Estimating diagnostic accuracy of the tuberculin skin test and abattoir meat inspection from bovine tuberculosis surveillance data

AIM: To extend the Bayesian formulation of the Hui-Walter latent class model to estimate diagnostic test parameters and true prevalence of bovine TB from surveillance data

INTRODUCTION

Bovine tuberculosis (bTB): serious disease of cattle
- Causative agent: Mycobacterium bovis
- Detection: single intradermal comparative tuberculin test (SICTT), supported by abattoir surveillance (1; figure 1)
- Heritability on the liability scale of SICTT responsiveness
  > 0.14 in Irish and 0.16 in British Holstein-Friesian (HF) dairy cattle (2,3,4)
- Diagnostic measures of SICTT accuracy
  - Specificity: ability to correctly identify infected cattle ~99.2-99.9% (1, 5)
  - Sensitivity: (ability to correctly identify non-infected cattle) ~72.0-100.0% (1, 5)
  - Imperfect accuracy results in misclassification of risk within breakdowns
  - Underestimation of heritability on the liability scale (6)

Aims:
- Extend the Hui-Walter latent class model: Bayesian framework of no ‘gold standard’ diagnostic test (7)
- Estimate diagnostic parameters and true prevalence from bTB surveillance data & infer true heritability

RESULTS

Table 1. Parameter estimates of diagnostic accuracy (with 95% Bayesian credibility intervals (95% BCI)) for the single intradermal comparative tuberculin test (SICTT), under ‘standard’ interpretation, a positive result is recorded when the Mycobacterium bovis-antigen response is more than 4mm greater than the M. avium-antigen response) and abattoir inspection from the conditional independence model including breakdown specific diagnostic parameter estimates.

Figure 1. Apparent Mycobacterium bovis infection prevalence (black spots) and superimposed estimated posterior mean of true prevalence (red line) with 95% Bayesian credibility intervals (broken grey lines) from the 409 herd breakouts in this study.

CONCLUSIONS:

- This study provides an extended Hui-Walter latent class model:
  - Estimation of diagnostic test parameters/true prevalence from bTB surveillance data (Table 1)
  - Assessment of diagnostic test performance at the population level
  - Estimates of test performance are within published range (1, 5)
  - Apparent prevalence are likely to be underestimated (Figure 1)
  - Correcting the heritability with diagnostic parameter estimates
  - True heritability estimates for SICTT responsiveness in the GB/Ireland of 0.16/0.19
  - Genetic variation > than initially estimated from surveillance data

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