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Estimating diagnostic accuracy of the tuberculin skin test and abattoir meat inspection from bovine tuberculosis 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
- Sensitivity (ability to correctly identify infected cattle) ~52.0-100.0% (1, 5)
- Specificity (ability to correctly identify non-infected cattle) ~99.2-99.9% (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



Surveillance of bovine tuberculosis (bTB) in Northern Ireland. The single intradermal compa Figure 1 A-C. Surveinance of bovine tuberculoiss (of 16) in Normer Ireland. The single intradermal comparative tuberculuin test (SICTT; A) involves separate intradermal injection of *Mycobacterium bovis* and *M. avium* antigens, and vorks on the premise that *M. bovis*-infected cattle tend to show a greater response to *M. bovis* than to *M. avium* antigens, whereas infection with other *Mycobacterium* spp. promotes the inverse. The SICTT skin change, the difference in response or reaction to the *M. bovis* and *M. avium* antigens, is measured 72 h after injection, whereby the size of the *M. avium* creation (**B**) is taken from that of the *M. bovis* antigens reaction. All test reactor cattle are compulsorily slaughtered, and undergo abattor inspection of animals for tuberculosis lesions at slaughter (C). Furthermore abattor meat inspection of all cattle at cluments for tuberculosis lesions and snaping TB control programme in *Northore*. slaughter for tuberculosis lesions is an integral part of the ongoing TB control programme in Northern Ireland

1) 73.000 HF dairy cows

- 2) 409 Northern Ireland (NI) HF bTB breakdowns 1995 -2010
- 3) Unrecorded data: not all cows with SICTT records had associated abattoir records

MATERIALS AND METHODS

- > Excluded abattoir records > 45 days of a positive SICTT result
- Reason: could not be certain when cows became infected
- 4) Hui-Walter no gold standard latent class methodology extended 2 additional multinomial counts: SICTT +/- cows have no abattoir record > Allow for breakdown specific variation in diagnostic sensitivity
- 5) Analyses in WinBUGS and R2WinBUGS package



Table 1. Parameter estimates of diagnostic accuracy (with 95% Bayesian creditability 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 breakdowns 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)
 - \rightarrow 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 Extended methodology applications:
- → Epidemiological analysis of other human/animal diseases with incomplete surveillance data for ≥ 2 tests

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