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Application of network analysis parameters in risk-based surveillance – Examples based on cattle trade data and bovine infections in Sweden

Jenny Frössling[a,b,*], Anna Ohlson[a,c], Camilla Björkman[c], Nina Håkansson[d,e], Maria Nöremark[a]

[a] *Department of Disease Control and Epidemiology, National Veterinary Institute, SE-751 89 Uppsala, Sweden*
[b] *Department of Animal Environment and Health, Swedish University of Agricultural Sciences, Box 234, SE-532 23 Skara, Sweden*
[c] *Department of Clinical Sciences, Swedish University of Agricultural Sciences, Box 7054, SE-750 07 Uppsala, Sweden*
[d] *Systems Biology Research Centre, Skövde University, Box 408, SE-541 28 Skövde, Sweden*
[e] *Division of Theoretical Biology, IFM Theory and Modelling, Linköping University, SE-581 83 Linköping, Sweden*

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ABSTRACT

Financial resources may limit the number of samples that can be collected and analysed in disease surveillance programmes. When the aim of surveillance is disease detection and identification of case herds, a risk-based approach can increase the sensitivity of the surveillance system. In this paper, the association between two network analysis measures, i.e. 'in-degree' and 'ingoing infection chain', and signs of infection is investigated. It is shown that based on regression analysis of combined data from a recent cross-sectional study for endemic viral infections and network analysis of animal movements, a positive serological result for bovine coronavirus (BCV) and bovine respiratory syncytial virus (BRSV) is significantly associated with the purchase of animals. For BCV, this association was significant also when accounting for herd size and regional cattle density, but not for BRSV. Examples are given for different approaches to include cattle movement data in risk-based surveillance by selecting herds based on network analysis measures. Results show that compared to completely random sampling these approaches increase the number of detected positives, both for BCV and BRSV in our study population. It is concluded that network measures for the relevant time period based on updated databases of animal movements can provide a simple and straight forward tool for risk-based sampling.

1. Introduction

Surveillance of infectious animal diseases constitutes an important part of the prevention of animal disease and can have several specific purposes, e.g. early detection, declaration of freedom or evaluation of control strategies. However, financial resources may limit the number of samples that can be collected and analysed, and a risk-based approach is then one alternative for increasing the case-finding capacity of the surveillance system. Infectious diseases are seldom homogeneously spread within the population and the benefits of searching "in the most likely place" when monitoring disease, in contrast to overall random sampling, have been previously discussed, e.g. by Cannon (2009) and Stärk et al. (2006).

Many livestock diseases can spread through direct contact between animals, and thus between herds through movements of animals. This is one of the major reasons for registering livestock transports in national databases (Anonymous, 2000). When the aim of surveillance is detection (eradication context, emergence of an exotic disease,

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[*] Corresponding author at: Department of Disease Control and Epidemiology, National Veterinary Institute, SVA, SE-751 89 Uppsala, Sweden. Tel.: +46 18 674359; fax: +46 18 674445.
E-mail addresses: jenny.frossling@sva.se, jenny.frossling@slu.se (J. Frössling).

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etc.), and when the disease is expected to spread through live animal contacts, animal movement data could be used in the selection of herds to be included in surveillance activities. In such cases, herds with many live animal contacts can be assumed to have a higher probability of infection, and sampling of these would therefore increase surveillance sensitivity.

Lately there has been an increasing number of publications analysing livestock movements (Dubé et al., 2009; Martinez-Lopez et al., 2009). For instance, the outbreak of foot-and-mouth disease in the United Kingdom in 2001 was the starting point for a number of studies within this field of research (e.g. see Ortiz-Pelaez et al., 2006). However, although analysis of animal contact patterns has already been suggested for targeting the surveillance of diseases (Christley et al., 2005; Martinez-Lopez et al., 2009; Blickenstorfer et al., 2011; Nöremark et al., 2011), to our knowledge there have been almost no published applications of the use of cattle movement network analysis for implementing a risk-based surveillance so far. There are many different network measures of centrality and, in 1979 in the context of social network analysis, Freeman discussed the importance of using meaningful and intuitively interpretable measures (Freeman, 1979). For surveillance activities that target herds with an increased risk of disease due to ingoing live animal contacts, an intuitive focus would be measures of contacts that have actually occurred, rather than measures describing the relative role of the herd in connecting the entire network (e.g. different measures of betweenness). Inclusion of measures of betweenness may, on the other hand, be more applicable in models simulating spread of disease. There are different network analysis parameters describing incoming contacts that may be applied for risk-based surveillance purposes. For example, the 'in-degree' measure (Wasserman et al., 1994) describes the actual number of ingoing animal contacts for a herd. In addition, Nöremark (2010) and Nöremark et al. (2011) described the 'ingoing infection chain', which includes secondary contacts in sequences, taking into account the temporal aspect and the order in which these contacts have occurred (Fig. 1).

Bovine respiratory syncytial virus (BRSV) and bovine coronavirus (BCV) are examples of pathogens that can spread through live animal contacts and also indirectly, e.g. through visitors and equipment (Elvander et al., 1998; Hägglund et al., 2006; Valarcher and Taylor, 2007; Bidokhti et al., 2009; Ohlson et al., 2010). Identified risk factors for BRSV and BCV infection in Sweden include large herd size (Tråvén et al., 1999; Norström et al., 2000; Ohlson et al., 2010) and being located in southern Sweden (Elvander, 1996; Beaudeau et al., 2010) where the herd density is higher compared to northern parts. Both diseases are distributed worldwide, causing enteric and respiratory disease in beef and dairy cattle (Clark, 1993; Valarcher and Taylor, 2007).

The aim of this study was to elaborate on the potential usefulness of including network analysis measures of animal movements in the design of surveillance programmes aimed at the detection of exotic diseases. In order to investigate potential association between network analysis parameters and the presence of disease, results from a serological survey of BRSV and BCV in Swedish cattle were combined with data of reported animal movements. BRSV and BCV were used as a proxy for exotic diseases, or other serious infections under surveillance, with similar contagiousness and routes of transmission. In other words, the study was not designed to investigate risk factors for these specific diseases. Simulated sampling from the study material was used to visualise and compare risk-based approaches to a random selection strategy.

2. Materials and methods

2.1. Data

Information about movements of individual cattle in Sweden 2006 was retrieved from the database of the Swedish Board of Agriculture (described in more detail by Nöremark (2010) and Nöremark et al. (2011)). Information about herd size, i.e. the number of cattle >1 year of age, and about the geographic location of herds was also included in that database. The regional cattle herd density was calculated for all herds in the study sample by dividing the total number of cattle herds by the total area of their three-digit postal code area.

In addition, results from a cross-sectional serological study investigating spatial patterns of BRSV and BCV in Swedish cattle were used. The design of the cross-sectional study and the analytical methods used are described in detail by Beaudeau et al. (2010). In short, a randomised subset of blood samples collected within the Swedish Bovine Viral Diarrhoea control programme was used. In the original study a total of 2763 samples from young stock >12 months of age in 2137 herds were collected between

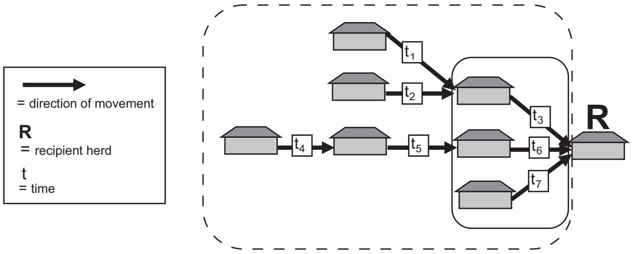

Fig. 1. Schematic illustration of the network measures 'in-degree' and 'ingoing infection chain'. The 'in-degree' for the recipient herd is 3 (herds included within the solid line), and assuming that t_1 and t_2 occur before t_3, that t_4 occurs before t_5 and that t_5 occurs before t_6, the 'ingoing infection chain' for the recipient herd is 7 (herds included within the dotted line).