a submission. Only the most frequent etiology/disease are presented. Less 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, Harm, Magstadt, Mainenti, Michael, Piñeyro, Rahe, Schumacher, Siepker, Sitthicharoenchai, 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 September. 1 to October. 15, 2022.

SDRS Advisory Group highlights:

• PRRSV (365) led cases with confirmed etiology, followed by *S. suis* (229), and *Influenza A* (196). PRRSV (346 of 1111) led the number of confirmed respiratory diagnoses, *E. coli* (117 of 420) lead the number of confirmed digestive diagnoses, and *S. suis* (36 of 67) led the number of confirmed neurological diagnoses.

• During September 12th to October 10th, there were spikes in the number of respiratory, systemic, and musculoskeletal confirmed diagnoses; during the same period there were spikes in *S.suis*, *G. parasuis*, Influenza A, *Trueperella pyogenes*, and *P. multocida*.

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 Senecavirus A in pigs from a historically negative national swine herd and in associated feed imports from an endemically infected country

Scott Dee[1], Karyn Havas[1], Gordon Spronk[1]
1 - Pipestone Applied Research, Pipestone, Minnesota, USA.

The full-text reference articles: Detection of Senecavirus A in pigs from a historically negative national swine herd and in associated feed imports from an endemically infected country

Introduction

The purpose of this report is to describe the initial clinical diagnosis of SVA in a swine farm from a historically naïve national herd, and the results of a diagnostic investigation designed to identify potential routes of entry of SVA to the country and the farm. For confidentiality, names of all countries and companies will not be disclosed. In July 2022, vesicular lesions were observed on the snouts and feet of pigs in the case pork production system. Diagnostic testing indicated the presence of SVA in vesicular fluids and ruled out FMDV. Prior to the onset of clinical signs, feed ingredients had been imported from other countries, several known to be endemically infected with SVA, and formulated diets contain these imported ingredients were being fed to pigs prior to and during the onset of clinical signs.

Materials and Methods

A diagnostic investigation was conducted to identify potential sources of viral entry. A total of 39 samples (dust and grain probe) were collected, including samples from facilities and equipment, i.e., floor surfaces from storage warehouses and associated driveways on affected farms and mills, along with feed mixers, from bulk-feed ingredients, including soybean meal imported from SVA-positive and SVA-negative countries, along with raw soybeans and corn gluten meal from SVA-negative countries, and micronutrients from SVA-positive countries, including valine, lysine, methionine, vitamin C, threonine, and tryptophan, were sampled. In addition, one tote bag containing lysine from an SVA-positive country was sampled, due to visible debris, i.e., feed dust and dirt observed on its external surface. Finally, dust samples of poultry feed and dust from associated feed storage areas, along with samples of dust from plant food, were collected. Samples were tested for the presence of SVA RNA by PCR. To validate the ability of the PCR assay to detect SVA RNA, six feed samples from an unaffected farm were spiked with vesicular fluid from affected pigs with clinical signs.

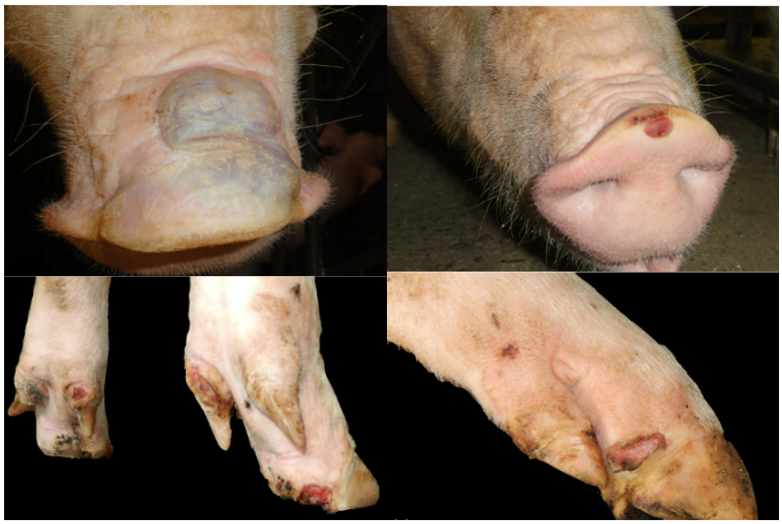


Figure 1. Seneca A virus lesions in sows: Top: *Left* snout, sow. A large vesicle typical of SVA infection is present on the dorsal aspect of the snout. *Right* Snout, sow. Ulcerated skin on the tip of snout after rupture of a vesicle. Bottom: Hooves, sows. Multifocal ulceration of the coronary band. Source: Segalés et al. 2016.

Major findings and implications

1. Across all samples tested, only samples from soybean meal imported from an SVA-positive country, and the sample from the external surface of the tote bag, from a different SVA-positive country, were positive for SVA RNA
2. All positive control samples were PCR-positive for SVA RNA.
3. The fact that clinical signs of SVA were noted in pigs being fed diets formulated with these imported ingredients suggests that infectious SVA could have been present in the feed.
4. This case describes the first potential link between the entry of a novel viral agent to a naïve national swine herd through the prior importation of feed ingredients from an endemically infected county.
5. It validates previously published laboratory data on feed risk.
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7. This could have been ASFV and FMDV, instead of SVA.
8. This case validates the need for a Responsible Imports program as part of the US SHIP.