

Title: "Assessing within-herd PRRS variability and its impact on production parameters",
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Scientific Abstract:

Porcine reproductive and respiratory syndrome virus (PRRSV) is one of the major health and economic concerns in the swine industry worldwide. Even though molecular diagnostic tools for PRRSV detection and classification have improved dramatically over the past years, the fact that this virus mutates rapidly combined with testing costs makes it difficult to understand and track PRRSV diversity in pig farms. The lack of understanding of PRRSV variability in swine herds in turn complicates outbreak investigations and prevention strategies in the field.

The objective of this study was to describe the genetic variability of PRRSV in swine farms with different production types (breeding and growing pig herds) and PRRS infection statuses (new outbreaks, vaccinated farms, "natural" PRRSV exposure). Five US swine herds (three farrow-wean herds namely Farms 1, 2 and 3, and two growing pig herds namely Farms 4 and 5) were enrolled in this project and followed up for 6 months to one year. Processing fluids, oral fluids and tonsil scrapings were sampled approximately once per month.

The study results suggested that PRRSV was more likely to be detected in processing fluids compared to tonsil scrapings (odds ratio (OR) = 3.86) in breeding farms; whereas oral fluids were outperformed by tonsil scrapings (OR = 0.26) in growing pig farms.

In addition, ORF5 sequencing in PF, OF, and TS samples validated the simultaneous detection and temporal dynamic of PRRSV lineages. Phylogenetic analyses on the PRRSV ORF5 gene in processing fluids identified the presence of multiple PRRSV (genetic identity > 98%) classified into different lineages in two breeding farms within and between sampling events. Both field lineages and modified live vaccine lineages (lineage L5) were observed in oral fluid and tonsil scraping samples for both growing herds.

This study showed moderate correlations between PRRSV detections and reproductive performance in breeding herds. PRRSV detection was indicative of a temporary surge in stillborn and mummified piglets in Farm 2 and 3 of the farrow-wean farms ((PF: $\rho = 0.86$, $p = 0.003$; TS: $\rho = 0.89$; $p = 0.001$) and mummified fetuses (PF: $\rho = 0.92$, $p < 0.001$; TS: $\rho = 0.92$; $p < 0.001$) and (stillborn: $\rho = -0.82$, $p = 0.002$; mummified: $\rho = 0.63$, $p = 0.04$) as well as higher pre-weaning mortality in Farm 3 ($\rho = -0.65$, $p = 0.03$).

Additional research is needed to attempt whole genome sequencing, which was not successful in the current study with the sample types collected herein.

These research results were submitted in fulfillment of checkoff-funded research projects. This report is published directly as submitted by the project's principal investigator. This report has not been peer-reviewed.

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