

Project Invitation: Assessing within-herd PRRS variability and its impact on production parameters

Arruda, A.G. and collaborators from UMN (Kumar, Schroeder, Vilalta), OSU (Pairis-Garcia), and NCSU (Almond, Ferreira)

We know that PRRS virus mutates and evolves quickly. We know there can be co-circulation of PRRS variants in a herd, and even within a single animal. We don't know whether that can impact health and production. We don't know how that affects the way we are currently sampling and assessing virus similarity within herds over time.

Project main goal:

This project aims to examine within-herd PRRSV variability over time for sow and growing pig sites under different PRRS immunity strategies (vaccinated, negative and positive herds), and investigate the association between within-herd PRRS variability and health and production parameters of interest to swine producers. We partnered up collaborators with a wide range of expertise to use whole genome sequencing (WGS) to provide insights on the likelihood of PRRS outbreaks

Objective 1: Describe PRRSV quasispecies within farms using a sample of farms of different demographic types and PRRS management strategies over a one-year time span; and investigate whether PRRSV variability has an impact on health and production outcomes.

Objective 2: Investigate and compare the use of WGS and different ORFs to determine the best predictor to identify and relate viruses within swine herds

Objective 3: Correlate PRRSV variants with production and disease metrics being due to "normal" within-herd virus evolution, vs. new PRRS introductions. And we will also look into the effect of PRRSV variants in production

Request:

We are looking to enroll 6 farms for this project, that has a duration of 1 year:

3 breeding herds (farrow-wean):

- 1 "naïve" herd (no PRRS for at least last 2 years) that just had an outbreak (farm will be enrolled as a new outbreak happens)
- 1 "vaccinated" herd (a herd that had a PRRS outbreak and has been vaccinated since then at least twice a year with a MLV)
- 1 "naturally exposed" herd (a herd that had an outbreak in the past year but is no longer exposing or vaccinating animals [herd will be still eligible if gilts are exposed off site and brought in after testing negative])

3 growing pig herds (finisher or wean-finish):

- 1 "naïve" herd (no PRRS for at least last 2 years) that just had an outbreak (farm will be enrolled as a new outbreak happens)
- 1 "vaccinated" herd (a herd that vaccinates each batch of animals using a MLV)
- 1 "positive" herd (a herd that had an outbreak in the past and is regularly exposed to live virus or a herd that is receiving known positive pigs from a positive source)

We would work with your veterinarian and your team to coordinate the submission of ~16 samples total in a monthly basis for 1 year (12 samplings). These samples will include a combination of processing fluids, oral fluids, and tonsil scrapings. All samples will be sent to the University of Minnesota monthly. Diagnostics is paid. Also, sharing production data will be a requirement.

Find more MSHMP science pages at: <https://z.umn.edu/SciencePages>

12/28/2018

