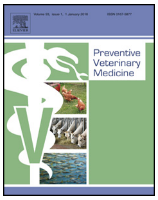
Preventive Veterinary Medicine 133 (2016) 73–83

Contents lists available at ScienceDirect

Preventive Veterinary Medicine

journal homepage: www.elsevier.com/locate/prevetmed



Bovine respiratory syncytial virus and bovine coronavirus antibodies in bulk tank milk – risk factors and spatial analysis

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ARTICLE INFO

Article history:
Received 10 January 2016
Received in revised form 29 June 2016
Accepted 3 September 2016

Keywords:
BRSV
BCoV
Risk factors
Serology
Spatial scan statistic
Dairy cattle

ABSTRACT

Bovine respiratory syncytial virus (BRSV) and bovine coronavirus (BCoV) are considered widespread among cattle in Norway and worldwide. This cross-sectional study was conducted based on antibody-ELISA of bulk tank milk (BTM) from 1347 herds in two neighboring counties in western Norway. The study aims were to determine the seroprevalence at herd level, to evaluate risk factors for BRSV and BCoV seropositivity, and to assess how these factors were associated with the spatial distribution of positive herds. The overall prevalence of BRSV and BCoV positive herds in the region was 46.2% and 72.2%, respectively. Isopleth maps of the prevalence risk distribution showed large differences in prevalence risk across the study area, with the highest prevalence in the northern region. Common risk factors of importance for both viruses were herd size, geographic location, and proximity to neighbors. Seropositivity for one virus was associated with increased odds of seropositivity for the other virus. Purchase of livestock was an additional risk factor for BCoV seropositivity, included in the model as *in-degree*, which was defined as the number of incoming movements from individual herds, through animal purchase, over a period of five years. Local dependence and the contribution of risk factors to this effect were assessed using the residuals from two logistic regression models for each virus. One model contained only the x- and y- coordinates as predictors, the other had all significant predictors included. Spatial clusters of high values of residuals were detected using the normal model of the spatial scan statistic and visualized on maps. Adjusting for the risk factors in the final models had different impact on the spatial clusters for the two viruses: For BRSV the number of clusters was reduced from six to four, for BCoV the number of clusters remained the same, however the log-likelihood ratios changed notably. This indicates that geographical differences in proximity to neighbors, herd size and animal movements explain some of the spatial clusters of BRSV- and BCoV seropositivity, but far from all. The remaining local dependence in the residuals show that the antibody status of one herd is influenced by the antibody status of its neighbors, indicating the importance of indirect transmission and that increased biosecurity routines might be an important preventive strategy.

1. Introduction

The overall health among Norwegian dairy cattle is good with few endemic infectious diseases present. Several infections, such as bovine tuberculosis, bovine brucellosis and bovine viral diarrhea (BVD), have been eliminated through successful control programs (Sviland et al., 2015a, 2015b; Åkerstedt et al., 2015). However, bovine respiratory syncytial virus (BRSV) and bovine coronavirus (BCoV) are endemic and prevalent in the national herd (Gulliksen et al., 2009). The prevalence of these infections is considered high in most parts of the world, and they cause disease problems leading to reduced animal welfare, increased use of antibiotics and financial loss for the farmer (Valarcher and Taylor, 2007; Boileau and Kapil, 2010; Sacco et al., 2014). BRSV causes respiratory disease, most often in young animals, and bronchopneumonia due to secondary bacterial infection is common (Larsen, 2000). BRSV was the most commonly isolated agent in respiratory outbreaks in cattle herds in a recent Norwegian study (Klem et al., 2014a). BCoV is the cause of calf diarrhea, respiratory disease and winter dysentery (contagious diarrhea in adult cattle) (Boileau and Kapil, 2010). Studies

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http://dx.doi.org/10.1016/j.prevetmed.2016.09.003

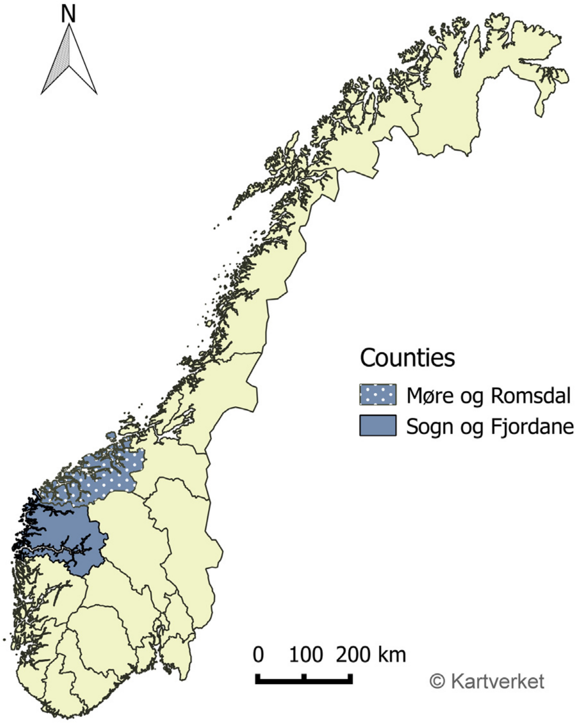

Fig. 1. Study area: Møre og Romsdal and Sogn og Fjordane county located at the northwest coast of Norway.

have shown significant effects of BCoV infection on production in terms of decreased milk yield and poor growth rate (Tråvén et al., 2001; Beaudeau et al., 2010b) which both result in economic loss.

Bulk tank milk (BTM) serology is a cheap and effective method used to screen herds for infectious diseases. However, due to long lasting seropositivity after infection, a herd will stay test-positive for many years after circulation of virus in the herd (Alenius et al., 1991; Tråvén et al., 2001; Klem et al., 2014b). Likewise, test-negative herds might have been virus free for years and serology on bulk tank milk is therefore an indicator of herd status with an inherent time-lag.

Herd level risk factors previously found to be of importance for BCoV status in Swedish dairy herds are herd size, not providing boots for visitors and geographic location (Tråvén et al., 1999; Ohlson et al., 2010). For BRSV seropositivity, herd level risk factors found to be of importance both in Scandinavia and beyond are herd size, age profile of the herd, type of production and existence of bordering cattle herds (Norström et al., 2000; Solís-Calderón et al., 2007; Ohlson et al., 2010; Saa et al., 2012).

Previous studies in Scandinavia have indicated large variations in prevalence of BRSV and BCoV between regions (Elvander, 1996; Tråvén et al., 1999; Beaudeau et al., 2010a; Klem et al., 2013), but spatial analyses involving BRSV and BCoV infections are infrequently reported. For control- and eradication purposes, locating high and low risk areas is important in order to know which control strategies should be applied to different regions. Risk factors like herd size, animal movement between herds, and proximity to neighbors are likely to vary geographically. However, it is currently not known how geographical differences in risk factors are associated with the spatial variation in prevalence of positive herds for these two viruses. Because the spatial pattern of antibody-positive herds may be largely driven by the spatial patterns of herd characteristics, such as herd size and distance to neighbors, spatial clusters of positive herds might only be reflecting the geographical distribution of known characteristics. Hence, it is of major interest to determine if adjusting for these factors changes the appearance of the spatial clusters.

BRSV and BCoV can be spread between herds by direct animal contact and indirect transmission. Direct contact includes physical contact between animals from different herds, for instance through shared pasture, or by live animal trade. Indirect transmission happens through passive transfer of animal secretions and excretions between herds by fomites like clothing or equipment.

The topography in western Norway, where the area under investigation is located, is characterized by mountains and fjords separating the herds and limiting direct contact. However, animal movements between holdings might provide an important route of transmission. *In-degree* is a measurement of animal contact which is defined as the number of incoming animal movements from individual herds, through animal purchase, over a defined time period (Nöremark and Widgren, 2014). Livestock movements are often registered in central databases which allows for calculation of *in-degree*, but factors affecting indirect transmission can be more difficult to assess because information on movement of people and biosecurity routines are not readily available in central registries. Nevertheless movement of people is associated with herd size, because larger herds have more visitors (Nöremark et al., 2013).

The aim of this study was to determine the spatial variation in herd-level prevalence of BRSV and BCoV, as measured by BTM-antibodies, across the study region in western Norway. Furthermore, the effect of the risk factors herd size, location, animal movement, and proximity to neighbors were evaluated and the effect of these risk factors on the spatial distribution of positive herds was assessed.

2. Materials and methods

2.1. Study population

This cross-sectional study was performed in “Sogn og Fjordane” and “Møre og Romsdal” counties on the west coast of Norway (Fig. 1). The region was thought to be a suitable study area because of an expected mix of BTM-positive and negative herds. One BTM sample from each of 1347 herds was collected by the dairy company (Tine, Norwegian Dairies SA), between December 2012 and June 2013. In 2013, 1854 herds delivered milk in the two counties, which means samples were collected from 73% of all eligible dairy herds. Milk samples were treated and analyzed as described in Section 2.2, and each herd was categorized as either positive or negative based on the BRSV and BCoV antibody test results, respectively. If a herd contributed more than one sample during the study period, only the result from the first sample was included. Prevalence estimates were calculated for the region as a whole and for each county separately. True prevalence was calculated using the Rogan-Gladen-estimator based on the sensitivity and specificity of the tests as specified by the manufacturer (Greiner and Gardner, 2000).

During the study period, 98% of all dairy herds were members of the Norwegian Dairy Herd Recording System (NDHRS) which provides reliable records on herd characteristics, production parameters and disease occurrence (Espetvedt et al., 2013). The medical company distributing the only registered BCoV vaccine in Norway was contacted to get information regarding the number of units sold. The use of the only registered BRSV vaccine was recorded by contacting the veterinary practitioners by phone. Veterinarians in all municipalities of the study area with more than 10 herds were contacted, covering 1295 of 1347 herds.