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Measuring the effect of disease diagnostic information on the mortality of growing pigs raised under field conditions

Edison S. Magalhães[1]; Pete Thomas[2];Giovani Trevisan[1]; Derald J. Holtkamp[1]; Christopher J. Rademacher[1]; Jeffrey Zimmerman[1]; Kent J. Schwartz[1]; Eric R. Burrough[1]; Daniel C. L. Linhares[1]

[1]Department of Veterinary Diagnostic and Production Animal Medicine, Iowa State University, Ames, Iowa.
[2]Iowa Select Farms., Iowa Falls, Iowa.

Statement of the problem

The increasing implementation of technologies in the swine industry produces a diverse and disperse availability of data streams within production systems (e.g., productivity, health, environment, diagnostic, logistic, and infrastructure). In the absence of connected data streams, producers will likely remain unable to tailor swine health and production management to specific swine populations/pig flows. Likewise, it will remain challenging to measure the effect of different risk factors associated with performance under specific production system's field conditions.

One example of these data streams available within swine production systems is diagnostic from tissues submitted to the veterinary diagnostic laboratories (VDL's). Due to ongoing infectious disease challenges, veterinarians use veterinary diagnostic data to support strategies to manage and prevent disease. The collection and submission of tissues to VDL`s is a common practice among veterinarians in the swine industry, providing crucial information in terms of the pathogens diagnosed and location/severity of lesions affecting the animals. Even though this data is frequently utilized immediately after the final diagnostic report provided by the diagnosticians, it becomes, for most of the times, stored and unutilized in databases without further application, creating a valuable historical database of pathogens occurring over time in the system. Thus, the aggregation of all retrospective diagnostic results that occurred throughout the lifetime of each closeouts of growing pigs (cohort) represent a potential important data stream for analysis to measure the association between disease occurrence and the growth performance, here measured by wean-to-finish mortality (W2F). The integration of disease diagnosis information with the other aforementioned data streams, such as the retrospective performance of the sow farms originating each growing group, can assist field veterinarians to make data-driven solutions on how to improve swine herd performance. Oliveira et al. (2009) and Larriestra et al. (2005) reported the importance of collective analysis of multiple characteristic associated with wean-to-finish (W2F) production.

Objectives

The objective of this study was to develop algorithms to aggregate and merge multiple data streams from a Midwestern production system (Iowa Select Farms), and to measure the association of disease diagnostic information on wean to finish (W2F) mortality, by analyzing the final data base, and the interactions occurring between key parameters from the sow farm along with the disease diagnosed through the growing phase. De Grau et al. (2005) and Alvarez et al. (2015) stated the impact that sow farm productivity and health have on the downstream performance of weaned cohorts.

Brief Materials and Methods Including Statistical Analysis

Disease diagnostic codes (DxCode) are assigned by diagnosticians to each tissue case received at the Iowa State University Veterinary Diagnostic Laboratory (ISU-VDL), based on submission information, laboratory assays, and compatible macroscopic and/or microscopic lesions. SAS scripts were built to match and merge DxCode data to productivity parameters and PRRS status data from breed-to-market, for all Iowa Select Farms (ISF) cohorts of growing pigs marketed from January 2018 to June 2019. The dataset included nursery, single stock W2F, and double stock W2F flows, as well as cohorts originated from single or multiple sow farms. The SAS scripts aggregated and merged productivity, sow farm PRRS status at weaning, and DxCode data into a single consolidated dataset, informing the pathogen(s) diagnosed throughout the growing phase of production for each cohort marketed. Furthermore, statistical analysis was conducted to: compare the mean W2F mortality for cohorts with DxCode allotted during the growing phase relative to those without DxCode allotted; compare the average age of the growing groups when tissue samples were submitted to the VDL and their respective W2F mortality, classifying age as early (first 21 days post-weaning), mid (22-69 days post-weaning), or late age of diagnosis (70+ days post-weaning); analyze the frequency of tissues submitted to the VDL, within the same cohort throughout the growing phase, classified as either "single" or "multiple" submissions; analyze the diversity of pathogens identified in each event of tissue submission, classifying as "single etiology" or "multiple etiology"; compare the mean W2F mortality of cohorts with DxCode assigned for PRRSV across the three aforementioned age groups; analyze cohorts with DxCode for PRRSV and their retrospective PRRS status at weaning (PRRSV-negative, endemic, or epidemic); analyze the interaction between cohorts with PRRS DxCode assigned and their retrospective sow farm pre-weaning mortality (PWM), described here in quartiles averages; compare the mortality difference among cohorts in 4 different categories of DxCode (PRRSV-negative and Influenza A virus (IAV)-negative, PRRSV-negative and IAV-positive, PRRSV-positive and IAV-negative, and cohorts with DxCode positive for both PRRS and IAV).

Significant Results

Our group developed automated algorithms for Iowa Select Farms (ISF) to integrate multiple available data streams (productivity, structural and management information, pig flow, and health status) with also the diagnostic codes data stream (disease diagnosis data from tissue(s) submitted to the ISU VDL). This study demonstrated the capability to capture and merge multiple longitudinal data streams from *breeding to weaning to marketing*, revealing the impact of disease diagnosed on growing groups along with other whole-herd drivers of wean-to-finish (W2F) mortality.

The algorithms were able to combine productivity, health information, and DxCode data into a single dataset, containing 1,742 closeouts marketed from January 2018 to June 2019. Of those, 434 closeouts (24.91%) had at least one DxCode assigned during the whole growing phase. The W2F percent mortality difference between closeouts groups with one or more DxCode allotted compared to no DxCode allotted was 2.22 (10.4%[a] vs. 8.18%[b]) (Figure 1). We conducted the following analyses within only the 434 closeouts with DxCode assigned: the mean W2F mortality of the closeouts classified as early stage, mid stage, and late stage of diagnosis was 11.5%[a], 10.1%[b], and 9.27%[b], respectively (Figure 2); for "single frequency" and "multiple frequency", the mean W2F mortality of the groups was 10.2%[a] and 11.4%[a], respectively (Figure 3); when comparing "single agent" and "multiple agent", the mean W2F mortality was 9.71%[a] and 11.2%[b] respectively (Figure 4); when comparing the age of groups assigned with DxCode for porcine reproductive and respiratory syndrome (PRRS) specifically, the observed W2F mortality for early detection, mid detection, and late detection closeouts were 14.7%[a], 11.4%[b], and 10.2%[b], respectively (Figure 5); when comparing the retrospective PRRS status in the sow farm when the cohorts were weaned, and the groups assigned with DxCode for porcine reproductive and respiratory syndrome (PRRS) specifically, the observed W2F mortality for groups with PRRS diagnosed throughout the growing phase and PRRS status negative, endemic, and epidemic were 12.4%[a], 11.4%[a], and 12.9%[a], respectively (Figure 6); when comparing the retrospective average pre-weaning mortality in the sow farm of the cohorts marketed, and the groups assigned with DxCode for porcine reproductive and respiratory syndrome (PRRS) specifically, the observed W2F mortality for groups with PRRS diagnosed throughout the growing phase and the pre-weaning mortality quartile average of 10.6%, 13.0%, 14.6%, and 17.3, were 10.9%[a], 11.7%[ab], 11.8%[ab], and 13.5%[b], respectively (Figure 7); the mean W2F mortality difference between groups assigned with influenza A virus (IAV), or groups assigned with a combination of IAV and PRRS was 3.16% (9.14%[a] vs. 12.3%[b]) (Figure 8).

Figure 1: W2F Mortality of groups with DxCode assigned compared to groups without any DxCode.

Closeouts with DxCodes assigned had ↑ W2F mortality

- 10.4%[a] (DxCode)
- 8.18%[b] (No DxCode)

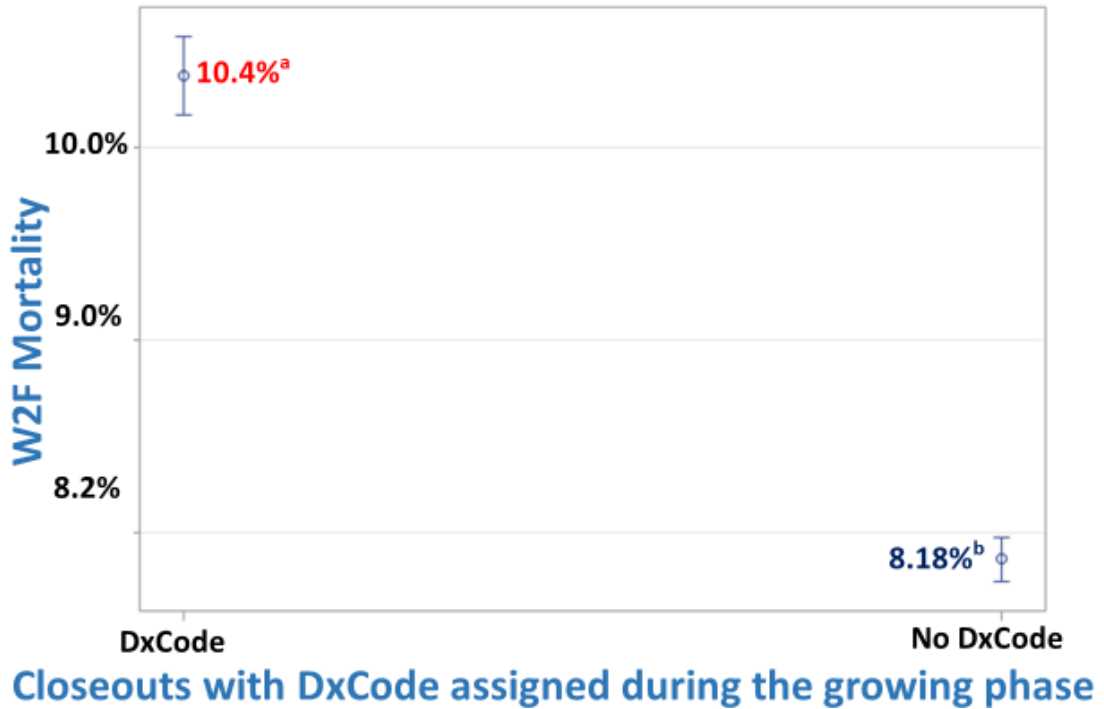**Closeouts with DxCode assigned during the growing phase**

Figure 2: W2F Mortality of groups with DxCode assigned by age when the tissue was submitted.

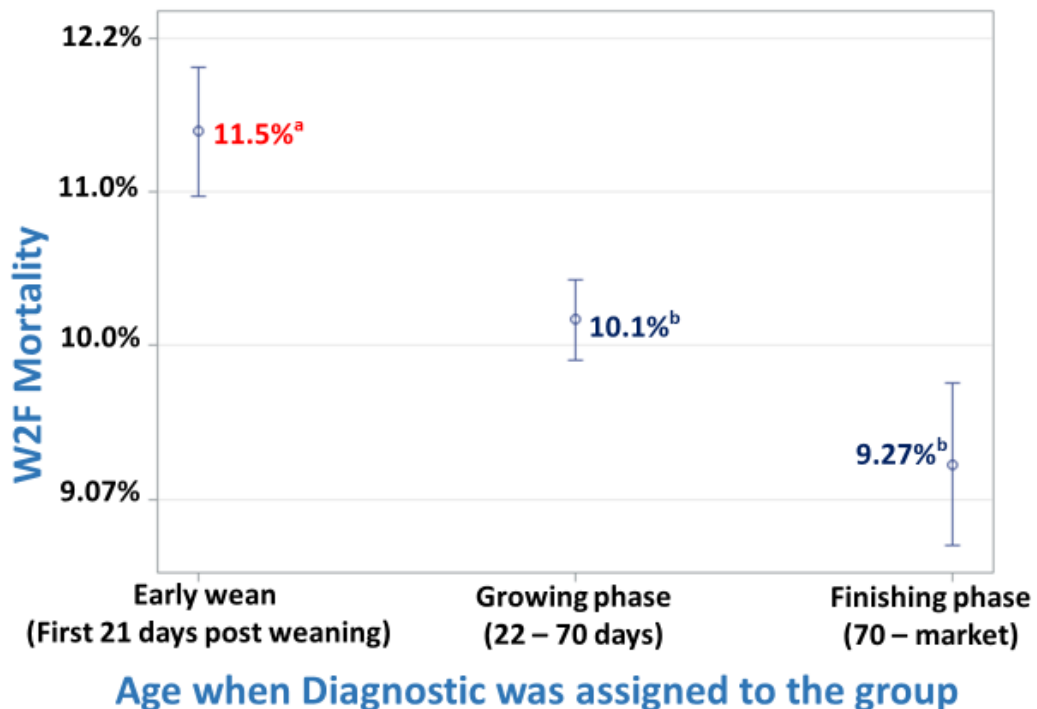**DxCodes submitted early in the nursery - ↑ W2F mortality**

- 11.5%[a] (Early wean — First 21 days post weaning)
- 10.1%[b] (Growing phase — 22 – 70 days)
- 9.27%[b] (Finishing phase — 70 – market)

Age when Diagnostic was assigned to the group

Figure 3: W2F Mortality of groups with DxCode assigned by the number of submissions.

No statistical difference between single and multiple DxCodes
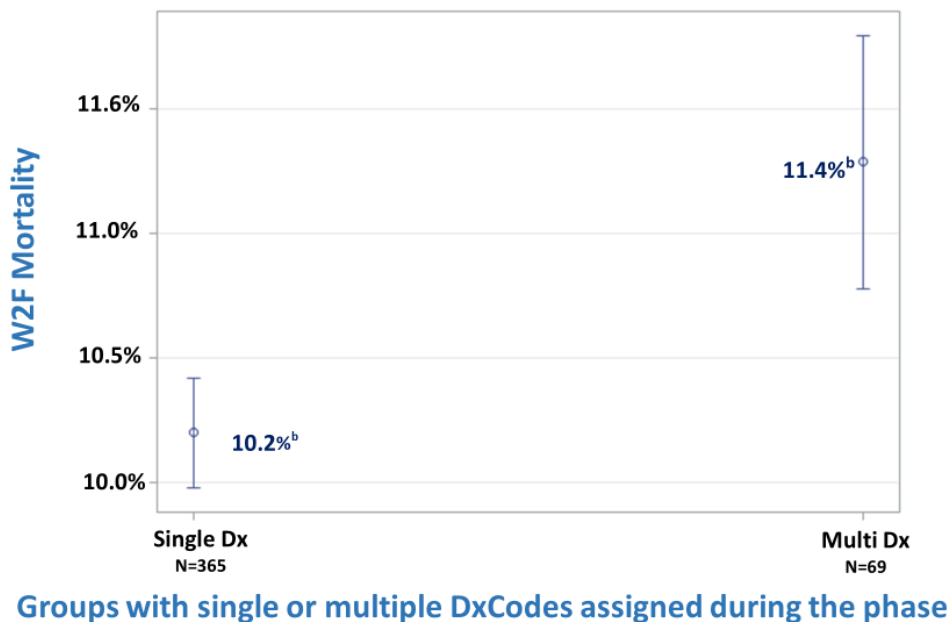
Figure 4: W2F Mortality of groups with DxCode assigned by the number of pathogens diagnosed.

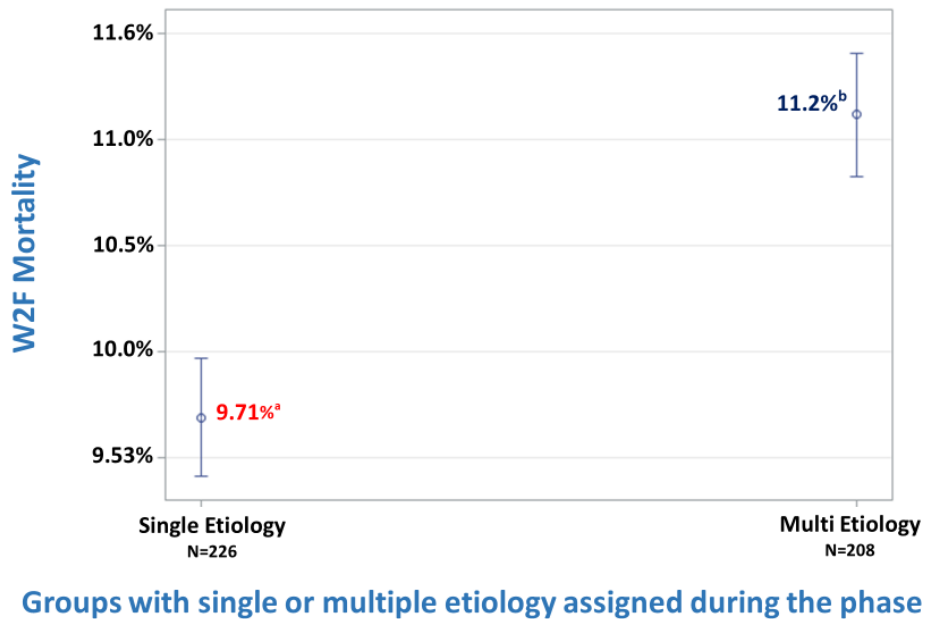## Groups with multiple etiologies had higher W2F mortality

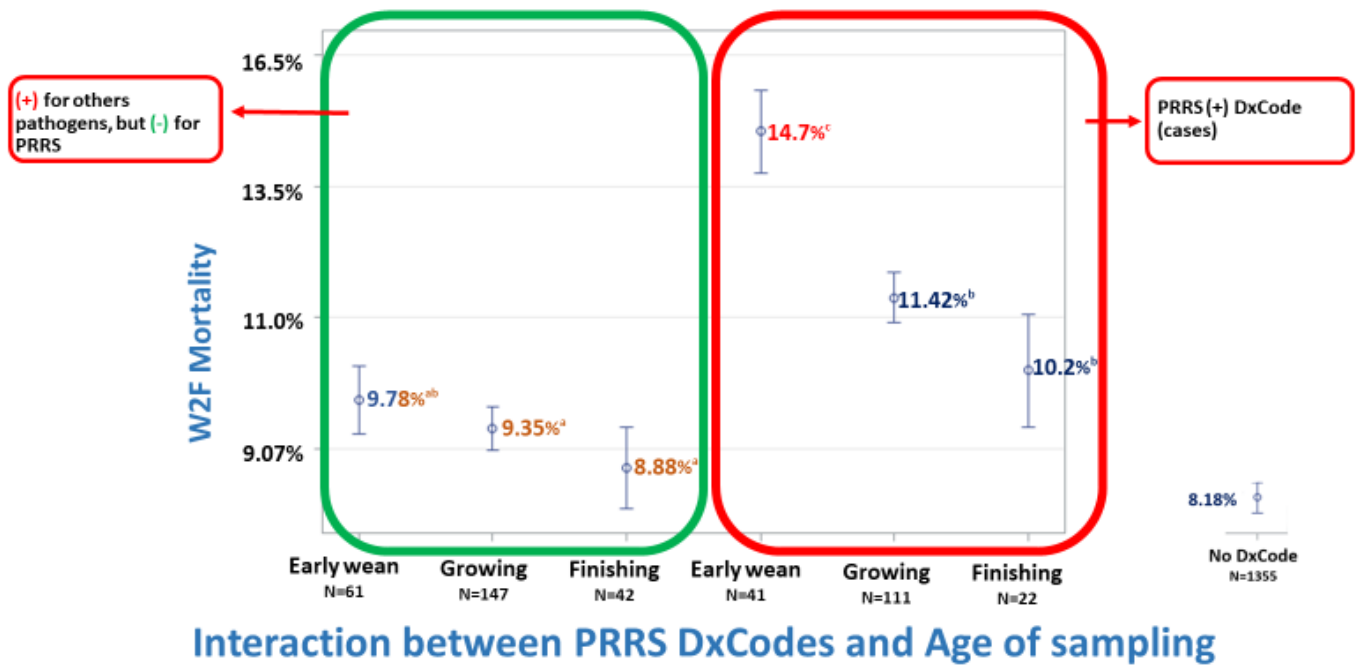Figure 5: W2F Mortality of groups with PRRS positive or negative DxCode assigned by age.

Figure 6: W2F Mortality of groups with PRRS positive or negative DxCode assigned and the previous sow farm PRRS status at weaning.
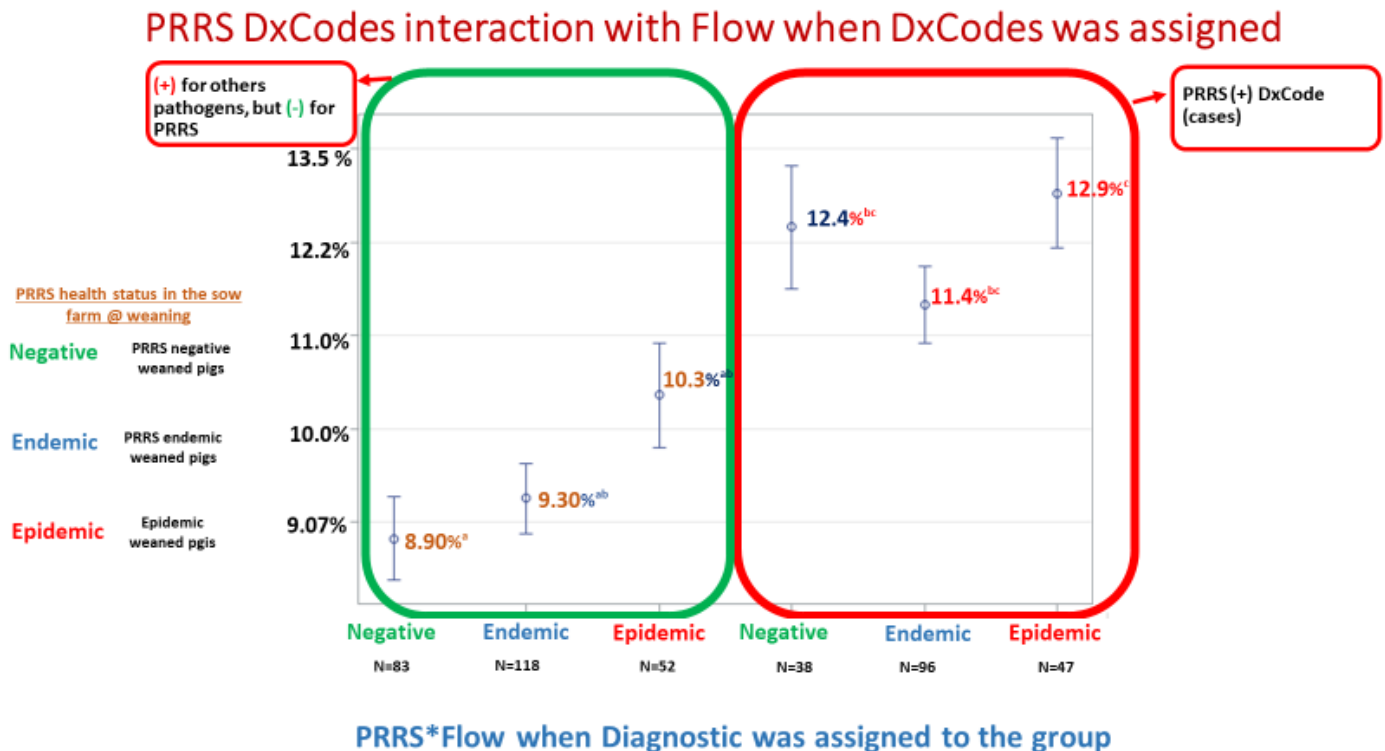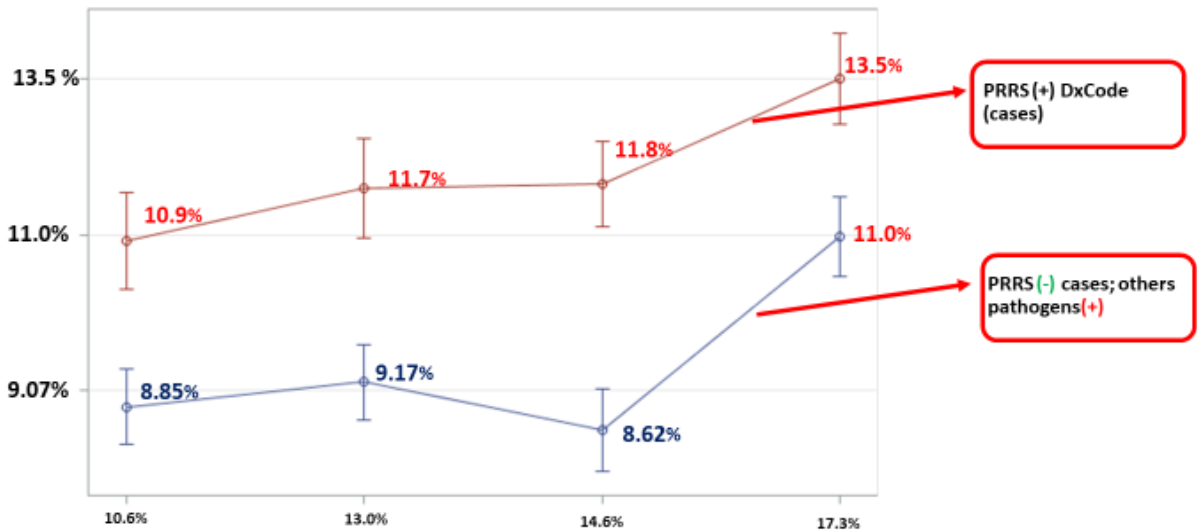
Figure 7: W2F Mortality of groups with PRRS positive or negative DxCode assigned by previous pre-weaning mortality of their progenies in the sow farm.
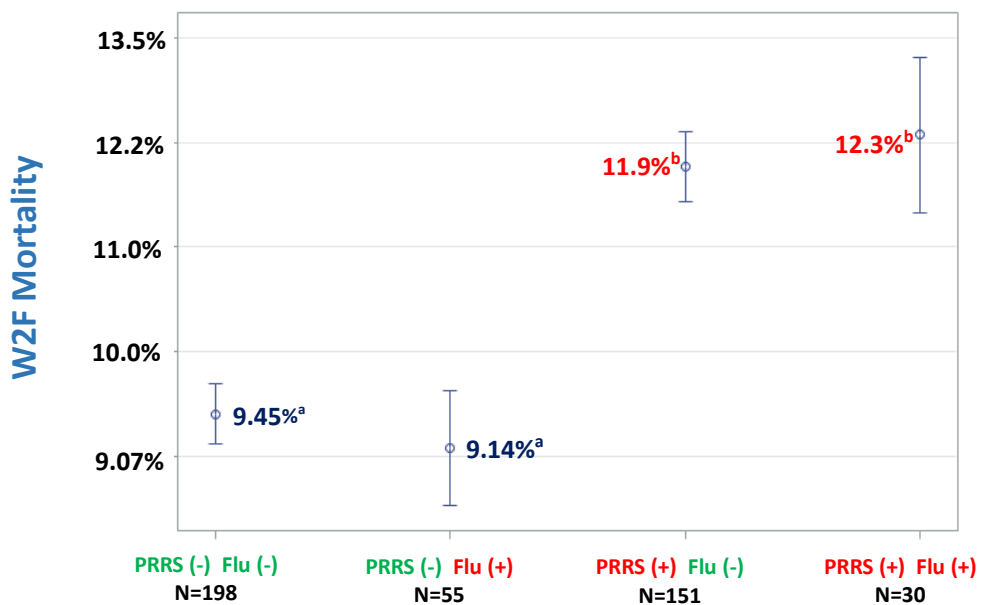

Figure 7: W2F Mortality of groups with PRRS positive or negative DxCode assigned and Influenza positive or negative DxCode.

After accomplishing the objectives of this proposal, we established a partnership with another production system - The Hanor Company – which provided all the aforementioned data streams through a cloud-based database, enabling automation of the process of importing the data periodically from the cloud on a real-time basis. We constructed a similar data integration and analysis model previously built for Iowa Select Farms, now for this new system, but with the capability of running the algorithms at the desired frequency (daily, weekly, or monthly), building a retrospective data management & analysis model that is fully automated from end-to-end. Results from the analysis with the new system also demonstrated the same trend observed with the previous one. Furthermore, we added a new data stream provided by the ISU-VDL through API`s, that included all Polymerase Chain Reaction (PCR) results for PRRSV in this production system, from 2018 to 2021. Thus, we could analyze the impact of sow farm performance with the detection of positive PCR`s for PRRS in the growing phase, and the results from tissues submitted to the VDL.

Discussion of how results can be applied by practitioners

This study demonstrated the importance of analyzing diagnostic data combined with other data streams. The cohorts with PRRSV DxCode were highly associated with increased W2F mortality. The W2F mortality of weaned groups with negative and epidemic status for PRRSV at weaning was similar when PRRS was diagnosed throughout the growing phase. Furthermore, cohorts originating from sow farms with high PWM (17.3%) had the worst W2F mortality. Co-infections were a common finding and were associated with higher W2F mortality than groups with single etiologies or no etiology. Timing of DxCode assignment was also important, i.e., earlier diagnosis was associated with higher W2F mortality. The present study focused on PRRSV positive DxCode due to high availability of information for this pathogen, concentrating on its interaction with and IAV, and other sow farm risk factors. Findings validated that the breeding herd health status is a good predictor of W2F health (Larriestra et al., 2006).

Take home message and what have we learned with this approach:

The main take home from this work is that swine production systems should utilize their internal retrospective data, in different approaches such as the one demonstrated in this study, to solve day-to-day issues and also support data-driven decisions. It is also important that they automate this process.

Results dissemination:

We will make this report available to share with the AASV members through newsletter and/or uploading to the AASV swine library. The preliminary results were published at the 2020 Leman conference, and the part of the final results at the 2021 AASV annual meeting. We will also work on a manuscript to be submitted to a peer reviewed journal, making the work available to the scientific community.

References

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