

## SWINE HEALTH

**Project:** Swine Disease Management Information Program # 20-109 IPPA  
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### Scientific Abstract:

This study combined epidemiological tools and concepts to structure and compare aspects and practices implemented in breeding herds following disease outbreaks. This project used porcine reproductive and respiratory syndrome-PRRS as a model and enrolled breeding herds that: (a) reported a PRRS outbreak and worked on a plan to control or eliminate the infection; (b) producers shared diagnostic results continuously; (c) herd veterinarian completed a short survey with information about the PRRS management plan and intervention practices for the outbreak; (d) shared weekly production data for 26 weeks prior to the outbreak, and until the herd achieved baseline production after the outbreak; (e) monitored the affected herd by sampling over time, with either weekly processing fluids or monthly suckling pig bleeding (n=30). Collected data under this integrative approach have allowed the implementation of the project in a standardized and sustainable fashion that can continuously receive and process data. This project was named PRRS Outbreak and Management Practices-POMP and can be expanded to incorporate other diseases beyond PRRS. The major finding was that large diversity of practices exists across the U.S. swine industry to control and eliminate PRRSV following an outbreak. An online platform with the results collected from the POMP enrollment survey having slice and filtering capabilities was created and publicly available at <https://www.fieldepi.org/POMP> for additional exploring. Overall the median time to low prevalence (TTLP) (25<sup>th</sup>-75<sup>th</sup> percentile) was 35 (29 - 49) weeks. This number is nine weeks longer than a previous study conducted by [Linhares et al.](#) about ten years ago. Reasons for the longer TTLP may include different viral populations (i.e., PRRSV evolving to gain persistence at the population level), a more sensitive sampling scheme (processing fluids outperform the herd sensitivity of serum-based monitoring), or a change in

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management practices including herd closure-associated practices, immunization practices, and bio-management activities. These farms were also monitored for time-to-baseline-productivity (TTBP), defined as the number of weeks it took for farms to recover the same quantity of piglets weaned per week that the farm had prior to the PRRSV outbreak. The median and 25<sup>th</sup>-75<sup>th</sup> percentiles were 22 (16 - 26), which is also six weeks longer than that observed with a cohort of 60 herds monitored ten years ago. Finally, the total loss (median, confidence interval) measured as the number of pigs per 1,000 sows weaned below the average before the outbreak was 4,092 (2,326 - 4,755). This represents an increased loss of 1,303 piglets per 1,000 sows than the observed ten years ago. The longer TTBP and higher total losses indicate opportunities for additional investigation on risk factors, including method of exposure, virus characteristics, and disease control-associated practices, including herd closure and internal biosecurity

Funds from this proposal were leveraged with an NPB-funded project # 19-178 (upon approval of both entities); those were used to explore next-generation sequencing and its feasibility to identify multiple PRRSV strains circulating in breeding herds and its association with key production parameters indicators. In summary, the recovery of PRRSV sequences by applying NGS in processing fluid samples provided scientific evidence supporting the detection of at least two wild-type PRRSV strains in a breeding herd (18 of 20) and recombination events (11 of 17). The presence of higher genetic variability in a breeding herd, i.e.,  $\geq 3$  strains, was associated with a 12-week increase in the median time to low prevalence when compared with herds that had  $\leq 2$  strains detected. The presence of  $\geq 3$  strains and recombination events were associated with increased total piglet losses of approximately 1,800 piglets per 1,000 sows. Also, resources of this proposal were used to fully sequence, characterize, and share information about the L1C variant strain. The novel way to visualize NGS outcomes provided better insights into the PRRSV dynamics and genetic variability in breeding herds. Please visit NPB # 19-178 grant final report delivered in November 2021 for more details.