

What drives sample size for detecting a pathogen? Part 1.

Key Points:

- When we test 30 samples, there are many assumptions behind the interpretation of our results.
- Optimum sample size depends on cost of sampling and implications of being wrong.
- Models such as this one are useful for helping us understand a disease and our management.
- This model was developed by Dr. Ana Alba Casals, a post doc in our Swine Group.

If we test 30 sera from weaned pigs and finding none to be PCR positive, we are 95% confident that the prevalence of PRRS is less than 10% in the population that we sampled. There are several assumptions in this calculation that we usually don't consider. And that's OK, because being quite confident that the pathogen is low prevalence is probably good enough in most circumstances.

We can never be 100% confident that a herd is free of a pathogen. We can get close if we test the entire herd with a test that is 100% accurate and assume that the PRRS virus would be detected if present (it just entered the herd on my boots, a sow just got some virus in her nose and tested positive - unlikely). We can increase our confidence by testing repeatedly, testing downstream flow, following negative gilts in the herd and testing high risk individuals (e.g. abortions, off-feed).

If we want to compare cost effectiveness of different sampling strategies, then the assumptions matter. Dr. Ana Alba Casals, a post doc in our Swine Group, is developing a model to compare consecutive sampling strategies for estimating our confidence that a herd has <5% prevalence. Regarding models, you might have heard the statement attributed to statistician George Box (1919 – 2013) "*all models are wrong; the practical question is how wrong do they have to be to not be useful?*" For Ana's model, the exact probabilities are no doubt incorrect, but the model is useful for helping us think through what might influence the outcome.

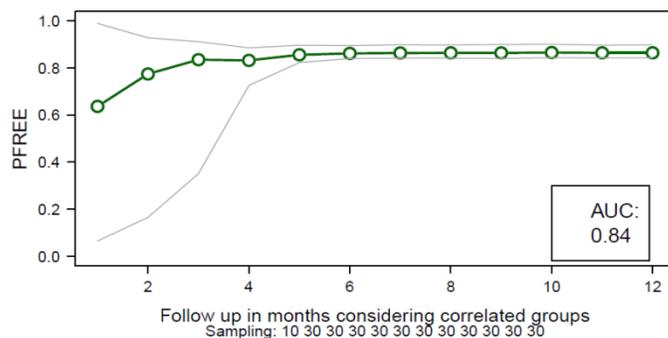
Factors that influence our confidence include:

- Sensitivity and specificity of the test being used. We generally assume 100% for both (no false positives or false negatives).
- Size of the herd. Our probabilities generally assume an infinitely large population.
- Representativeness of the sample to the herd as a whole. There are three considerations here; (1) we test weaned pigs because we believe this is the high risk group in the herd and findings in the weaned pigs can be applied to the herd as a whole, (2) the pigs sampled are "randomly" selected from those to be weaned that week. We might select high risk pigs (light, barrows, gilt litters) but this is an unrepeatable observation and (3) the correlation between this week's (group) results and consecutive weeks in the farm.
- Our confidence that the first test at 12 weeks after last exposure will yield no positive results (<5%). Since we are not very confident on our first test, we often start with a low sample size such as 10 pigs and we will assume that we are only 50% confident that our first sample of 10 will be negative.
- The likelihood that the herd is infected with a new PRRS virus between tests. We feel more confident adding previous testing together if incidence of new infection is low. In the strictest sense, we are only as confident as our most recent test.

So, let's look at a commercial herd with high incidence (once every 3 years) and a goal to be stable (status 2vx or 2fvi). At 16 weeks after infection, we'll take our first sample. We can set a detection limit of ≤ 5% as our indication of low prevalence (and maybe negative). We'll test 10 pigs on our first test and increase the sample to 30 if all 10 were negative. And we'll test 30 monthly after that. Suppose that we are 50% confident that our first sample will be negative. And suppose that we have a moderate correlation for prevalence between consecutive weeks ($r=0.71$).

This last assumption deserves elaboration. If all weeks of weaned pigs were homogenous, that is perfectly correlated, we would only need to test one week. But we know we can detect a positive sample this week and negative next week. So, in the middle stages of eliminating virus from a sow herd, the consecutive weeks are not perfectly correlated.

D: Commercial herd with medium incidence taking 340 samples



In the figure above, we are roughly 60% confident that the herd is <5% prevalence after our first negative test of 10 samples. After finding 30 negative, we are approximately 80% confident. And we gradually increase to about 84% confident. If we lower the risk of new infection, our confidence would increase. And, the longer we test negative, the higher our correlation between weeks will become and our confidence will increase – this is not in the model at this time.

We'll show a comparison of a few more scenarios next week. Bob Morrison