The importance of including intra-herd transmission in a foot and mouth disease model

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Introduction

Foot and mouth disease is one of the most economically important livestock diseases in the world. In recent years large-scale epidemics have been observed in Taiwan in 1997 (Donaldson, 1997), the UK in 2001 (Anonymous, 2001), and Argentina in 2001, resulting in the slaughter of more than 4 million animals in the UK (DEFRA, 2002) and 178 million doses of vaccine distributed in Argentina (OIE, 2002).

Simulation modeling has been used to predict the spread and control of FMDV if it were endemic (Carpenter and Thieme, 1980) or introduced into a non-infected country (Garner and Lack, 1995; Jalvingh et al., 1997; Keeling et al., 2001; Miller, 1979; Morris, 2001; Bates et al., 2003). If a model fails to take the dynamics of intra-herd transmission into consideration, the model simplifies the behavior of virus transmission and tacitly assumes that once a herd is infected (even by only one animal), it becomes infectious at some level after the predicted incubation period passes. In addition, models lacking the intra-herd component fail to capture information that may be useful to control of the disease. The purpose of this paper was to predict and evaluate intra-herd transmission of FMDV in a hypothetical 1000-cow dairy herd, assuming a range of animal-to-animal contact rates and alternative clinically-infected prevalence cut-points for diagnostic and disposal delays of an FMD-infected herd.

Methods

The intra-herd transmission model was programmed in EXCEL[®] and was one component of a larger simulation model that also included an inter-herd transmission component. The model was stochastic, in that it included uncertainty information for various parameters. The model consisted of 5 FMD disease states: susceptible, latently infected, subclinically or clinically infectious and immune.

For the purpose of illustration, we assumed a hypothetical 1000-cow dairy herd to be infected with FMDV. A total of 5,000 iterations were performed to assess the distribution of outcomes. The expected distribution of disease prevalence, by infection state, and the number (and 90% prediction interval (PI)) of infected and infectious cows for 5,000 iterations were calculated.

Results

In the scenario examined in this paper, it was assumed that 50%, or 500 cows, would be infected 9 days after an infected cow was introduced into the herd (Fig. 1). By day 13, nearly the entire herd was expected to be infected. There was a similar

pattern seen with respect to the number of infectious cows in the herd, lagged by 4 days. In addition, the pattern for prevalence of animals with clinical disease is illustrated in the second panel of the figure. There it illustrates that while a substantial number of cows are infectious approximately 2 weeks post herd infection, a relatively small percentage are showing clinical signs. Thus clinical detection of FMD would be unlikely during the early period when prevalence of infectious cows is high.
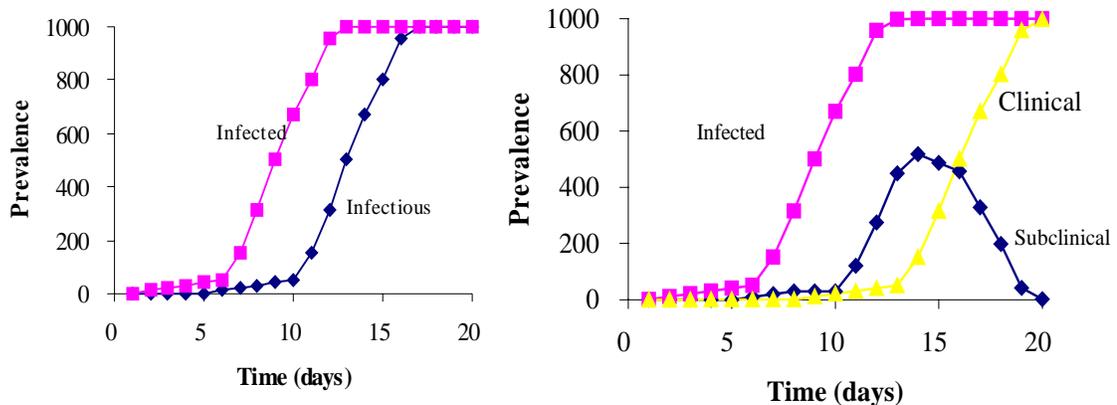

Figure 1. The expected prevalence of FMD infection in a hypothetical 1000-cow dairy herd.

The importance of not delaying the detection or depopulation of an infected herd is illustrated in figure 2. Assuming that FMD would be detected in this herd once 1%, or 10 cows, showed clinical signs, more than 400 cows (180 – 800, 90% PI) would be infectious. The number of infectious cows grew by approximately 150 per day for the 3 days following the day of diagnosis. While the mean number of infectious cows was approximately 50 on the day of diagnosis, it increased fairly linearly and reached approximately 700, 5 days post-diagnosis.
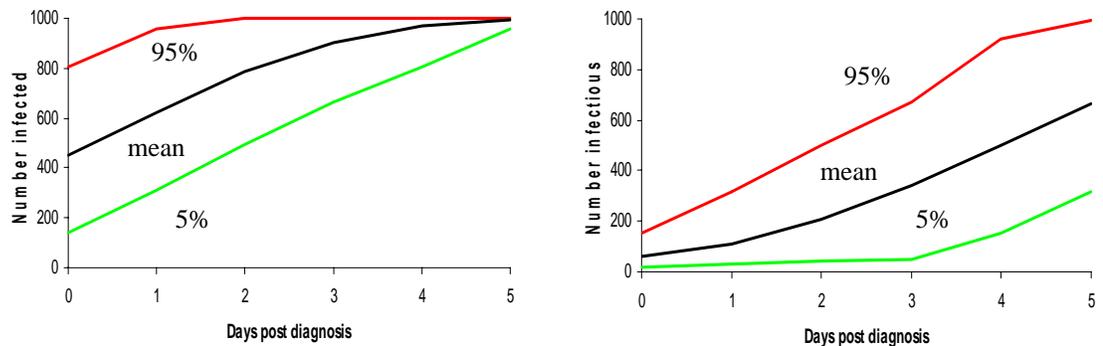

Figure 2. The mean and 90% prediction interval of the number of infected and infectious cows in a hypothetical 1000-cow dairy herd infected with FMDV.

Discussion

Simulation results generated from the intra-herd model illustrate the explosive nature of FMD. The intra-herd transmission projected here for a typical intensively managed dry-lot type of dairy herd has important implications for diagnostic medicine in developing herd and regional biosecurity programs, as well as for our ability to make a timely diagnosis of FMD. A challenge facing diagnostic medicine is the need to develop screening strategies for replacement livestock, as part of herd biosecurity aimed a minimizing introduction of FMDV into a herd. In order to minimize inter-herd transmission, regional, state, and national biosecurity also will require new diagnostic approaches that detect the virus much earlier than is possible using the current clinical signs signalment. The current surveillance strategy that relies solely on clinical signs of FMD will allow the infection to incubate and for many animals to transmit the virus to other herds after being culled or removed from the infected herd. In light of the potential for real-time diagnostic capability for FMDV detection, this traditional approach will need to be augmented by diagnostic surveillance that actively seeks out the virus, rather than waits for clinical signs to develop.

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