From network analysis to risk analysis—An approach to risk-based surveillance for bovine tuberculosis in Minnesota, US

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ABSTRACT

Bovine tuberculosis (bTB) was first detected in 2005 in cattle in northwestern Minnesota (MN) through slaughter surveillance. By the end of 2008, 12 cattle herds were infected with bTB, and the main cause for infection was determined to be the movement of infected animals between herds. Bovine tuberculosis was contained in a smaller area in northwestern Minnesota classified as modified accredited (MA), corresponding to a prevalence inferior to 0.1% in cattle. From January 2008 to 2011, all cattle movements within the bTB MA were recorded electronically. The primary objectives of this study were to characterize cattle movements within this region and identify cattle herds with higher risk of bTB introduction based on network parameters and known risk factors from the published literature. During the period that data was collected, 57,460 cattle were moved in 3762 movements corresponding to permits issued to 682 premises, mostly representing private farms, sale yards, slaughter facilities and county or state fairs. Although sale yards represented less than 2% of the premises (nodes), 60% of the movements were to or from a sale yard. The network showed an overall *density* of 0.4%, a *clustering coefficient* of 14.6% and a *betweenness centralization index* of 12.7%, reflecting the low connectivity of this cattle network. The degree distribution showed that 20% of nodes performed 90% of the movements. Farms were ranked based on the total risk score and divided into high, medium, and low risk groups based on the score and its variability. The higher risk group included 14% ($n = 50$) of the farms, corresponding to 80% of the cumulative risk for the farms in the bTB area. This analysis provides a baseline description about the contact structure of cattle movements in an area previously infected with bTB and develops a framework for a targeted surveillance approach for bTB to support future surveillance decisions.

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1. Introduction

The State-Federal program for eradication of Bovine tuberculosis (bTB) in cattle populations in the US was initially developed in 1917 and has been efficient in reducing disease prevalence, nearly to the point of eradication (National Research Council, 1994). The backbone of the surveillance system for detecting infected animals is slaughter surveillance, which has an estimated median time-to-detection at the herd level of 5.75 years, after bTB is introduced into a herd (Fischer et al., 2005), and an estimated very low herd-level sensitivity (USDA-APHIS-VS, 2009a). Individual animal ante-mortem tests for bTB

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are available; however, testing is not routinely performed. Currently, individual ante-mortem animal testing is only performed prior to cattle movements from states or zones that are not bTB free or during disease eradication efforts in infected areas.

The main problems with the current surveillance system include: (i) the long time-to-detection (often identifying disease years after its introduction into an initially disease-free population); and (ii) the unequal probability of inspection of cattle farms of different types and sizes, with large dairy herds being tested more frequently than small beef herds (for example, due to the former sending more cattle to slaughter) (USDA-APHIS-VS, 2009b). The delay in detection allows bTB to spread to other animals and other herds. Once detected, this results in high eradication costs due to the widespread herd tracing and animal depopulation that is required. In order to detect bTB cases earlier in disease free areas, and as a consequence minimize the spread of disease, factors associated with a greater risk of disease introduction or transmission should be incorporated into the surveillance system. In the field of animal health, risk is defined in the Animal Health Code (OIE) as "the likelihood of the occurrence and the likely magnitude of the biological and economic consequences of an adverse event or effect to animal or human health" (OIE, 2012). This is the concept behind *risk-based surveillance* programs, which seek to focus funding and resources toward subsets of the population with a higher risk of the health event of interest, improving surveillance system sensitivity and cost-effectiveness (Stärk et al., 2006).

A recent assessment conducted by the United States Department of Agriculture (USDA) – Animal and Plant Health Inspection Service (APHIS) identified a variety of risk factors associated with bTB infection in US areas without a wildlife reservoir, including the importation and comingling of Mexican-origin steers, the management and biosecurity practices used by calf raisers for dairy replacement heifers, and the influx of purchased cattle (USDA-APHIS-VS, 2009b). The role of cattle movement has also been identified to be of primary importance, particularly in low prevalence or disease-free areas, where disease can be introduced through the importation of cattle from infected areas (Bessell et al., 2012; Gilbert et al., 2005; Gopal et al., 2006). Because cattle movements are directed, since cattle moves from one farm to another and not in both directions, these risks (risk of becoming infected and likelihood of transmitting infection to other farms) may be different depending on a herd's management factors. These include whether the herd engages primarily in selling or buying cattle, and the origin of the latter. Characterizing patterns of cattle movements before a disease outbreak occurs is thus critical to identifying which herds have the highest risk of infection and which would be most likely to transmit an infection to others. Furthermore, the identification of high risk herds, based on cattle movements, do not exclude the role of wildlife for disease spread after it is present, but highlight the importance of cattle movements as the primary source for disease introduction in a disease free area (Mintiens et al., 2008; Natale et al., 2009).

Network analysis, a methodology arising from the social sciences with recent applications to the spread of human and animal infectious diseases, has proven to be an useful tool in understanding the structure of contacts within and between animal populations as well as the role of high risk herds in the transmission of infectious diseases in livestock (Bigras-Poulin et al., 2006; Dubé et al., 2008; Volkova et al., 2010). In a network analysis framework, a population is described in terms of a set of nodes and the edges that describe the interactions between them. In the case of describing the spread of bTB between cattle premises (e.g. herds, sale yards, fairs, etc.), nodes represent cattle premises, where an edge between two herds represents the movement of animals from one premise to another and a potential pathway for disease introduction. A variety of measures have been developed to characterize network features, including measures of *connectedness*, *clustering*, and *distance*, as well as the specific role of individual nodes in the network, including measures of importance or *centrality* (Wasserman and Faust, 1994). Certain network measures have been linked with the risk of infection, such as *in-degree*, the number of incoming connections to a node; while others have been associated with both the risk of infection and also of transmitting disease to other nodes in the network, such as *betweenness centrality* (Frössling et al., 2012; Keeling and Eames, 2005; Pastor-Satorras and Vespignani, 2001).

Given the association of livestock movements with outbreaks of bTB (Gilbert et al., 2005), the objectives of this study were (1) to characterize cattle movements in the region of a past bTB outbreak and (2) to identify herds with a higher risk of becoming infected and/or of infecting other herds based on known risk factors related with cattle movements and network analysis parameters. The ultimate goal was to develop a risk-based surveillance framework for bTB, in order to identify in which herds to focus surveillance resources to minimize disease burden and reduce the cost of disease control. We made use of cattle movement data collected following a recent bTB outbreak in Minnesota. Bovine tuberculosis was first detected in 2005 in cattle in northwestern Minnesota through slaughter surveillance. By 2009, 12 cattle herds were found to be infected with bTB. Almost all herds in the outbreak could be linked to an infected herd through cattle movements (Shaw, 2008). Bovine tuberculosis was contained in a smaller area in northwestern Minnesota classified as modified accredited (MA) (Carstensen and Doncarlos, 2011), corresponding to a prevalence inferior to 0.1% in cattle (USDA-APHIS, 2005). In 2011, the state was declared bTB free. From January 2008 to 2011, cattle movements within the MA region were recorded electronically as part of an eradication program.

The USDA recently issued a document outlining a new approach to bTB surveillance. This included the development of targeted approaches, with the objective of responding to the new challenges posed by this disease. Of greater importance are the following: most cases detected at slaughter are imported animals (mostly from Mexico), the risk for wildlife reservoirs to emerge, and the greater cost of disease control and eradication due to increased herd size and long distance cattle movements across the country (USDA-APHIS-VS, 2009c).

The objectives of this analysis are supported by the hypothesis that the assumption of randomness does not