Interpretation of Spot Test Results in BVD Prevalence Survey

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ABSTRACT

Targeted disease control at population level requires the identification of infected herds. Spot testing offers advantages both with respect to practicability and effective use of resources. Depending on the biology of the pathogen and the diagnostic test used, the optimum number of animals per spot test may differ. For many endemic diseases the presence of a low number of previously exposed animals does not provide evidence of an active infection in the tested herd. A Bayesian finite mixture modelling approach is presented to make optimal use of information provided by spot tests. The method accounted for within and between herd variability and allowed for diagnostic test classification error. Applying a mixture model to data collected for a cross-sectional study estimating the seroprevalence of bovine viral diarrhoea virus (BVDV) in Scottish beef suckler herds, three distinct exposure cohorts were identified: young stock with no evidence of recent exposure to BVDV; young stock with a seroprevalence between 26 and 39%; and young stock with a very high seroprevalence. The different exposure cohorts differed in various aspects, e.g. farms with a seronegative spot test tended not to house cattle on premises away from the home farm whereas herds with a high BVDV seroprevalence amongst young stock tended to show BVD related health issues. The method presented makes best use of the data available and seems attractive for surveys where sampling variability within and between herds is expected.

KEYWORDS

Spot test, cut-off value, within herd seroprevalence, BVD

INTRODUCTION

Robust prevalence estimation is a necessary step in defining appropriate disease control measures at the population level. Sampling all herds or flocks, let alone testing all individuals comprising a population is seldom feasible. Spot testing, using a subgroup as a proxy for a herd or flock, offers advantages both with respect to practicability and effective use of resources (Houe, 2006). Such an approach, however, relies on an appropriate interpretation protocol to classify the infection status of an animal group. Defining such a classification system is additionally complex when based on a single serological test, which *per se* does not allow a differentiation between a current and historic infection of individual animals in the spot test.

The result of a spot test is interpreted by defining cut-off values which take into account the characteristics of the diagnostic test used and the biology of the disease (Donald et al., 1994). Defining a single cut off value for the simple distinction between previously exposed and unexposed herds makes poor use of the available data by reducing the results of a group of animals to a single binary outcome. Extensive empirical experience may justify more elaborate interpretation keys (Table 1); however both mentioned methods lack formal validation on whether the cut-off values are relevant and justifiable. We present a formal approach for the interpretation of spot test results emphasising the added value of using more than a single cut off value.

Material and Methods

To avoid arguably arbitrary cut-off values, separating infected from non infected groups, we use a Bayesian finite mixture modelling approach (Diebolt and Robert, 1994) to interpret spot test results. There were two distinct levels of sampling variability which had to be modelled for such analysis to be robust: within and between herd sampling variability. We do not ask how many farms show evidence of exposure to a pathogen (e.g. 1 or more seropositive animals), but rather ask how many distinct exposure cohorts can be identified in the study population (e.g. one, two or more distinct exposure cohorts). The latter question is of greater epidemiological value as it makes better use of all data, potentially allowing for more than just a binary separation into an exposed and unexposed group. We used Bayesian latent class methods to develop a mixture model comprising either binomial or beta-binomial densities with an explicit disease free cohort. Starting with a single seroprevalence cohort, models with increasing numbers of prevalence cohorts were fitted (including with and without the disease free cohort) and their goodness of fit to the data compared using Bayes factors. The method also accounted for classification error from the diagnostic tests (Joseph et al., 1995). We adopted non-informative priors for all model parameters.

We used data from a cross-sectional study estimating the prevalence of active bovine viral diarrhoea virus (BVDV) infection in Scottish beef suckler herds. BVD is an endemic condition of cattle, inflicting substantial losses to both beef and dairy enterprises worldwide. Data was collected from 301 beef suckler herds using a stratified random sampling design based on agricultural census data. Blood samples from typically 10 animals per herd were serologically tested for previous exposure to BVDV and a standardised questionnaire on general farm management as well as specific animal health aspects was conducted.

Results

Our mixture model has optimal goodness of fit when the model comprises three cohorts, with the explicit inclusion of a disease free cohort (Figure 1). The properties of these three cohorts include: i) cohort 1 consists of herds with young stock which show no evidence of former exposure to BVDV; ii) herds in cohort 2 have young stock with a median seroprevalence between 26.3% and 38.5%; iii) herds in cohort 3 have young stock with a median seroprevalence between 91.9% and 99.8%. Cohort 3 shows strong evidence for active infection; in the case of BVD this can be interpreted as previous or current presence of a persistently infected (PI) animal in the sampled herd.

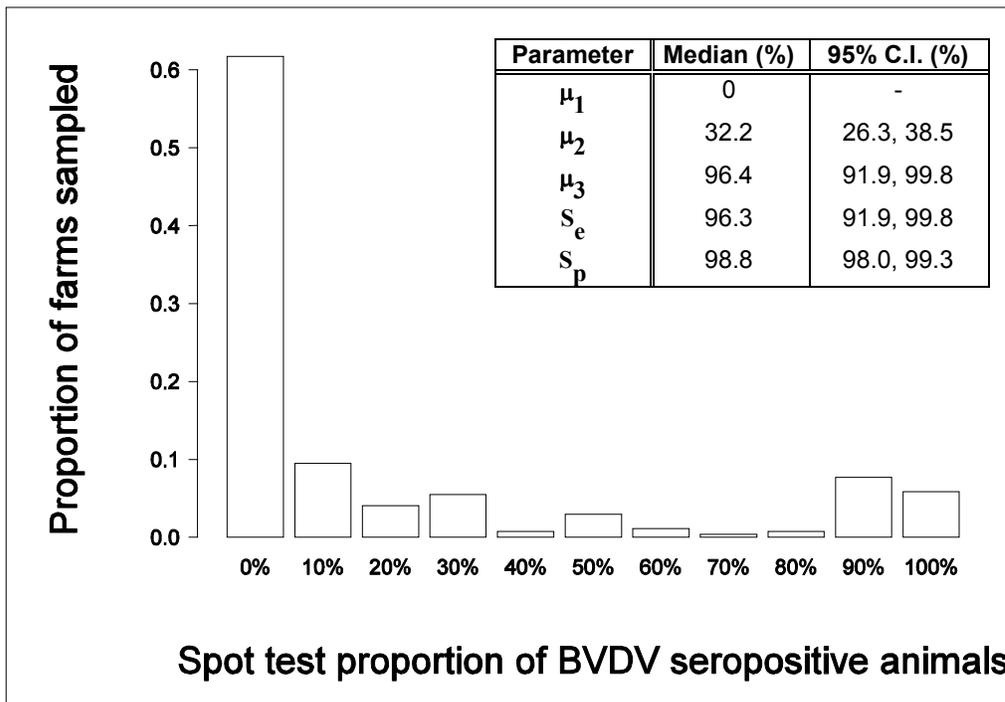| Parameter	Median (%)	95% C.I. (%)
μ_1	0	-
μ_2	32.2	26.3, 38.5
μ_3	96.4	91.9, 99.8
S_e	96.3	91.9, 99.8
S_p	98.8	98.0, 99.3

Figure 1: Observed spot test results from young stock on 301 Scottish beef suckler herd with mixture model parameter estimates. The estimated BVDV seroprevalence in each of the three observed cohorts are denoted by μ_1, μ_2, and μ_3; mean diagnostic test sensitivity by S_e and specificity by S_p.

Various management practices were distributed neither in a balanced way between the three exposure cohorts nor proportionally to the number of exposed animals in individual herds. For example, presence or absence of the following covariates characterised the different cohorts. Herds of cohort 1 tended not to house animals away from the home farm, herds in cohort 2 generally did not restrict access to the farms and farm managers of cohort 3 herds were more likely to believe that their cattle were affected by BVD.

Discussion

An empirical classification protocol based on spot tests comprising 10 young stock developed by the SAC Premium Cattle Health Scheme identifies five categories including categories where a biosecurity failure is suspected with increasing likelihoods of having a PI animal in the tested group (Table 1). Houe (2002) reports that for the identification of herds with and without PI animals, spot tests comprising 5 animals offer a high degree of accuracy. The method presented above allowed the identification of three cohorts when applied to the described survey data. Depending on the aim, the optimal sample sizes for spot tests vary and the proposed method assists an assessment of how detailed an interpretation is supported by the collected data.

Table 1: Empirically evolved interpretation protocol developed by the SAC Premium Cattle Health Scheme for spot tests comprising 10 randomly sampled animals in the age range 8 to 12 months, assuming the samples were taken from an animal group that had been managed as one unit for several months.

Spot test result	Interpretation
All samples are BVDV seronegative	There is no evidence of exposure to bovine viral diarrhoea Virus (BVDV) infection in the tested group, i.e. the animals of this unit have never been in contact with animals infected with BVDV.
Less than 3 animals are BVDV seropositive	There is evidence of exposure to BVDV infection on the farm. This may be due to a failure in biosecurity or the presence of a persistently viraemic animal elsewhere on the farm. It is unlikely to be due to the presence of a persistently viraemic animal in the tested group.
3 to 5 animals are BVDV seropositive	Comment as above, but the probability of a persistently viraemic calf in the tested group is higher.
More than 5 animals BVDV seropositive	There is evidence of exposure to BVDV infection and there is a high probability of a persistently viraemic animal being present in the tested group.
More than 5 animals are positive for BVDV antibody, but with low titres	These results are consistent with group vaccination against BVDV, with no evidence of recent exposure to active BVDV infection.

CONCLUSION

Our objective was to infer the distribution of within herd BVDV seroprevalence across all young stock in beef suckler herds in Scotland. This distribution was used to define herds in which recent active infection with BVDV was very likely. The observed sample data supports the discrimination of three distinct seroprevalence cohorts. Therefore the method presented seems attractive for surveys where sampling variability within, as well as between, herds or flocks is expected.

The analysis of farm data showed that various management practices were distributed neither equally between the three exposure cohorts nor proportionally to the number of exposed animals in individual herds. The different seroprevalence cohorts were distinctively characterised by the presence or absence of specific risk factors for disease transmission, an observation which supports the existence of at least three different categories of herds, where each category might play a different role in the survival of endemic disease at the population level.

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