

# Potential for Transmission of Endemic Infections in Scottish Livestock Networks

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## ABSTRACT

Understanding how the network of livestock farms connected by the movements of animals affects the potential for transmission of infections is essential for predicting and controlling the spread of livestock diseases. Here we reconstruct the Scottish sheep, cattle and all major livestock (sheep, cattle, pigs and goats) farm networks from July 2003 to June 2007. For each network, we calculate the basic reproduction number for an infectious disease over a one-year interval, as relevant to chronic endemic infections. We then partition the contribution to the transmission potential from the first (mean movement rates per farm), second (variance and covariance of movement rates on and off individual farms) and higher order properties of the network. By weighting the contacts between farms in three different ways, we address a set of epidemiological scenarios: highly transmissible infections with high on-farm prevalence, rare infections with low on-farm prevalence, and an intermediate scenario. We identify which features of the farm contact networks and which farms in a given network contribute the most to the potential for spread of endemic livestock infections, and how these contributions vary depending on the weighting of the contacts between the farms.

**KEYWORDS** contact networks, basic reproduction number, livestock

## INTRODUCTION

Animal movement is a major mode for the spread of livestock infections (Fèvre, Bronsvoort et al. 2006). Livestock movements connect the farms into networks. Understanding how the properties of these contact networks affect the potential for transmission of infections among the farms is crucial for designing efficient control programmes. Here, we consider the effects on the potential for transmission of chronic endemic infections. We calculate the basic reproduction number,  $R_0$ , the expected average number of secondary infected farms from a single primary infected farm, for such an infectious disease spreading through a farm network. There are a number of endemic infections specific for sheep or cattle, and some food-borne pathogens are potentially transmissible among all the major livestock species farmed in Scotland (sheep, cattle, pigs and goats), for example, *Cryptosporidium* spp (Tzipori 1983; Olson, Thorlakson et al. 1997), *Giardia intestinalis* (Ey, Mansouri et al. 1997; Olson, Thorlakson et al. 1997) or *Yersinia enterocolitica* (McNally, Cheasty et al. 2004; Milnes, Stewart et al. 2008). These infections are often asymptomatic and long-lasting in the livestock carriers, and persistent in livestock populations. We therefore individually consider: a) the sheep movement network, b) the cattle movement network, and c) the network of movements of all the major livestock species. We evaluate these networks in Scotland over four one-year intervals.

## MATERIALS AND METHODS

Records of livestock movements between Scottish farms from July 2003 to June 2007 were extracted from Scottish Animal Movement System and Cattle Tracing System of British Cattle Movement Service, and processed in Python programming environment and SAS® 9.1.3 software for Windows (SAS Institute Inc.) as previously described (Volkova, Savill et al. 2008). The data were divided into four one-year intervals: 01/07/2003-30/06/2004, 01/07/2004-30/06/2005, 01/07/2005-30/06/2006 and 01/07/2006-30/06/2007. The June/July dividing date precedes the major peak in sheep movements in the autumn; seasonality in livestock movements was not considered further. Livestock movements to slaughter, to shows, outside Scotland and those with incomplete histories were excluded. Each farm population (sheep, cattle, all livestock) was analyzed as a closed network considering all animal movements between the farms, either direct or via a Scottish livestock market. For the network of all livestock, the transmission of an infection between farms was assumed to occur through any movement of sheep, cattle, pigs or goats.

For each farm contact network and one-year interval,  $R_0$  was partitioned into components corresponding to different moments of the network. The contributions of the first order moments can be evaluated by

calculating the mean number of contacts for a farm in the network [quantity 1]. The contribution of the second order moments can be calculated by further accounting for the variances and covariances of the movement rates on and off individual farms [quantity 2], and obtaining the ratio of this quantity 2 to quantity 1, as previously shown (Woolhouse, Shaw et al. 2005). These calculations were done with SAS® 9.1.3 software. The contribution of the higher order moments was evaluated by representing the network as the farm contact matrix, calculating the magnitude of the dominant eigenvalue of this matrix (Barbour 1978; Diekmann, Heesterbeek et al. 1990) [quantity 3], and then obtaining the ratio of quantity 3 to quantity 2. The eigenvalues were calculated using ARPACK FORTRAN77 code libraries (Lehoucq, Sorensen et al. 1997).

We address different epidemiological scenarios for an endemic disease by weighting each directed contact between a pair of farms in a network in a given year in three ways: 1) present or absent (unweighted); 2) weighted by the number of batches of animals moved; and 3) weighted by the total number of animals moved. Model (1) is appropriate for a highly transmissible infection with high on-farm prevalence (likely to be transmitted by any movement); (3) is appropriate for a rare infection with low on-farm prevalence (the probability of transmission is low and linearly dependent on the total number of animals moved); and (2) refers to an intermediate scenario.

We have recently developed an approximate method to identify a 20% subset of farms contributing the most to  $R_0$  for endemic infections in a farm network. Here we apply this methodology and quantify the effects of targeted removal of this subset of farms on the transmission potential in the Scottish cattle and sheep networks, and how the effects vary between the models (1)-(3) and the years of study. We further evaluate the usefulness of the farm contact information from the preceding (rather than current) year, as this information is more readily available in practice.

## RESULTS AND DISCUSSION

First, the higher order moments of the farm contact matrices have a substantial impact on the relative magnitude of the potential for transmission of endemic infections between the farms. There is apparent year-to-year variability in these effects. The full effects of the networks' structure on the transmission potential cannot be evaluated from knowledge of the means, variances and covariances of the farm contact rates, but require information on the complete contact matrices. These observations stress the importance of collating comprehensive information on livestock movements among the farms.

Second, the contributions of the higher order and lower order moments of a given network substantially differ depending on how the contact between the farms is weighted. The choice of weighting would be determined by the detailed epidemiology of the infection.

Third, heterogeneities in contact patterns of individual farms affect the magnitude of the potential for transmission of endemic livestock infections. The farms can be ranked in their individual contributions. Using an approximate method, we find that the top ranked 20% of farms in Scottish sheep and cattle networks are contributing more than 80% to the transmission potential for chronic endemic infections amongst the farms each year. Control efforts targeted at these farms are likely to be efficient in reducing the transmission potential. In practice, the pattern of infectious contacts between farms can be altered through such interventions as livestock movement restrictions or pre-movement testing.

Fourth, the subset of farms contributing the most to  $R_0$  for chronic endemic infections changes through time, and archived information on the preceding year's farm contacts is of limited usefulness. Efficient targeting of interventions requires deriving and differentiating the characteristics of the farms that consistently versus intermittently appear among those contributing the most to the transmission potential.

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