Can you estimate PRRSV piglet prevalence using family oral fluids? Yes, you can.

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Key points:
- For aggregate samples like family oral fluids (FOF), appropriate sample sizes are calculated using the estimated proportion or prevalence of PRRSV-positive litters, not PRRSV-positive piglets.
- This study showed the relationship between the piglet level prevalence, litter-level prevalence based on serum testing, and litter-level prevalence based on FOF testing in a farrowing room.
- Using the tables provided, the piglet-level prevalence can be estimated from FOF-positivity rates.

Background:

In aggregate sampling, two or more animals are represented in a single sample obtained in one sampling event. For example, one udder wipe or family oral fluid sample (FOF) represents one litter of piglets or one farrowing crate. FOF is an oral fluid sample obtained when fluid is wrung off a rope chewed by a dam and her piglets. Since the unit to be sampled is the entire litter and not the individual piglet, sample size considerations must be done at the level of the litter, not individual pigs. The litter-level PRRSV prevalence in a farrowing room, or proportion of PRRSV-positive litters in a room, is a key assumption for estimating the number of litters to be sampled (sample size) for PRRSV RNA investigation by reverse transcription polymerase chain reaction (RT-PCR).

Since the swine industry is accustomed to the conventional piglet-level prevalence, it becomes important to characterize a link between the piglet and the litter prevalence levels. This study characterized the relationship between piglet- and litter-level prevalence of PRRSV in farrowing rooms. In addition, the expected FOF positivity rate (apparent litter prevalence) is characterized alongside the previously mentioned proportions.

Methods

A stochastic mathematical model was used to characterize the link between the three prevalence levels. All mathematical modeling was done on R statistical software; the data sources and methods are described in detail in the published paper (see link below), and the R codes used can be found at https://github.com/onyechux/Prevalence-simulations.

Results and discussion

There was a linear relationship between the piglet-level prevalence (PP), true litter-level prevalence (TLP), and apparent litter-level prevalence (ALP), where the PP consistently had higher values. The relationship between all three prevalence levels is shown below for a 56-crate room, with a baseline clustering of 0.61. Please refer to the supplemental file of the article in the provided link below to retrieve TLP and ALP values at more PP, room sizes, and clustering scenarios.

Clustering (spatial heterogeneity) of PRRSV-infected piglets was measured from retrospective (published) data; the baseline (0.61) may be used to guide sample size estimates; however, an alternative value of clustering may be used (estimated) given other factors that could influence the spatial distribution of PRRSV-infected piglets. Such factors include the PRRSV variant, bio-management practices (e.g., cross-fostering), previous monitoring results, etcetera. Incorporating clustering adds precision to estimating appropriate sample sizes and is one more way to tailor conventional statistical concepts to better fit peculiarities with PRRSV monitoring and surveillance in contemporary swine populations.

Piglet-level prevalence * (%)	Litter prevalence based on sera (95% quantiles) ** (%)	FOF-based prevalence (95% quantiles) *** (%)
1.00	5.36 (1.79, 7.14)	2.06 (1.07, 3.53)
5.00	8.93 (7.14, 12.50)	6.48 (5.30, 8.58)
10.00	14.29 (10.71, 17.86)	11.25 (9.31, 13.92)
15.00	19.64 (16.07, 23.21)	16.35 (14.47, 19.21)
20.00	23.21 (21.43, 26.79)	21.60 (18.73, 24.19)
25.00	28.57 (25.00, 32.14)	26.66 (23.50, 29.31)
30.00	33.93 (30.36, 37.50)	31.35 (28.77, 34.33)

* The proportion of PRRSV-positive piglets in a farrowing room
** The proportion of litters with at least one PRRSV-positive (viremic) piglet in a farrowing room
*** The expected proportion of litters to test PRRSV RT-PCR positive on family oral fluids.

Conclusions

All three prevalence levels have been mathematically characterized and linked; piglet-level prevalence in a farrowing room can therefore be estimated from the results of FOF testing using provided tables. Linking all three proportions also allows for comparing sample sizes to make sampling choices; for example, a practitioner can calculate and compare appropriate sample sizes at the piglet- and litter levels that will have an equivalent power to detect one or more PRRSV-infected units and decide what sample type (serum or FOF) would be most convenient to obtain at that time.

The full peer-reviewed paper can be found here: https://porcinehealthmanagement.biomedcentral.com/articles/10.1186/s40813-023-00300-x