Swine Disease Reporting System
Report # 60 (February 07, 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 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, Kinath Rupasinghe, Eric Burrough, Phillip Gauger, Christopher Siepker, Panchan Sitthicharoenchai, 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.

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 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.

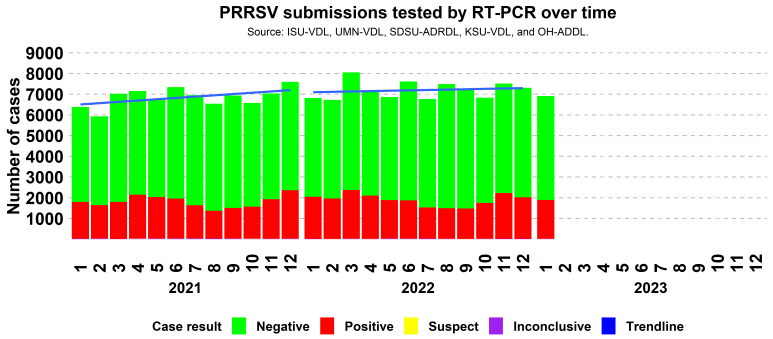
Audio and video reports: Key findings from SDRS projects are summarized monthly in a conversation between investigators and available in the form of an "audio report" and "video report" through Spotify, Apple Podcast, Google podcast, SwineCast, YouTube, LinkedIn, and the SDRS webpage.

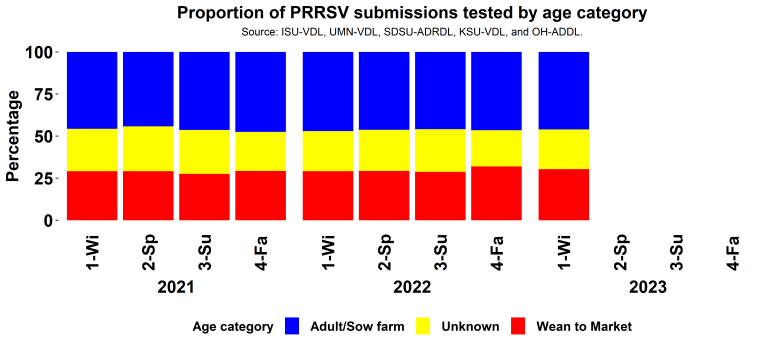
Advisory Group: Reviews and discusses the data, providing their comments and perspectives monthly: Mark Schwartz, Paul Sundberg, Paul Yeske, Tara Donovan, Deborah Murray, Scott Dee, Brigitte Mason, Peter Schneider, Sam Copeland, Luc Dufresne, Daniel Boykin, Corrine Fruge, William Hollis, and Rebecca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

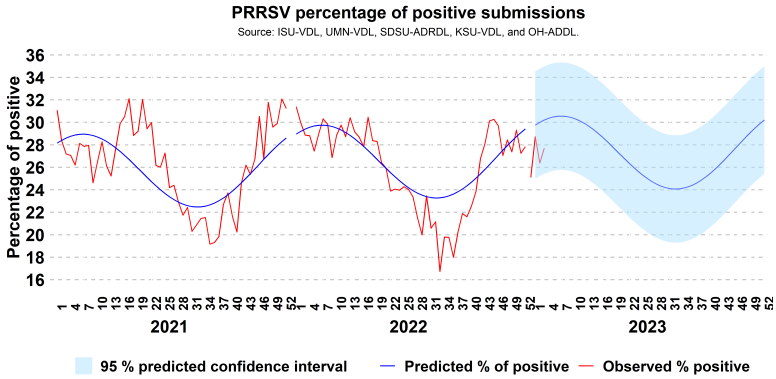
In addition to this report, interactive dashboards with aggregated test results are available at www.fieldepi.org/SDRS.

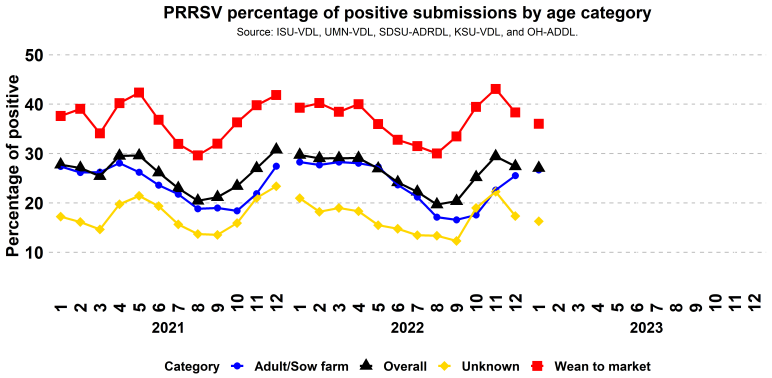
Note: This report contains data up to January 31, 2023.

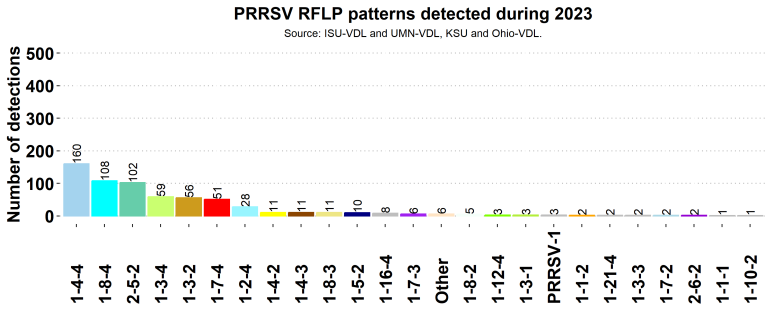
Topic 1 – Detection of PRRSV RNA over time by RT-qPCR.











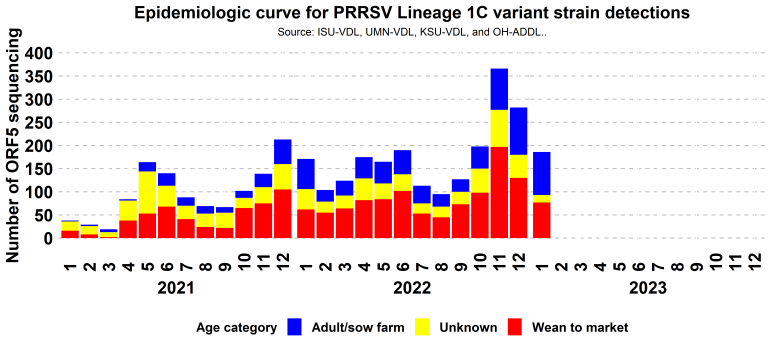


Figure 1. Top: *Left*: Results of PRRSV RT-PCR cases over time; *Right*: Proportion of accession ID cases tested for PRRSV by age group per year and season. **Middle**: *Left* Expected percentage of positive results for PRRSV RNA by RT-qPCR, with 95% confidence interval band for predicted results based 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 2023; *Right*: Epidemiological curve of detection for PRRSV Lineage 1C variant strain.

SDRS Advisory Group highlights:

- Overall, 27.06% of 6,913 cases tested PRRSV-positive in January, similar to 27.42% of 7,312 in December;
  - Positivity in the adult/sow category in January was 26.68% (849 of 3,182), similar to 25.54% (861 of 3,371) in December;
  - Positivity in the wean-to-market category in January was 36.03% (756 of 2,098), a moderate decrease from 38.31% (841 of 2,195) in December;
- Based on the number of sequences detected and classified as L1C variant, the states with high activity are Missouri (90), Iowa (58), and Minnesota (17) during January 2023;
- The advisory group highlighted that 2023 might be a year with high activity of PRRSV. An increase in the number of growing sites closely monitoring for PRRSV activity and detection of the circulating (different PRRSV strains) has contributed to leveling up the PRRSV detection. The advisory group keeps reminding of the need to continue improving biosecurity practices in growing sites to decrease lateral infections and pressure of infection.

Topic 2 – Enteric coronavirus RNA detection by RT-qPCR

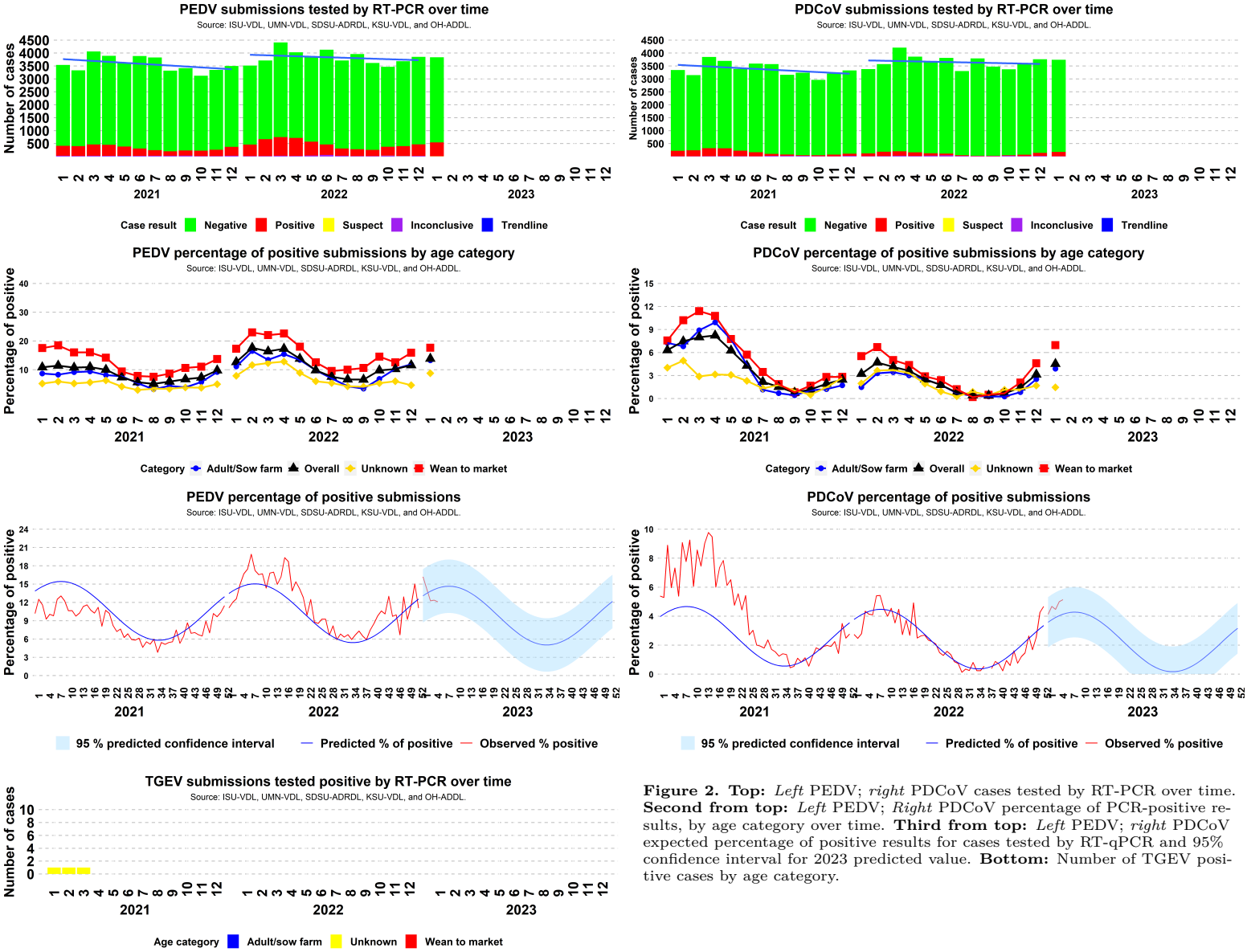


Figure 2. Top: *Left* PEDV; *right* PDCoV cases tested by RT-PCR over time. **Second from top:** *Left* PEDV; *Right* PDCoV percentage of PCR-positive results, by age category over time. **Third from top:** *Left* PEDV; *right* PDCoV expected percentage of positive results for cases tested by RT-qPCR and 95% confidence interval for 2023 predicted value. **Bottom:** Number of TGEV positive cases by age category.

SDRS Advisory Group highlights:

- Overall, 13.88% of 3,832 cases tested PEDV-positive in January, a moderate increase from 11.58% of 3,850 in December;
  - Positivity in the adult/sow category in January was 13.29% (154 of 1,159), similar to 11.9% (150 of 1,260) in December;
  - Positivity in the wean-to-market category in January was 17.68% (284 of 1,606), similar to 15.94% (248 of 1,556) in December;
- Overall, 4.52% of 3,740 cases tested PDCoV-positive in January, similar to 3.14% of 3,761 in December;
  - Positivity in the adult/sow category in January was 3.89% (44 of 1,131), similar to 2.52% (31 of 1,230) in December;
  - Positivity in the wean-to-market category in January was 6.97% (110 of 1,579), a moderate increase from 4.6% (70 of 1,523) in December;
- There was 0 positive case for TGEV RNA in January, 2023 over a total of 3,651 cases tested. It has been 22 months (with a total of 75,544 cases tested) since the last TGEV PCR-positive result;
- The advisory group highlighted lessons learned from the 2021 PDCoV and 2022 PEDV unexpected outbreaks that could help to contain the spread of future outbreaks. Sampling and testing growing animals at placement and marketing periods to identify positive sites help in better addressing biocontainment measures, pig flow, transportation cleaning/disinfection, biosecurity auditing coupled with continuous employee training on biosecurity practices, and monitoring farm warehouse entries were highlighted as potential improvements that could be made to help the swine industry in reducing enteric coronavirus outbreaks.

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

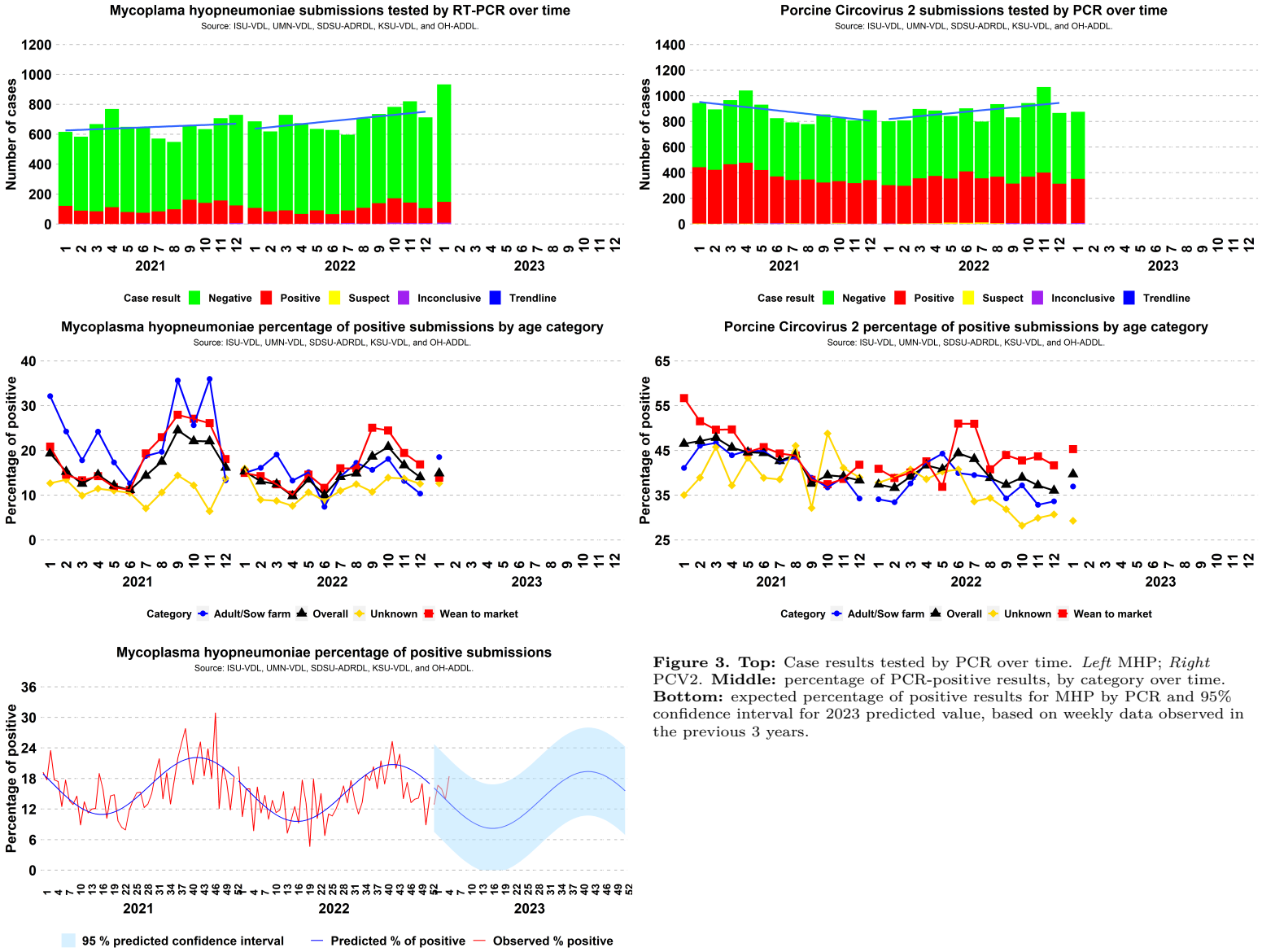
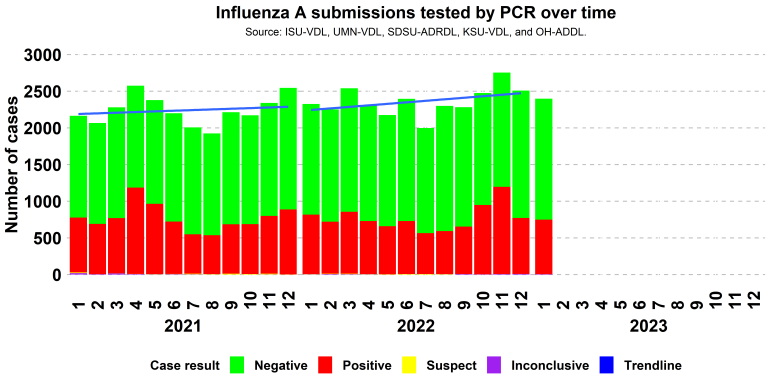


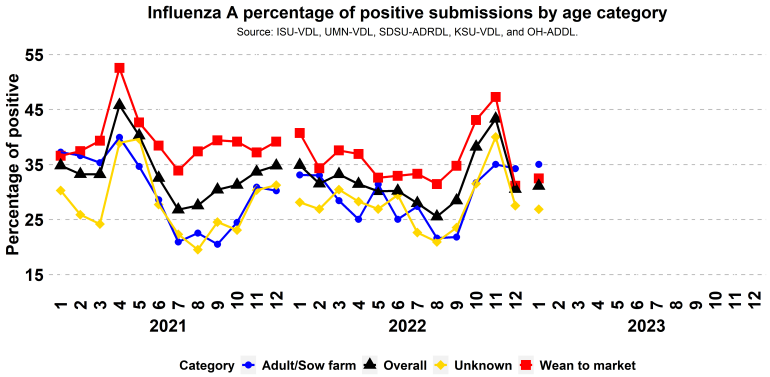
Figure 3. Top: Case results tested by PCR over time. *Left* MHP; *Right* PCV2. **Middle:** percentage of PCR-positive results, by category over time. **Bottom:** expected percentage of positive results for MHP by PCR and 95% confidence interval for 2023 predicted value, based on weekly data observed in the previous 3 years.

SDRS Advisory Group highlights:

- Overall, 14.9% of 933 cases tested *M. hyopneumoniae*-positive cases in January, similar to 14.03% of 713 in December;
- Positivity in the adult/sow category in January was 18.52% (50 of 270), a substantial increase from 10.37% (17 of 164) in December;
- Positivity in the wean-to-market category in January was 13.9% (57 of 410), a moderate decrease from 16.87% (55 of 326) in December;
- Overall MHP-percentage of positive was within state-specific baselines in all 11 monitored states;
- Overall, 39.68% of 867 cases tested PCV2-positive in January, a moderate increase from 36.04% of 863 in December;
- Positivity in the adult/sow category in January was 36.94% (157 of 425),a moderate increase from 33.63% (151 of 449) in December;
- Positivity in the wean-to-market category in January was 45.28% (163 of 360), a moderate increase from 41.67% (125 of 300) in December;
- The levels of *M. hyopneumoniae* detection in Adult/sow farm decreased in 2022 (14.55% of 1,391 sow farms submissions were PCR-positive), being the lowest level since 2011 (19.21% of 406 sow farms submissions were PCR-positive), and the prediction model supports a decrease in the overall detection of *M. hyopneumoniae* in 2023;
- The advisory group highlighted that strategies to eliminate and control *M. hyopneumoniae* in the past years have been successful, contributing to the decreased percentage of positive submissions in sow farms. High stock of negative gilts at the end of the elimination process was highlighted as a key factor in having a successful elimination program.

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





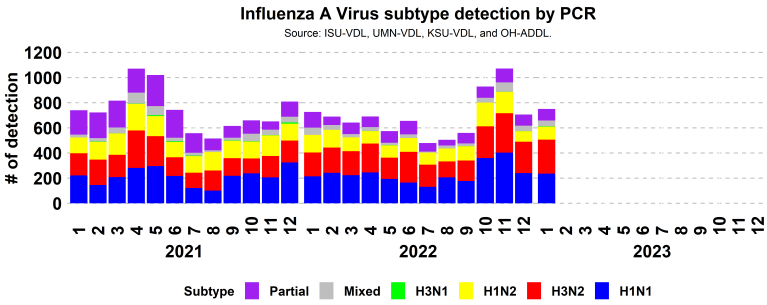


Figure 3. Top: *Left* Results of IAV PCR cases over time. *Right* Percentage of IAV PCR-positive results, by category over time. **Bottom:** Number of IAV subtyping PCR detection over time; (Partial - only hemagglutinin or neuraminidase region detected; Mixed - 3 or more haemagglutinin and neuroamnidase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

SDRS Advisory Group highlights:

- Overall, 31.12% of 2,394 cases tested IAV-positive cases in January, similar to 30.56% of 2,500 in December;
  - Positivity in the adult/sow category in January was 35.04% (157 of 448), similar to 34.27% (171 of 499) in December;
  - Positivity in the wean-to-market category in January was 32.48% (370 of 1,139), similar to 31.15% (343 of 1,101) in December.
- Overall, 6.27% of 750 samples had mixed subtype detection in January, similar to 6.09% of 706 in December;

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

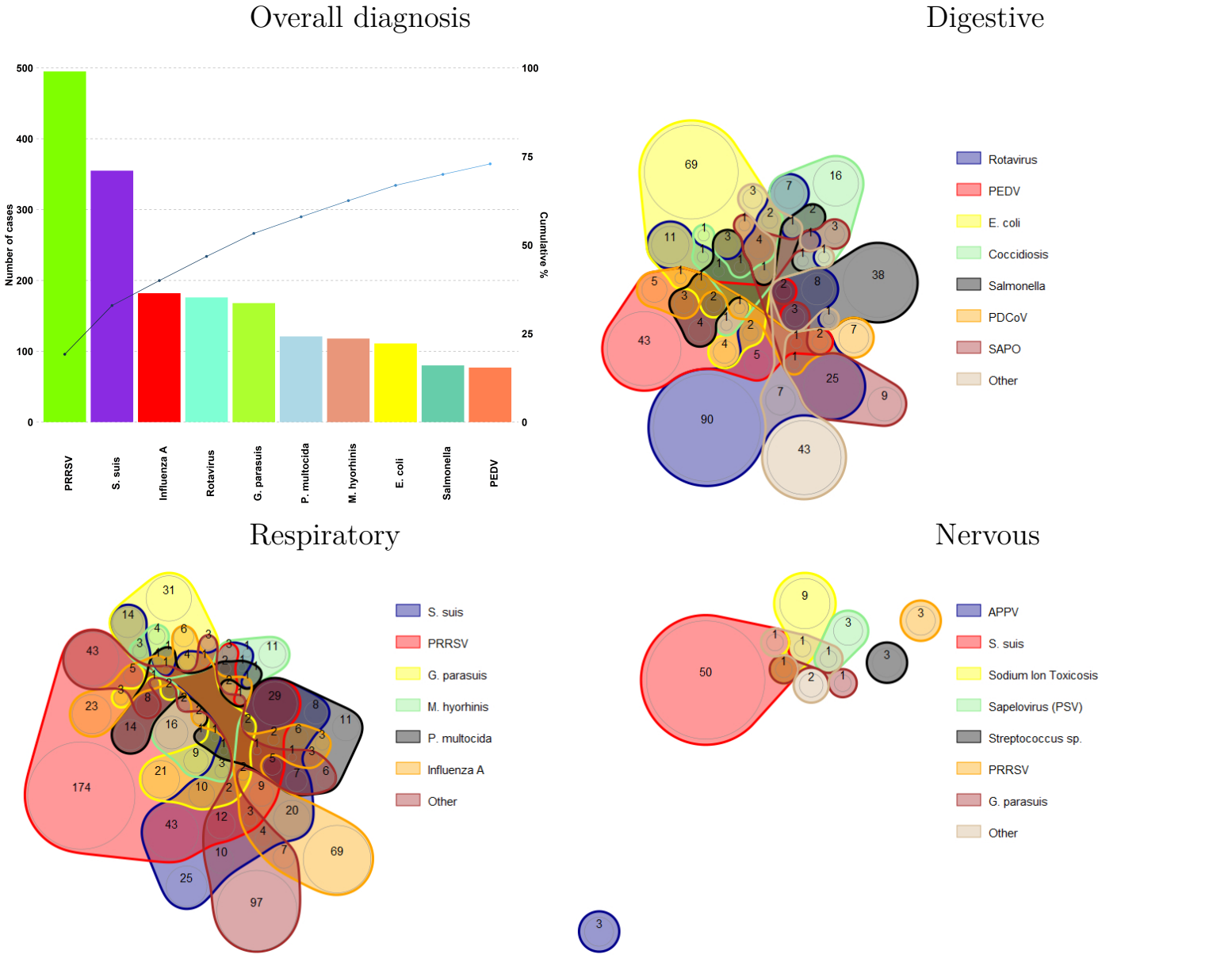


Figure 4. ISU-VDL most frequent overall confirmed tissue disease diagnosis. The presented system is described in the title of the chart. Colors represent one agent; line intersections present diagnosis of 2 or more agents within a submission. Only the most frequent etiology/disease are presented. Less 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 December. 1 to January. 23, 2023.

SDRS Advisory Group highlights:

• PRRSV (495) led cases with confirmed etiology, followed by *S. suis* (355), and Influenza A (182). PRRSV (456 of 1429) led the number of confirmed respiratory diagnoses, Rotavirus (176 of 601) lead the number of confirmed digestive diagnoses, and *S. suis* (52 of 83) led the number of confirmed neurological diagnoses.

• During the weeks of January 6th to 19th, there were spikes in the number of digestive, cardiovascular, and respiratory systems confirmed diagnosis;

• During December 19th to January 16th, there were spikes in the number of PEDV, PDCoV, and PCV2 confirmed diagnosis. Even though there were a restricted number of cases, signals were detected in the number of *A. pleuropneumoniae* (APP) and Mulberry heart disease confirmed diagnosis.

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.*

Risk of pathogen carryover in feed and within the mill environment after mixing and batch sequencing of contaminated feed

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1 - Kansas State University, Manhattan, Kansas, USA.

Introduction

Feed biosecurity practices historically have focused on preventing the feed introduction of bacterial biological hazards, specifically the bacterium Salmonella. Multiple points of entry of biological hazards into a feed mill exist and can include raw ingredients, transport vehicles, and people. With the introduction of porcine epidemic diarrhea virus (PEDV) to the United States, the focus of feed biosecurity advanced to also consider the risk of feed serving as a means by which swine viruses could infect susceptible populations of animals. Much of the research focused on swine feed biosecurity in the mid-2010s focused on PEDV, but recent research has also focused on African swine fever virus (ASFV). While Schumacher et al. (2017) used PEDV, a recent project was conducted that used similar procedures to characterize the spread of ASFV within a feed mill. The objectives of the current study were to: 1) evaluate feed batch sequencing as a mitigation technique for ASFV contamination in a feed mill; 2) determine if a feed sampling method could identify ASFV following experimental inoculation; and 3) evaluate the distribution of ASFV in a feed mill following manufacture of contaminated feed.

Materials and Methods

Batches of feed were manufactured in a BSL-3Ag containment facility at Kansas State University's Biosafety Research Institute in Manhattan, Kansas. First, the pilot feed manufacturing system mixed, conveyed, and discharged an ASFV-free diet. Next, using the same equipment, a diet was manufactured that contained feed inoculated with ASFV reaching a final concentration of 5.6 $\times$ 10^4 TCID50/g. Then, four subsequent ASFV-free batches of feed were manufactured. After discharging each batch into a biohazard tote, 10 feed samples were collected. In addition, environmental swabs from 18 locations within the pilot feed mill were collected after each batch was discharged. Feed and environmental samples were analyzed using a qPCR specific for the ASFV p72 gene.

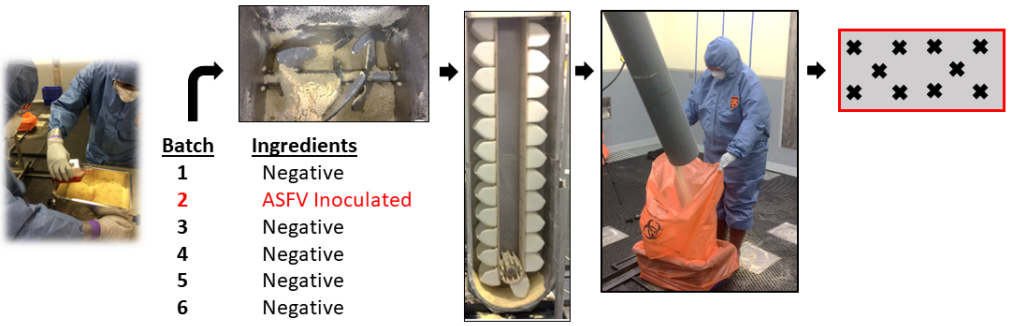

Figure 1. Procedures to mix and batch sequence virus-contaminated feed..

Major findings and implications

1. Swine viruses such as PEDV and ASFV rapidly distribute within feed mills following inoculation under experimental conditions, and decontamination of feed mills is extremely challenging;
2. Sequencing batches of feed decreases concentration of ASFV in feed, but does not eliminate it;
3. Movement of people can significantly contribute to the spread of ASFV in a feed mill environment;
4. ASFV genetic material is incredibly stable in feed or on environmental surfaces over time;
5. The stability of ASFV genetic material can help aid in diagnostic investigations, although infectious characteristics have not yet been evaluated for ASFV-inoculated feed or environmental samples;
6. Important biosecurity principles within the feed supply chain include: preventing entry of the pathogen during ingredient receiving, monitoring and exclusion of foot traffic by high-risk individuals, prevention of cross-contamination, and proactive mitigation using thermal processing or chemical additives.

The full-text reference articles: Schummacher et al., 2017, Elijah et al., 2021, and Elijah et al., 2022