RESEARCH ABSTRACT

SWINE HEALTH

Title: Design and analysis of PRRSv surveillance: temporal and spatial sampling, mapping, monitoring and automated rapid detection of outbreak – **NPB #11-165**

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Scientific Abstract:

In animal disease testing at the population level, traditional calculation methods relate the power of detection to sample size using probability models, e.g., binomial distribution.1 These probability models are based on the assumption that all individuals have the same chance of acquiring disease. In contemporary animal production systems, however, a hierarchical structure exists. For example, a farm may consist of multiple buildings and each building usually contains multiple pens of animals. Farm sample size may be calculated using classic formulas, but there is a lack of guidance about how to subsequently allocate sampling across strata. Despite the fact that strata are not necessarily homogenous in terms of disease status, it is common for samples to be collected from selected strata, leaving other strata unsampled: (1) for convenience, (2) for lack of formal guidance regarding sample allocation across strata, and (3) under the assumption that certain strata are most representative of the farm's disease status. For optimal disease detection at the farm level, a mathematically more intuitive way to allocate samples would be even distribution across the different strata. But does sampling from one stratum vs. multiple strata differ in the power of disease detection? If multiple strata sampling is preferable, is even distribution of samples across the strata the optimal strategy? If not, what are the formulas for sample size calculation and allocation for populations with a two-level structure? The objective of this project is to address these questions from a mathematical perspective.

A pivotal part of disease surveillance is the repeated disease diagnostic testing to monitor the status of the disease. Despite their importance, little work has been done to address the common questions of sampling frequency as well as sample size for repeated testing. We develop mathematical relationships between the sample size, sample frequency and the other parameters in disease detection, ie, the prevalence, the desired detection time and the desired power of detection. We also develop a web application called SSF (Sample Size and Frequency), built upon the Shiny web-application framework. SSF provides easy-to-use and instantly displayed calculation of sample size and frequency based on a custom-defined scheme of their own choosing.