

Estimation of the basic reproductive ratio (R_0) of BoHV1 on field data

Transmission in Dutch dairy herds in past and present

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Objective of the study

In the Netherlands, bovine herpesvirus 1 (BoHV1), the causative agent of infectious bovine rhinotracheitis (IBR), is endemic. The basic reproductive ratio (R_0) of an infection is the number of cases one infectious individual generates on average over the course of its infectious period, in a fully susceptible population. The R_0 of BoHV1 is an important parameter for the design of future control programs. The aim of this study was to estimate the R_0 of BoHV1 on recent field data of dairy herds with an IBR outbreak and to compare it to earlier estimates of the nineties.

Background

Since the nineties, the Dutch dairy industry has gone through a substantial change. The average herd size doubled and when earlier the whole herd was housed in one building, nowadays the subgroups within a herd (e.g. calves, heifers, dry cows, lactating cows) are often housed in separate units or even in other herds. There is a growing number of young stock raisers that focus exclusively on the raising of replacement heifers. A mandatory national BoHV1 eradication program has been in place for a short period from 1998 to 1999 and was cancelled due to vaccine contamination issues. Since then, farmers could voluntarily participate in an IBR control program. A new plan for mandatory BoHV1 eradication on dairy farms started on April 1st, 2018.



Methods

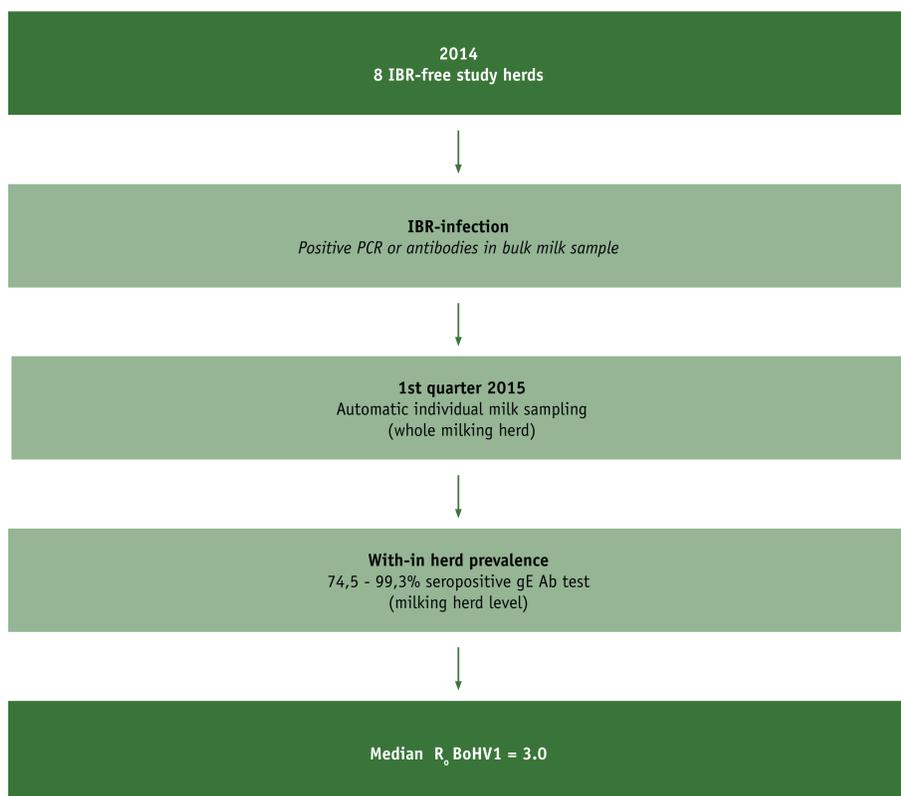
For this study, all lactating cows in eight dairy herds that lost their 'IBR-free' status in 2014 (either because of positive BoHV1 PCR on nasal fluid or antibodies in bulk milk sampling) were sampled in individual milk for antibodies (IDEXX IBR gE Ab Test) in the beginning of 2015. Information from the national identification and registration database was used to determine herd size and cattle movements of the herds. The proportion of positive BoHV1 samples in each herd was used to estimate the R_0 of BoHV1 with a deterministic final size model.

Results

The selected herds had on average 118 milking cows, which was significantly larger than the average Dutch dairy herd with 98 milking cows. In the year before the outbreak, 50.0% of the herds purchased cows and 87.5% grazed their cows, which was slightly higher than the Dutch average of 47.3% and 75.0%, respectively. In all outbreak herds, the percentage of infected animals was high and varied from 74.5% to 99.3%. Nevertheless, these large outbreaks often were subclinical. The low number of seronegative animals were mostly young heifers that were added to the milking herd after the epidemic had ceased. The average time between the outbreak and sampling was 8.2 months (range 4.4 to 14.2). A longer period may have resulted in an underestimation of the herd prevalence on farm level because some seropositive cows might have been replaced by naive heifers. The infection seemed often limited to the lactating herd and did not spread to young stock, thereby forming a new susceptible group for reactivating cattle. The median R_0 in this study was 3.0 (range 1.8 to 5.1). This number was comparable to earlier scientific work on the basic reproductive ratio of BoHV1 about twenty years ago.

Conclusion

BoHV1 spreads fast within a herd ($R_0=3.0$) and most lactating animals became infected. When compared to transmission studies in the nineties, it seems that the initial spreading of IBR within an uninfected population is not different in small or large herds. The current R_0 can be used for future modelling and communication purposes.



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