



Swine Disease Reporting System Report # 36 (February 2, 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:

Iowa State University: Giovani Trevisan, Edison Magalhães, Leticia Linhares, Bret Crim, Poonam Dubey, Kent Schwartz, Eric Burrough, Phillip Gauger, Pablo Pineyro, Christopher Siepker; Rodger Main, Daniel Linhares.

Project coordinator Giovani Trevisan. Principal investigator Daniel Linhares.

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

Kansas State University: Rob McGaughey, Eric Herrman, Roman Pogranichniy, Rachel Palinski, Jamie Henningson.

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

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 report: Benchmarks patterns of PRRSV RFLP pattern detected at the ISU-VDL 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: Clayton Johnson, Mark Schwartz, Paul Sundberg, Paul Yeske, Rebecca Robbins, Tara Donovan, Deborah Murray, Scott Dee, Melissa Hensch, Brigitte Mason, Randy Jones.

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, 2021.

Swine Disease Reporting System:

Domestic Swine Disease Surveillance



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Top: *left*: Results of PRRSV RT-PCR cases over time. $\mathit{Right:}\ \mathsf{Proportion}\ \mathsf{of}\ \mathsf{accession}\ \mathsf{ID}\ \mathsf{cases}\ \mathsf{tested}\ \mathsf{for}\ \mathsf{PRRSV}\ \mathsf{by}\ \mathsf{age}$ Figure 1. group 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 the 25 most frequently detected RFLP patterns left year of 2020; right year of 2021

SDRS Advisory Group highlights:

• Overall, 28.24% of 6,083 cases tested PRRSV-positive in January, a moderate decrease from 30.52% of 7,262 in December;

• Positivity in adult/sow category in January was 27.62% (770 of 2,788), similar to 27.79% (924 of 3,325) in December;

• Positivity in wean-to-market category in January was 39.23% (687 of 1,751), a substantial decrease from 46.03% (933 of 2,027) in December;

• Overall PRRSV-percentage of positive cases was within 3 standard deviations from state-specific baselines in all 11 monitored states;

• There were several reports of clinical outbreaks in all age groups associated with PRRSV belonging to RFLP 1-4-4 or Lineage 1C, particularly in the Midwest region. Colder weather and environmental condition may have favored the regional spread of this strain. Limited herd immunity to this particular strain may have contributed to the magnitude of the outbreak.

Swine Disease Reporting System:

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Percent Positive

24

Percent Positive

2500





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

Predicted % of positive

95 % predicted confidence interval

SDRS Advisory Group highlights:

• Overall, 11.19% of 3,386 cases tested PEDV-positive in January, similar to 10.15% of 3,587 in December;

• Positivity in adult/sow category in January was 9.01% (96 of 1,065), similar to 10.19% (115 of 1,129) in December;

• Positivity in wean-to-market category in January was 18.09% (229 of 1,266), a moderate increase from 15.87% (208 of 1,311) in December;

• Overall PEDV-percentage of positive cases was within 3 standard deviations from state-specific baselines in all 11 monitored states:

- Overall, 6.39% of 3,193 cases tested PDCoV-positive in January, a moderate increase from 4.03% of 3,399 in December;
 - The overall PPDCoV detection was outside of the upper boundaries of the forecasted levels between January 18 to 30;
 - Positivity in adult/sow category in January was 7.42% (73 of 984), a moderate increase from 3.51% (37 of 1,055) in December;
 - Positivity in wean-to-market category in January was 7.67% (91 of 1,187), similar to 6.16% (75 of 1,218) in December;
 - Overall PDCoV-percentage of positive cases was 3 standard deviations from state-specific baselines in OK and KS;

• There was 1 positive case for TGEV RNA in January, 2021 over a total of 3,136 cases tested. Sample was identified as been collected in the state of MN;

• The advisory group pointed out that the increase in PDCoV detection is likely to be related to resources and regional connections that may have facilitated the agent's spread across farms. Additional reminding was that as PDCoV is not as clinically significant as PEDV, so it is possible that PDCoV increased infection went subclinical in farms across other regions.

Observed % positive

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Figure 3. Left top: results of 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, 19.9% of 573 cases tested *M. hyopneumoniae*-positive cases in January, a moderate decrease from 22.46% of 748 in December;

• As expected the observed overall detection of *M. hyopneumoniae*-positive cases is following the forecasted expected decrease in the levels of detection for this time of the year.

Swine Disease Reporting System: Disease Diagnosis Reports



Topic 4 – Disease diagnosis at the ISU-VDL.



Figure 4. Most frequent disease diagnosis by physiologic system at ISU-VDL . Presented system is described in the title of the chart. Colors represent one agent and/or the combination of 2 or more agents. Only the physiologic systems with historic number of cases per season above 100 are presented in the report.

Note: Disease diagnosis takes one to two weeks to be performed. The graphs and analysis contain data from December 1, 2020 to January 17,2021.

SDRS Advisory Group highlights:

• PRRSV (194 of 1114) continues to lead the number of respiratory diagnoses. Rotavirus (147 of 525) continues to lead the number of digestive diagnoses. *Streptococcus suis* (43 of 93) continues to lead the number of neurological diagnosis;

• For the week of January 11, there was a significant disease diagnosis increase (signal) for cases classified as integument.

Swine Disease Reporting System Bonus Page



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Diagnostic

Laboratory

In the SDRS report 35, the SDRS Advisory Group brought to attention the re-emergence of a PRRSV strain classified as RFLP 1-4-4 in the Minessota (MN) and Iowa (IA) region with reports of detection of this strain in other states. PRRSV open read frame-5 (ORF5) sequences shared with the SDRS project by the **ISU and UMN-VDL** were used to conduct a cluster analysis to characterize and visualize genetic variability over time and across states. After removing sequences classified as a vaccine-like (n=100), ORF5 sequences from 2017 (n=417), 2018 (n=563), 2019 (n=481), and 2020 (n=656) were retained. Only states having more than 10 ORF5 sequences were retained for cluster analysis over states. As expected and over time, a genetic evolution for PRRSV classified as RFLP 1-4-4 was observed from 2017-2019. A considerable change was detected in 2020 forming a distinct cluster from the previous years (Fig. 1). Across states, large genetic variability was identified. Very distinct clusters like the one for North Carolina (n=138) and another for Oklahoma (n=94) were revealed. Additional clustering were revealed for Missouri (n=42); Ohio (n=27) and Indiana(n=75); Kansas (n=17); Texas (n=58); and another cluster for IA (n=523), Illinois(n=235), Michigan (n=13), Nebraska (n=123), and MN (n=546) (Fig. 1).



Figure 1. Discriminant analysis of principal components (DAPC) for restriction fragment length polymorphism (RFLP) 1-4-4 for the years 2017-2020 (*right*) and across states (*left*). Groups are shown by different colors and inertia ellipses, while each dot represents an individual porcine reproductive and respiratory syndrome virus (PRRSV) open read frame-5 (ORF5) sequence.

Pairwise comparison over time within the state of MN and IA were additionally conducted. A pairwise distance decrease from 2.22% in 2019 (n=96) to 1.05% in 2020 (n=211) was revealed for sequences recovered from MN (Fig. 2). In sum, there is supportive evidence to demonstrate that PRRSV strains classified as RFLP 1-4-4 kept evolving over time. Considerable change occurred in 2020, forming a very distinct cluster. Large variability was encountered across states, and ORF5 sequences recovered from geospatial related states shared more similarity. The number of recovered ORF5 sequences classified as RFLP 1-4-4 in MN more than doubled in 2020 compared with 2019. A substantial decrease in pairwise distances was contributed by the detection of close genetic related sequences. The encountered results support the field observation of more detection of a PRRSV RFLP 1-4-4 strain in MN. Connections between farms like transportation routes (semen, feed, hauling), animal placement, or weather conditions may help to spread this strain to other production areas. As a reminder, biocontainment and bioseurity practices can be helful to reduce the spread of this and other agents across farms.



Figure 2. Pairwise distances within PRRSV strains classified as RFLP 1-4-4 over time for sampels collected in the state of Minnesota

Highlights:

- PRRSV strains classified as RFLp 1-4-4 still evolve over time with a distinct cluster being identified in 2020;
- Across states there are considerable genetic diversity for the 1-4-4's;
- More similar 1-4-4's have been detected in Minnesota during 2020.

Note: Contact the SDRS project if you would like to share your work on the bonus page.

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