How many PRRSV variants can we find in a swine farm in a sampling event?

Cheng T[1], Campler M[1], Ferreira J[2], Schroeder D[3], Yang M[3], Mor S[3], Arruda A[1].
[1]The Ohio State University. [2]North Carolina State University. [3]University of Minnesota

Why did we do this?

Even though PRRSV diversity has been recognized,, current sampling and diagnostic strategy schemes used by field veterinarians (i.e. sequencing of part of the PRRSV genome using one sample per swine site) have not been well evaluated for this highly mutating RNA virus. This becomes important when considering the potential consequences derived from conclusions made on current diagnostic knowledge. Field veterinarians should preferably be using the most recent tools while helping our clients on a regular basis (e.g. is this a new virus? And if so/ if not: do I need investments on biosecurity to improve prevention? etc.).

What did we want to do?

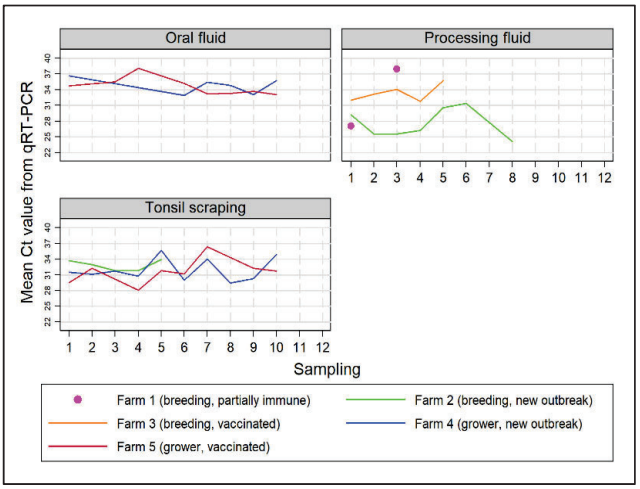
The objective of this study was to describe the genetic variability of PRRSV in swine farms with different production types (breeding and growing pig herds) and PRRS infection statuses (new outbreaks, vaccinated farms, "natural" PRRSV exposure).

How did we do it?

Five US swine herds (three farrow-to-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 for 6 months to one year. For the breeding herds, farms were either "naturally" infected (no vaccine used- Farm 1), recently infected (active outbreak – Farm 2), or actively vaccinated (using a MLV vaccine- Farm 3). For the growing pig herds, farms were either recently infected (active outbreak- Farm 4), or actively vaccinated (using an MLV vaccine- Farm 5). Processing fluids (PF; breeding herds), oral fluids (OF; growing pig herds) and tonsil scrapings (TS; both herd types) were collected approximately once per month.

What did we find?

PRRSV was detected by RT-PCR in approximately 25% of TS, 22% of PF, and 25% of OF throughout the study period. See the figure below for detailed Ct values over time.



When analyzing ORF5 sequences (34 PF, 7 OF and 12 TS), up to 3 different PRRSV lineages could be found in a single sampling event (month) for single farms. More specifically, we identified the presence of multiple PRRSV classified into different lineages (L1H, L1A, and L8) in two breeding farms (Farms 2 and 3) within the same sampling events using PF. Furthermore, both a field lineage (L1A) and a modified live vaccine lineage (lineage L5) were observed using OF and TS samples for both growing herds (Farms 4 and 5). We also observed different PRRSV lineages detected from month-to-month for most herds.

Additionally, we reported that TS appeared to be a useful sample type for PRRSV detection in growing pig herds (regardless of vaccination status), but not for breeding herds, in which processing fluids appeared to be a better option.

So what?

Our study demonstrates the co-circulation of multiple lineages of PRRSV including wild and vaccine strains in commercial breeding and growing swine herds. This implies the deficiency in the common practice identifying the sequences of dominant PRRSV in the field, i.e., simply submitting samples with the highest viral concentrations (lowest Ct). As such, we recommend that sequencing results based on ORF5 and only one sequenced sample per site for a given point in time should be interpreted with caution; especially when trying to make conclusions regarding source of a new outbreaks and the possibility of PRRS re-emergence in swine herds. Sequencing multiple samples in a sampling event would likely give a more comprehensive picture of PRRSV diversity within swine herds.

Questions? arruda.13@osu.edu