

“How can farm structure and demography influence pathogen persistence within a herd?”

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Key Point:

Farm structure and demography can influence the persistence of pathogens within a herd by altering transmission dynamics.

Introduction

Foot and mouth disease (FMD) is one of the most contagious and economically relevant diseases affecting livestock and is rapidly transmitted between hosts. Typically, FMD models consider farms as the epidemiological unit of analysis, ignoring key characteristics of a farm that may have an effect on within-herd pathogen dynamics. However, oversimplifying a swine farm's structure and demographic qualities may lead to erroneous conclusions when considering the between-herd spread of FMD.

What did we do?

We developed a stochastic disease transmission model to simulate the spread of FMD virus in a farrow-to-finish and farrow-to-wean swine farm and compared those predictions to a model in which farm structure and demography was ignored (homogenously-mixed). The model classified pigs into 5 mutually exclusive states: susceptible, latently infected, subclinically infected, clinically infected, and recovered. The number of pigs in each of the states was calculated and reported at the room and herd-level for 50 days. For each simulation we calculated the mean time to detection based on the proportion of animals with clinical signs (Kinsley et al., 2016) and reported the duration of the epidemic.

What did we find?

We found that the mean time to detection was about 11.5 days in all scenarios (Table 1).

Feature	Farrow to finish	Farrow to wean	Homogenously-mixed
Time to detection (days) (95% interval)	11.50 (11.39, 11.62)	11.56 (11.42, 11.70)	11.41 (11.28, 11.54)
Duration of epidemic (days) (95% interval)	--	--	45.94 (45.53, 46.34)

Table 1: Mean time to detection and duration of the epidemic for the farrow to finish, farrow to wean, and homogenously mixed populations.

However, the duration of the epidemic varied between scenarios. The homogenously-mixed population experienced a phenomenon termed “epidemic fadeout”, in which the pathogen became extinct in the population due to the low number of infected individuals and the stochastic nature of the disease. In contrast, sufficient numbers of infected and susceptible pigs remained in the farrow to finish herd to maintain the infection within this population. This maintenance of infection was even more evident in the farrow to wean herd where the number of infected individuals fluctuate as births of susceptible piglets sustain the infection process. These fluctuations can be seen in

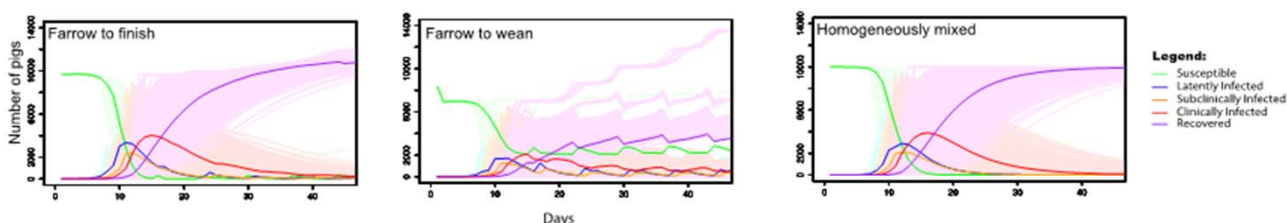


Figure 1: Epidemic curves for the farrow to finish, farrow to wean and homogenously mixed population. Lighter, thinner lines represent the results of 1,000 simulations. Thicker, darker lines represent the mean of the simulations.

What does this mean?

Our results indicate that FMD persistence within a population is dependent on farm structure and availability of susceptible individuals as seen in the ongoing infection in the farrow to finish and farrow to wean herds, which are both birthing susceptible piglets on a weekly basis. Moreover, our results indicate that the homogenous-mixing assumption may be sufficient to model FMD spread when only average outputs are modeled but that farm structure and demography need to be considered to more accurately model deviations from the outputs.

Farm structure is also likely contributing to the prolonged duration of infection within the herd, as the limitation of interactions between individuals slows the spread of infection. These findings may extend beyond the study of FMD in swine herds. Therefore, we suggest that farm structure and farrowing rates be considered when aiming for pathogen elimination within a herd.

References: Kinsley, A. C., Patterson, G., VanderWaal, K. L., Craft, M. E., & Perez, A. M. (2016).. *Frontiers in Veterinary Science*, 3, 44.