Swine Disease Reporting System
Report # 46 (December 7, 2021)

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 the input of our advisory group, which consists of veterinarians and producers across the USA 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 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, and Kansas State University VDL.

Collaborators:

Swine Disease Reporting System office: Principal investigator: Daniel Linhares, Project coordinator: Giovani Trevisan, Communications: Edison Magalhães.

Iowa State University: Gustavo Silva, Bret Crim, Kent Schwartz, Eric Burrough, Phillip Gauger, Pablo Pineyro, Christopher Siepker, Rodger Main.

Project coordinator Giovani Trevisan. Principal investigator Daniel Linhares.

University of Minnesota: Mary Thurn, Paulo Lages, Cesar Corzo, Jerry Torrison.

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

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

Ohio Animal Disease and Diagnostic Lab.: Melanie Prarat, Yan Zhang, Richard French, 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, USA state, specimen, and age group.

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 SwineCast, YouTube, LinkedIn, and the SDRS webpage.

Advisory Group: Reviews and discusses the data, providing their comments and perspectives on a monthly: Mark Schwartz, Paul Sundberg, Paul Yeske, Tara Donovan, Deborah Murray, Scott Dee, Melissa Hensch, Brigitte Mason, Peter Schneider, Sam Copeland, and Luc Dufresne.

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 November 30, 2021.

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

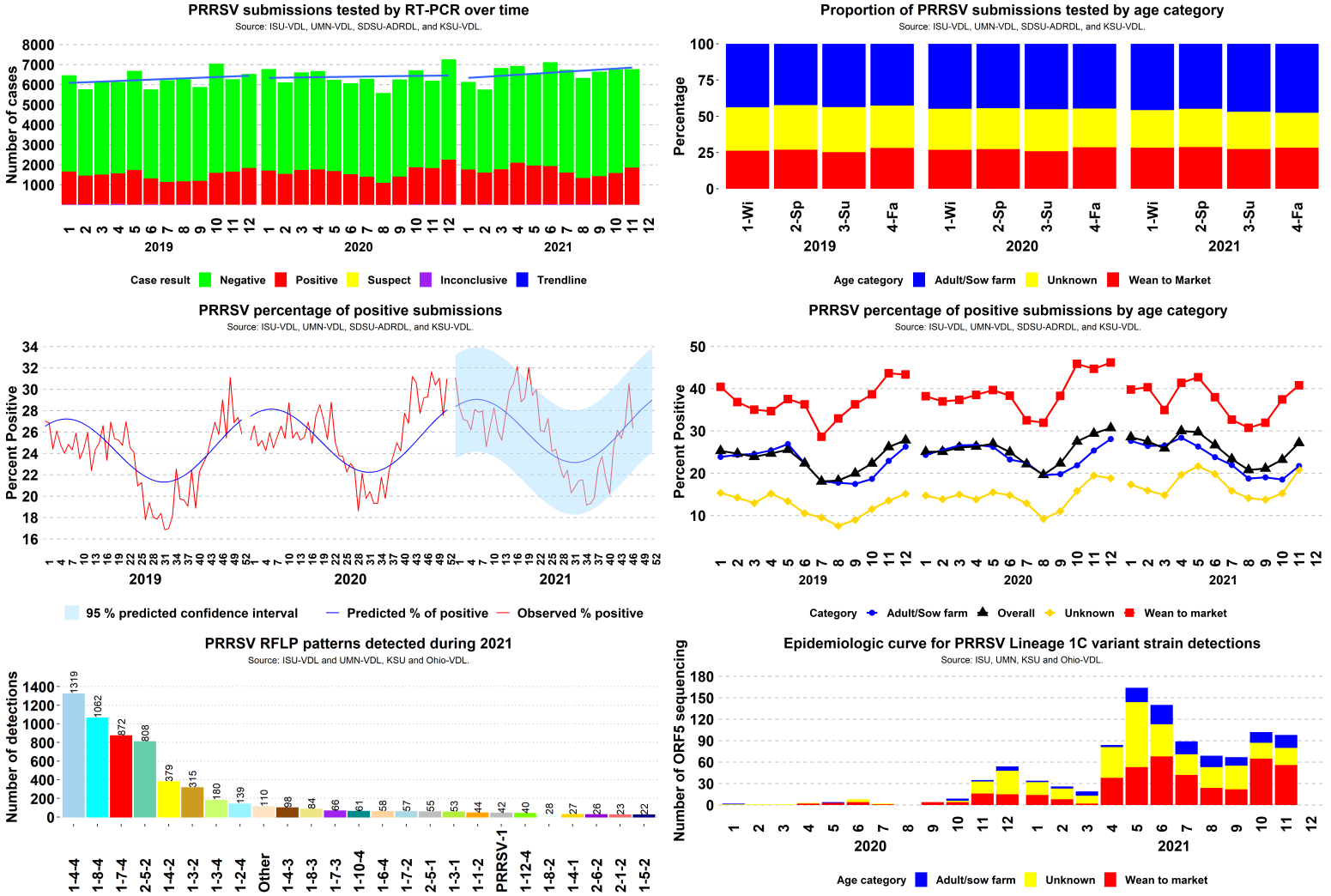

Figure 1. Top: *left*: Results of PRRSV RT-PCR cases over time. *Right*: Proportion of accession ID cases tested for PRRSV by age group per year and season. **Middle**: *Left* expected percentage of positive results for PRRSV RNA by RT-qPCR, with 95% confidence interval band for predicted results based 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 druing 2021; *right* Epidemiological curve of detection for PRRSV Lineage 1C variant strains.

SDRS Advisory Group highlights:

- Overall, 27.18% of 6,774 cases tested PRRSV-positive in November, a moderate increase from 23.2% of 6,759 in October;
- Positivity in adult/sow category in November was 21.71% (689 of 3,173), a moderate increase from 18.51% (585 of 3,160) in October;
- Positivity in wean-to-market category in November was 40.82% (820 of 2,009), a moderate increase from 37.46% (733 of 1,957) in October;
- Overall PRRSV-percentage of positive cases was wihin 3 standard deviations from state-specific baselines in OH;
- During November 72.45% (71) of the PRRSV L1C variant strains were detected in IA and other 25.51% (25) in MN;
- A moderate increase in detection of PRRSV in breeding herds occurred in November, and agreed with past reports that have highlighted that spike in grow-finish pigs (seen since September) usually is followed by increased activity in breeding herds;
- The advisory group has highlighted that during the last decade, the U.S. swine industry has considerably raised the bar on biosecurity and biocontainment practices to contain the spread of pathogens across farms. Still exist opportunities to improve practices across all the swine industry sectors. The most commonly raised opportunities are:
  - Implementing entry benches, usage of site-specific clothing and a shower in/shower out process.
  - Better transport truck wash facilities and increase the capacity of washing trucks specially before leaving the packing plant.
  - Separation of trucks, people, maintenance crew movement between breed to wean farms and growing sites.
  - Focus on growing sites biosecurity as like reducing caretakers circulation across multiple finishing sites within a day.
- Also, the advisory group reminds that some regions have considerably evolved the level of biosecurity and biocontainment practices that further implementations will require a considerable amount of investments.

Topic 2 – Detection of RNA of enteric coronavirus by RT-qPCR

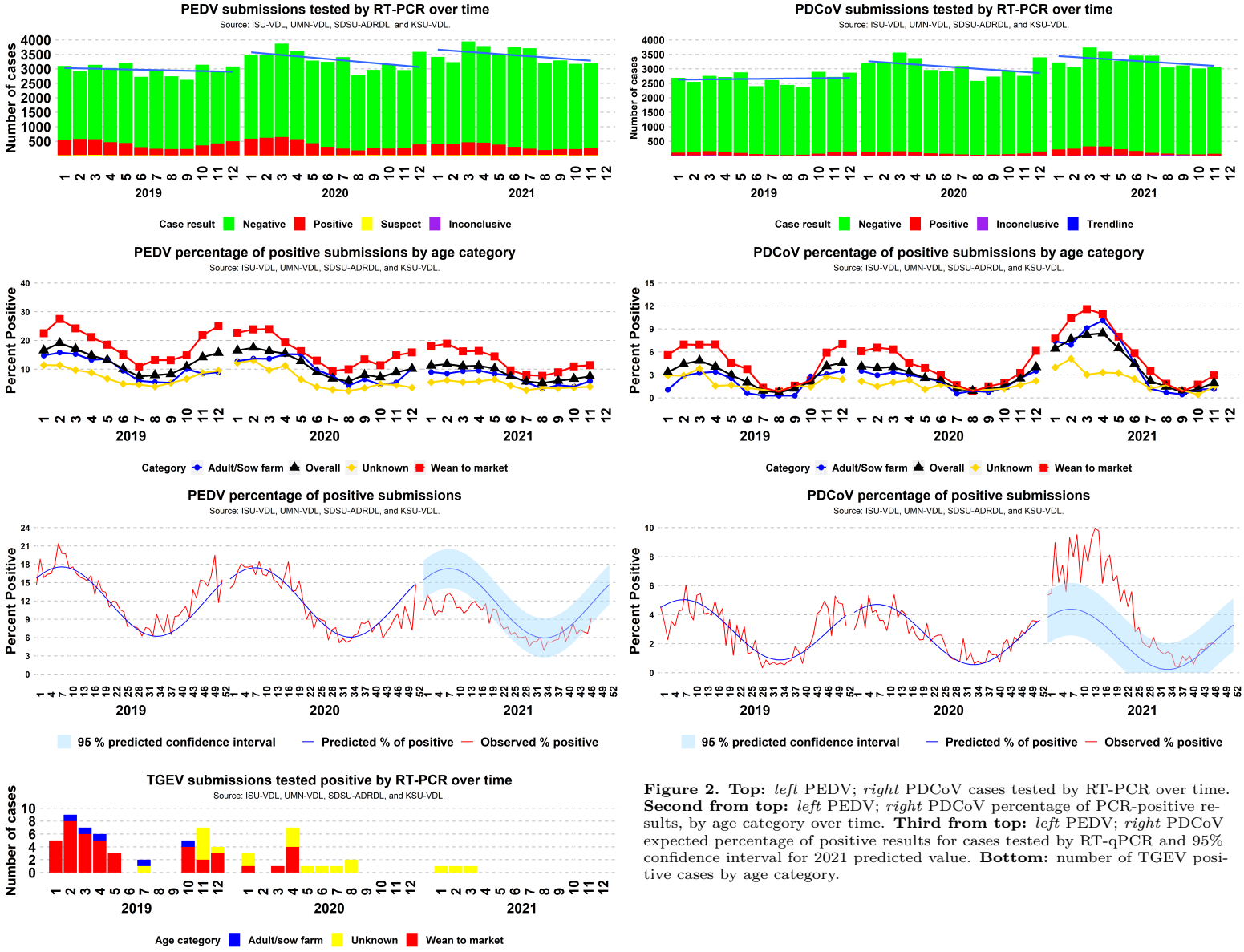

Figure 2. Top: *left* PEDV; *right* PDCoV cases tested by RT-PCR over time. **Second from top:** *left* PEDV; *right* PDCoV percentage of PCR-positive results, by age category over time. **Third from top:** *left* PEDV; *right* PDCoV expected percentage of positive results for cases tested by RT-qPCR and 95% confidence interval for 2021 predicted value. **Bottom:** number of TGEV positive cases by age category.

SDRS Advisory Group highlights:

- Overall, 7.53% of 3,202 cases tested PEDV-positive in November, similar to 6.67% of 3,177 in October;
  - Positivity in adult/sow category in November was 5.88% (58 of 987), similar to 3.94% (38 of 964) in October;
  - Positivity in wean-to-market category in November was 11.39% (147 of 1,291), similar to 10.97% (140 of 1,276) in October;
  - The overall PEDV-percentage of positive cases was 3 standard deviations from state-specific baselines in IL and OK;
- Overall, 1.96% of 3,057 cases tested PDCoV-positive in November, similar to 1.16% of 3,016 in October;
  - Positivity in adult/sow category in November was 1.17% (11 of 939), similar to 1.1% (10 of 905) in October;
  - Positivity in wean-to-market category in November was 2.94% (36 of 1,225), similar to 1.73% (21 of 1,212) in October;
  - Overall PDCoV-percentage of positive cases was 3 standard deviations from state-specific baselines in all 10 monitored states;
- There was 0 positive case for TGEV RNA in November, 2021 over a total of 2,837 cases tested;
- The advisory group has suggested that the detection of PEDV is following the expected trend of detection for November. The same comments on biosecurity and biocontainment practices shared in the PRRSV section apply to enteric coronavirus.

Topic 3 – Detection of *Mycoplasma hyopneumoniae* (MHP) DNA by PCR.

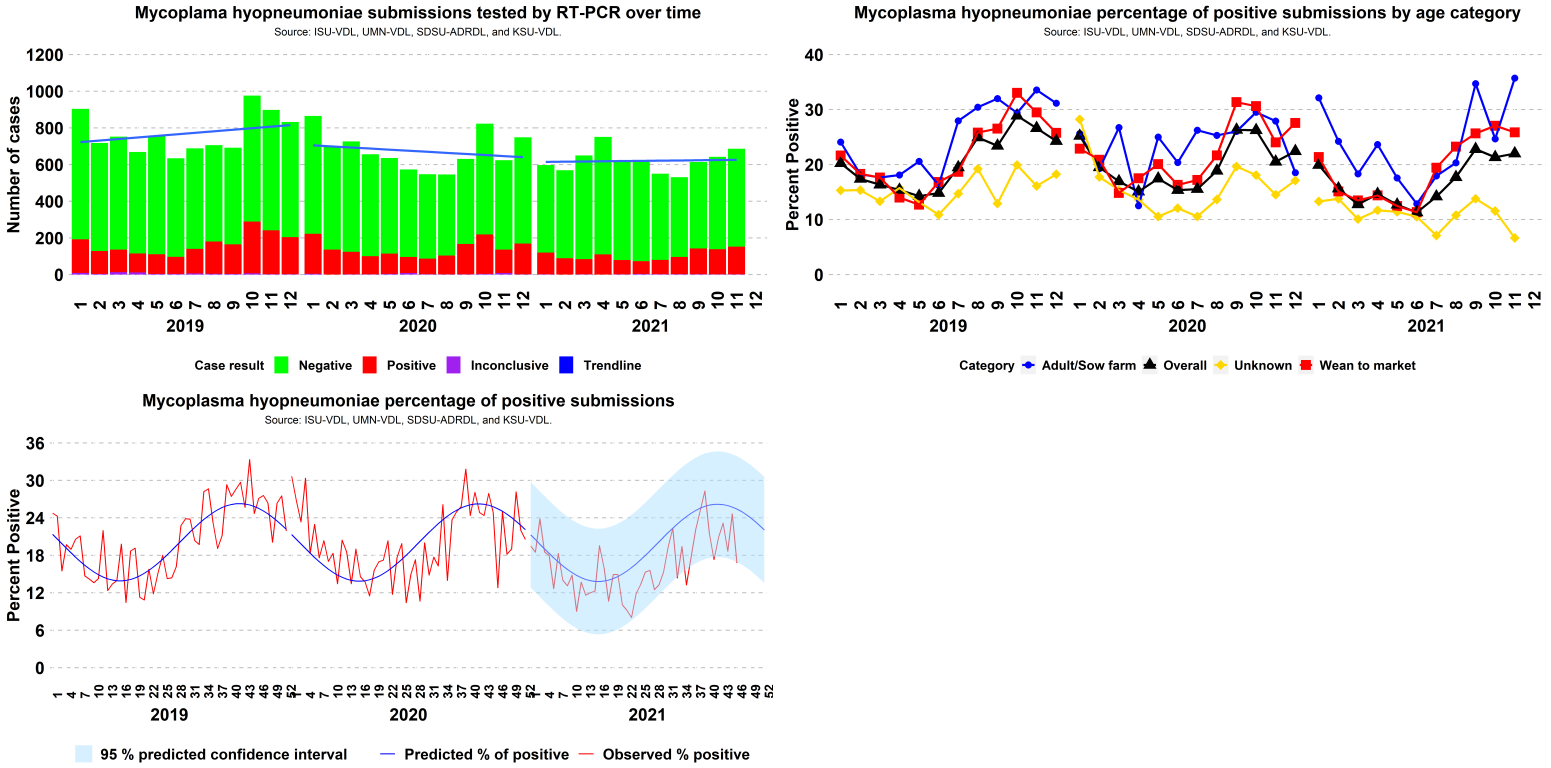

Figure 3. *Left top*: results of *M. hyopneumoniae* (MHP) PCR cases over time. *Right top*: percentage of MHP PCR-positive results, by category over time. *Bottom*: expected percentage of positive results for MHP by PCR and 95% confidence interval for 2020 predicted value, based on weekly data observed in the previous 3 years.

SDRS Advisory Group highlights:

- Overall, 22.01% of 686 cases tested *M. hyopneumoniae*-positive in November, similar to 21.34% of 642 in October;
  - Positivity in adult/sow category in November was 35.71% (40 of 112), a marked increase from 24.68% (19 of 77) in October;
  - Positivity in wean-to-market category in November was 25.86% (98 of 379), similar to 27.06% (92 of 340) in October;
  - Overall MHP-percentage of positive was within expected state-specific baselines in all 11 monitored states;
- The advisory group considered that the recent increase in detection of *M. hyopneumoniae* is according to the expected for this time of year.

Topic 4 – Confirmed tissue cases etiologic/disease diagnosis at the ISU-VDL.

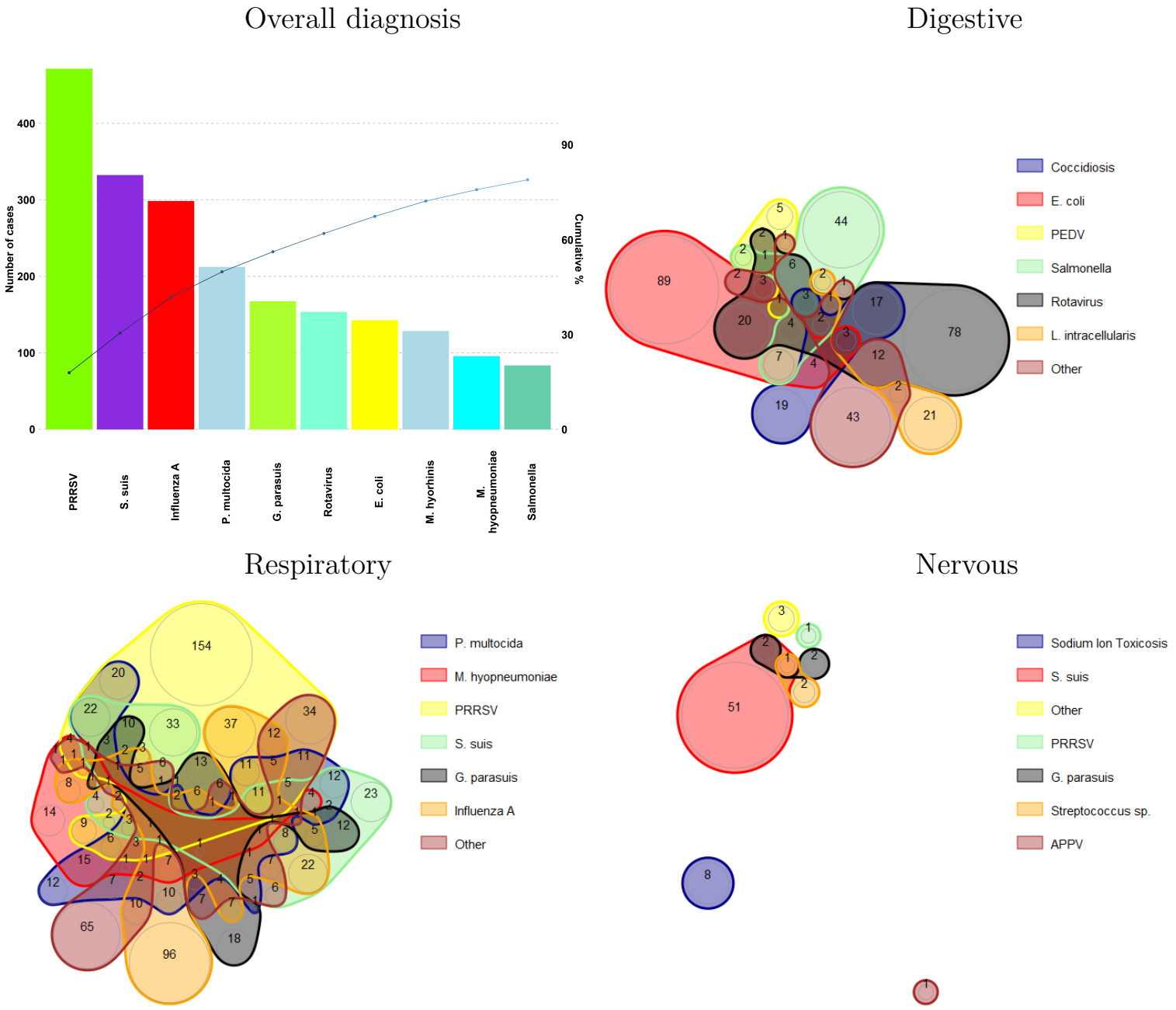

Figure 4. ISU-VDL most frequent overall confirmed tissue disease diagnosis. The presented system is described in the title of the chart. Colors represent one agent. Line intersections present diagnosis of 2 or more agents within a submission. Only the most frequent etiology/disease are presented. Less frequent etiology/disease are grouped as other. Non-confirmed diagnoses are not presented. Note: Disease diagnosis takes 1 to 2 weeks to be performed. The graphs and analysis contain data from Oct. 1 to Nov. 18, 2021.

SDRS Advisory Group highlights:

- PRRSV (471) leads cases with confirmed etiology/disease, followed by *S. suis* (332), and Influenza A (298). PRRSV (449 of 1627) leads the number of confirmed respiratory diagnoses, *Rotavirus* (153 of 512) leads the number of confirmed digestive diagnoses, and *S. suis* (54 of 74) leads the number of confirmed neurological diagnosis.
- During October 24 to 30, there was a significant increase (signal) in tissue diagnosis of respiratory, systemic, and cardiovascular-blood-endocrine-immune agents, with an uptick in diagnosis of: PRRSV, PCV2, *M. hyopneumoniae*, *G. parasuis*, and *S. suis*;
- During November 5 to 18, there was a significant increase (signal) in tissue diagnosis of Influenza A;
- The advisory group has associated the uptick of respiratory agents with seasonal swings and cooler temperatures. Also, pigs in some areas went through a significant amount of viral challenges what may have created an opportunity for the expression of secondary agents.

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.*

Understanding the persistence of Senecavirus A in breeding herds

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Senecavirus A (SVA) is well known for causing a vesicular disease that is visually indistinguishable from other government-monitored vesicular diseases such as foot-and-mouth disease (FMD). For this reason, this virus has been responsible for a rampant increase in the number of foreign animal disease (FAD) investigations in the U.S. Based on the USDA's FAD Investigation report, in 2019, a total of 2,517 FAD investigations were conducted, with 1,845 (73%) of them being for swine vesicular diseases.
It is currently unknown for how long SVA stays active within a sow farm after its introduction. At the University of Minnesota (UofM), we began addressing this question by conducting a study funded by the AASV Foundation. Processing fluids (PF) samples were collected from 10 sow farms undergoing an SVA outbreak and tested for SVA using PCR. One farm had semen and tissues from heat check boars tested to assess their potential role in the persistence of the virus in the breeding herd. All farms were sampled and tested for different periods before and/or after SVA signs were detected.
The virus was detected in PF from all farms, and intermittent detection for up to 21 weeks after the first SVA clinical signs were seen, with an average of 11.8 weeks. Interestingly, Farm 1 had SVA-positive PF three weeks before clinical signs were evident. Furthermore, Farms 1, 3, 4, and 5 were positive two weeks before clinical signs, and Farms 1, 4, 5, and 9 were positive one week before clinical SVA signs were seen (Figure 1). Heat check boars could potentially act as a source of SVA infection to naïve gilts and sows over time and after an outbreak. In two semen collection time-points, 7 out of 9 and 1 out of 16 boars tested had SVA positive semen by PCR at 7 and 18 weeks after outbreak detection, respectively. Furthermore, the boar with SVA-positive semen in the second collection time-point was euthanized and had its testicles tested at 22 weeks after the outbreak. Testicular tissues contained a significant amount of SVA genetic material and had positive in-situ hybridization signal, which indicates the presence of SVA replication in the testes.

The data collected in this study shows that SVA continues to circulate in breeding herds for a significant amount of time after clinical signs have been detected. Since SVA signs in breeding herds are usually seen for two weeks after the outbreak, producers and practitioners should be cautious when classifying the herd as stable based upon weaning SVA-negative piglets. Our study demonstrated that the absence of clinical signs does not necessarily indicate that the virus is no longer present within the herd. Processing fluids have been successfully used for monitoring PRRS in disease elimination protocols, and it appears that this tool might be helpful for the control of SVA. Heat-check boars also appear to play an essential role in the persistence of SVA in a sow farm, so strategic sampling and testing of these animals is advised. This study contributes to the SVA-epidemiology knowledge in sow farms by increasing the understanding of SVA persistence and transmission, which can help develop strategies to control SVA and its impact on pig production systems.

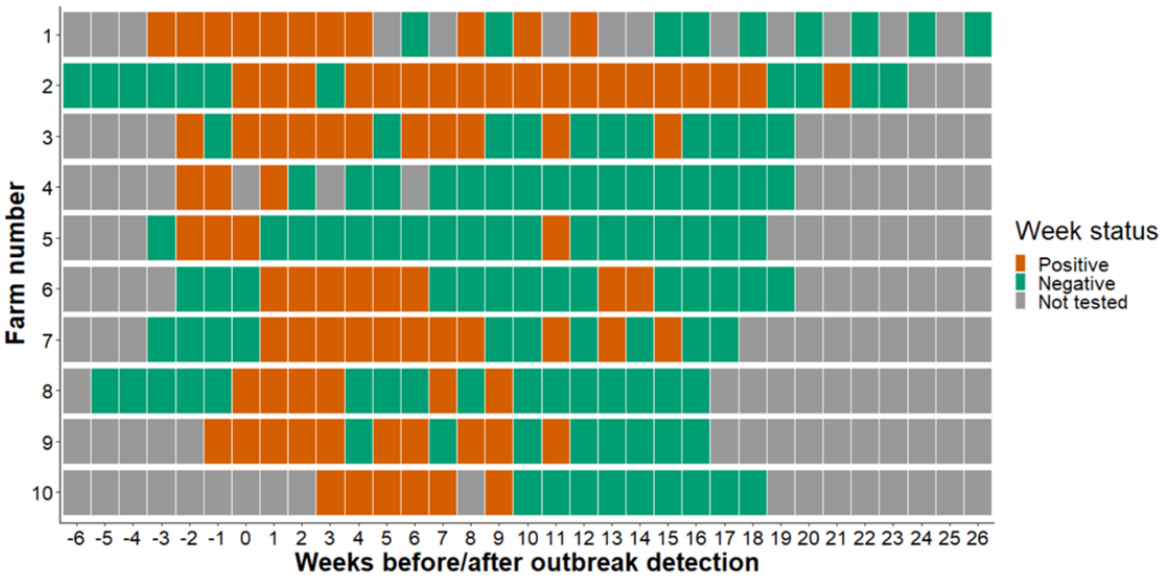

Figure 1. Weekly status to Senecavirus A (SVA) by processing fluids samples in 10 sow farms before and after SVA outbreak detection.

Highlights:

- Senecavirus A (SVA) continues to be responsible for an important number of FAD investigations;
- SVA continued to circulate in breeding herds for up 21 weeks after farmworkers detected clinical signs;
- Heat check boars may contribute to the persistence of this virus in the population.