***In-silico* characterization of the relationship between PRRSV prevalence at the individual piglet level and prevalence at the litter level in a farrowing room**

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**Introduction:**

Monitoring/surveillance remains an integral component of PRRSV control and elimination programs. Sampling for monitoring/surveillance is generally guided by assumptions, paramount of which is the assumed prevalence of the disease in the population to be sampled1. With the recent paradigm shift in US breeding herds’ PRRSV surveillance, from individual-animal-based sampling to aggregate sampling2, the unit for which prevalence is estimated for these aggregate samples shifts from the individual animal to the animal group giving the sample, for example, the litter, in the case of family oral fluids (FOF)3. To the best of the authors’ knowledge, no published work describes how the mentioned prevalence types relate. Therefore, the objective of this study was to characterize the relationship between the proportion of viremic piglets in a farrowing room, the proportion of litters with at least one PRRSV-positive piglet (True litter prevalence, TLP), and the proportion of PRRSV-positive litters likely to be detected by FOF (Apparent litter prevalence, ALP).

**Materials and methods:**

*Parameters from the referenced study*: Based off the study4 of Almeida et al., a predictive model was first built to characterize the relationship between within-litter prevalence (the proportion of viremic piglets within a litter) and the probability of a positive FOF sample from that litter.

*Stochastic model*: Farrowing rooms were simulated with a fixed number of litters (crates), using piglet-level PRRSV prevalence (PP) ranging from 0 to 40%. The number of piglets within each litter was drawn from a discrete empirical distribution. The number of viremic piglets in each litter was sampled from a recursive binomial model, using a clustering factor ranging from 0 (random distribution of PRRSV-positive pigs between litters) to 1 (PRRSV-positive pigs are clustered within the fewest number of litters possible). To fit the clustering factor to Almeida data...We further conducted an *in silico* model using the stochastic model abovementioned and a factorial design using four levels for the clustering factor {0, 0.3, 0.61, 0.9} and four levels for the number of crates in a room {12, 24, 56, 102}. The TLP per iterated room was obtained as the proportion of litters with at least one viremic pig, and the apparent litter prevalence was obtained as the predicted proportion of the litters in an iterated room that will be PRRSV-positive by FOF testing. A total of 5000 iterated rooms were obtained by monte carlo simulation, and the median values of TLP and ALP were obtained. All analyses were done on R statistical software5.

**Results:**

Chart

Description automatically generatedThe median clustering obtained from Almeida’s study was 0.61. The degree of clustering influenced the relationship between PP, TLP, and ALP (Figure 1).

**Discussion and conclusion:**

The results of this study demonstrate how PP, TLP, and ALP (by FOF) in a farrowing room compare. This study provides insight to swine practitioners on comparable prevalence values to be used in estimating sample sizes for either serum or FOF sampling for PRRSV surveillance in weaning age pigs. The results of this study also provide a framework for estimating the proportion of viremic piglets within a farrowing room, given the results of FOF testing. This study not only scaled and measured the distribution (clustering) of PRRSV-positive pigs from a previous study, but also utilized this clustering scale in estimating PRRSV litter-level prevalence at different piglet-level prevalence scenarios; adding to the series of studies6,7 that are tailoring conventional sample size concepts to better fit the peculiarities in typical US swine barns and the ecology of PRRSV.

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