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A longitudinal study of the dynamics of bovine corona virus and respiratory syncytial virus infections in dairy herds

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ABSTRACT

The objective of this study was to examine the dynamics of bovine corona virus (BCV) and bovine respiratory syncytial virus (BRSV) infections in dairy herds over a 3-year period. The status of 79 dairy herds located in two Northern and two Southern Regions of Sweden were surveyed by measuring antibody concentrations to BCV and BRSV in pooled milk samples from primiparous cows, and in bulk-tank milk twice annually.

In the Southern Regions the percentage of antibody-positive herds remained persistently high (75–100%), whereas in herds based in the Northern Region, the percentage of positive herds for BCV and BRSV was 38–80% and 0–80%, respectively, with antibody levels to BRSV decreasing over time. Pooled milk samples of 'home-bred' primiparous animals were found to be most useful in terms of monitoring herd status but could gradually be replaced by bulk-tank sampling once freedom from infection was established.

Introduction

Bovine corona virus (BCV) and bovine respiratory syncytial virus (BRSV) are significant pathogens of both beef and dairy cattle worldwide (Clark, 1993; Valarcher and Taylor, 2007). A survey in England and Wales based on virus antibody concentrations in bulk-tank milk (BTM) samples, found prevalences of 100% (Paton et al., 1998). BCV can cause diarrhoea in calves and winter dysentery in adult cattle as well as respiratory disease of variable severity (Stair et al., 1972; Saif et al., 1986; Saif, 1990; Alenius et al., 1991). Infection with BRSV can lead to outbreaks of severe respiratory disease (Verhoeff et al., 1984; Elvander, 1996; Viuff et al., 1996).

Outbreaks of both viral infections typically occur during the housing (winter) period (Stott et al., 1980), and it remains unclear how the virus survives during the intervening seasons. It is possible that factors such as latency/reactivation, low level circulation of virus within and/or between herds or reservoir hosts may play a role. Sequencing indicates that virus within herds during an outbreak is identical, but varies both temporally and spatially between outbreaks, suggesting that outbreaks are caused by 'new' virus rather than through latency or the existence of carrier animals (Larsen et al., 2000; Liu et al., 2006; Bidokhti et al., 2012).

Both infections have significant negative effects on both herd health and animal performance (Tråvén et al., 1999; Beaudeau et al., 2010; Ohlson et al., 2010a) and there is a clear association between higher levels of herd biosecurity levels and lower prevalence of herd infection (Ohlson et al., 2010b). In order to control these infections better, it is important to clarify further some aspects of their epidemiology and to evaluate the accuracy of diagnostic procedures. To the authors' knowledge, very few longitudinal studies charting the epidemiology of BCV and BRSV infections in cattle herds have been performed. Van der Poel et al. (1993) investigated BRSV infection in six dairy herds over a 1-year period and found a rise in titres but not seroconversion in antibody-positive animals during the summer period. Hägglund et al. (2006) conducted a 1-year serological study of calves in a region of southern Sweden where both BCV and BRSV are endemic and found seroconversion to occur in animals mainly during the winter.

The within-herd spread of both BCV and BRSV is highly effective with the result that all susceptible animals typically become infected (Alenius et al., 1991; Hägglund et al., 2006; Bidokhti et al., 2009). Sampling a subset of young animals has previously been used in testing for bovine viral diarrhoea virus (BVBV) (Houe, 1992). Bulk tank milk (BTM) is also convenient way of monitoring infection status in dairy herds, and the relationship between the BTM antibody titre and the serological status of young animals has previously been evaluated for BVDV (Houe, 1994). However, such an approach has not been used to investigate if there is an association between BTM antibody concentrations and the serological status of young animals to BCV or BRSV.

The main objective of this study was to investigate the dynamics of BCV and BRSV infection in dairy herds and to assess if these

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dynamics varied between geographical areas. The antibody status of 79 herds located in four regions of Sweden was recorded over a 3-year period. A secondary aim was to evaluate if there was an association between the percentage IgG positivity in BTM samples, and the antibody status of younger cows in order to determine if the former could be used as an estimate of the latter.

Materials and methods

Study population

Four study areas within the counties of Halland, Gotland, Jämtland and Västerbotten were selected (Fig. 1). The selection was based on previously estimated differences in herd prevalence of antibodies in BTM samples, and on regional differences in herd density. The prevalence of antibodies in BTM was estimated to be 90–94% and 84–89% in Halland, 95–100% and 84–89% in Gotland, 75–79% and 41–51% in Jämtland, and 70–74% and 41–51% in Västerbotten to BCV and BRSV, respectively (Elvander, 1996; Tråvén et al., 1999). The corresponding herd densities in 2006 were 0.09, 0.11, 0.005 and 0.007 herds/km^2, respectively (Swedish Board of Agriculture, 2007).

A sample of 20 herds was selected from each area: 10 herds with 30–80 cows and 10 with >80 animals. These represented 'average' and 'large' sized herds under current dairy farming conditions in Sweden (the mean herd size in Sweden was 48 in 2006).

The vast majority of Swedish dairy herds have a non-seasonal calving pattern, and vaccines against BCV and BRSV are rarely used. Herds were eligible for inclusion in the study if their owners were members of the local livestock association and had enrolled in the National Animal Disease Recording System (Emanuelson, 1988), and Swedish Official Milk Recording Scheme (Olsson et al., 2001). Currently >90% of Swedish dairy cows are enrolled in these programs (Mörk et al., 2010). Selected herds were geographically spread over the selected areas, were included once farmer consent was obtained, and were routinely visited by personnel from the local livestock association. Vaccination against BRSV and BCV was not used in participating herds and all were free of BVDV infection as defined by the Swedish eradication program (Lindberg and Alenius, 1999). The herds were also included (in the spring sampling of 2008) as a part of a risk factor study (Ohlson et al., 2010b).

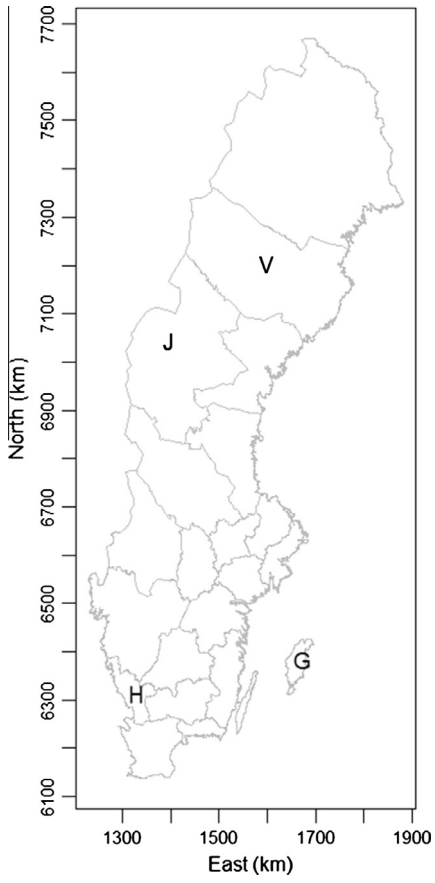

Fig. 1. Map of Sweden illustrating the boundaries of the four areas surveyed. H, Halland; G, Gotland; J, Jämtland; and V, Västerbotten. Map created using *R* statistical package (TEAM, 2008).

Using farm location details provided by the Swedish Board of Agriculture in 2005, kernel smoothing techniques were applied to illustrate the spatial distribution of dairy farms throughout Sweden, expressed as the number of farms/100 km^2. These analyses were based on a regular grid of 2578 × 2578 cells calculated using the Spatial Analyst extension in ArcGIS (version 9.3, ESRI). The bandwidth parameter for the kernel function (used to control the amount of smoothing of the estimated density surface) was fixed at 30 km, and was calculated using the normal optimal method (Bowman and Azzalini, 1997). The locations of the 79 herds were superimposed on this plot to demonstrate the spatial distribution of the study herds relative to the overall national distribution of at risk herds (Fig. 2).

Sampling procedures

Herds were sampled before (September–October) and after (April–May) the housing season for three consecutive years (from September 2006 to May 2009). For each herd, on each sampling occasion, a pooled milk sample was collected from the five youngest home-bred primiparous cows, and a BTM sample was also obtained, which included milk from the sampled primiparous animals. Sampling was performed by personnel from the local livestock association. Ten millilitre test tubes containing 1.5 mg of the preservative bronopol (2-bromo-2-nitropropane-1.3-diol) were used and samples were not diluted or centrifuged and were stored at −20 °C until analysed. There were 432 pooled samples in total with corresponding BTM samples. Farmers were informed of the antibody status of their herd by mail after each sampling, based on the results obtained from the pooled primiparous cow sample. Herd owners also received basic information regarding the clinical signs and transmission routes of BCV and BRSV infection, as well as advice on biosecurity.

Milk analysis

Samples were analysed for IgG to BCV (Alenius et al., 1991) and BRSV (Elvander et al., 1995) using commercially available indirect ELISAs (Svanovir BCV-Ab and BRSV-Ab, Svanova Biotech). Test sensitivity was estimated at 84.6% (BCV) and 94.6% (BRSV), respectively, and specificity at 100% for both (individual samples, Svanova Manual). There were no data relating to herd sensitivity/specificity for BTM samples. The optical density (OD) at 450 nm was corrected by subtraction of the negative control antigen OD. To adjust for possible day-to-day variation in analysis, the percentage positivity (PP) was calculated as (corrected OD/positive control corrected OD) × 100. For the BTM samples, a PP value of <5 was considered negative. This corresponded to the corrected OD of 0.05, with the positive control having an OD of '1'. This cut-off had previously been used to detect antibodies to BCV and BRSV in BTM (Elvander, 1996; Paton et al., 1998; Hägglund et al., 2006). For the pooled milk samples a PP < 20 was deemed negative, closely corresponding to the corrected OD of 0.20, the cut-off for negative individual samples for both BCV and BRSV, as recommended by the manufacturer.

Assessment of infection dynamics

Changes in test results from <20 to >20 for primiparous animal sample pools, and from PP < 5 to PP ⩾ 5 for BTM samples, were classified as a change in herd status from antibody negative to positive and the reverse situation resulted in herds changing from positive to negative status.

Statistical analysis

A Kruskal–Wallis equality-of-populations rank test was used to compare median herd size between the areas for each of the two herd-size groups, and also to compare median PPs in BTM between negative and positive herds based on the primiparous pooled sample. The proportion of positive herds in each region on each sampling occasion was compared using a Fisher's exact test. The association between herd antibody status to BCV and BRSV was evaluated using the χ^2 test, repeated for each sampling occasion.

Results

Of the 79 herds initially sampled in the autumn of 2006, 73 remained in the study for the duration of the survey period and six dropped out as the farms ceased milk production. Two additional herds entered the study: 'Halland' in spring 2007 and 'Jämtland' in autumn 2007. For the Gotland region, samples during the autumn 2008 period were lost during transport. Fig. 2 illustrates the distribution of the selected herds and the herd densities in these areas. Median herd size at the start of the study was 45 for the 30–80 group and 110 for the >80 sized herds: there were no