

Influence of disease control zones on dairy cattle movement patterns

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Purpose:

Many countries with endemic bovine tuberculosis (bTB) have established control zones around regions where farms with higher infection risk exist. This can significantly influence the structure of cattle movement networks, which has important implications for modelling disease transmission dynamics. Here, movement data from dairy herds in New Zealand were analysed (1) to explore the spatial relationships between network trade communities and the five major disease control areas (DCA) and (2) to identify demographic factors that predict community membership.

Methods:

Dairy cattle movement data from July 2008 and June 2011 were retrieved from the Livestock Improvement Corporation (LIC) database. The movement data were aggregated by year and the Clauset-Newman-Moore algorithm for directed networks was then used to detect communities amongst the LIC dairy farms. The association between community membership and DCA was analysed using Mantel test. A multinomial regression model was constructed to predict the major community membership.

Results:

The geographical distributions of the major network communities were relatively stable over time and we restricted the remaining analyses to data from July 2009 through June 2010. During this period, 747,802 individual animals were moved between the 12,288 LIC farms in 42,149 distinct batch movements. The algorithm detected 408 communities, although only 35 of these communities contained more than 10 farms and the largest five communities included 9,508 farms (77.4%) of the studied population. Farms in the same DCA were more likely to be in the same community ($p < 0.001$). In addition to DCA, numbers of culling and new calves born in the previous year were useful predictors for the major community membership.

Conclusions:

The community structure of dairy cattle movements in New Zealand is strongly influenced by DCA. However, there is still significant trade between farms in different DCAs, which may be contributing to the spread of bTB.

Relevance:

It is important to account for network community structure when planning disease control strategies and when developing rules to generate cattle movement patterns in disease simulation models.