Bayesian accuracy estimates of environmental sampling for determining herd paratuberculosis infection status and its association with the within-herd prevalence in Québec dairy herds

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BACKGROUND

Environmental sampling (ES) is the most cost-effective diagnostic strategy to determine paratuberculosis herd status. In Canada, two studies have reported Bayesian accuracy estimates for ES. However, there are no reports about diagnostic accuracy of ES in the Québec context where small herds (average herd size = 76 cows), mostly housed in tie-stall barns (91%) are predominant (Canadian Dairy Information Center, 2021). Further, MAP herd-level prevalence has been suggested to be lower in Québec than the rest of Canada (Kelton et al., 2016; Corbett et al., 2018).

OBJECTIVES

1) Estimate the sensitivity (Se) and specificity (Sp) of bacterial culture of ES for determining MAP infection status in Québec dairy herds, using a Bayesian Latent Class Model (BLCM)
2) Explore the association between the number of positive environmental samples and apparent and true MAP within-herd prevalence based on individual fecal culture (IFC).

MATERIALS AND METHODS

Study design and sample collection: Retrospective analysis of environmental and individual fecal samples collected from 87 Québec dairy herds.

Participant herds		
Study source	Herds from a case-control study (n=53)	Herds from another studies (cross-sectional; cohort) (n=34)
Individual sampling (IFC)	Random sample of 30 cows, ≥2 lactations	All the adult cows, ≥1 lactation
Environmental sampling (ES)	6 samples (manure pit x 2, gutter x 2, other site of manure accumulation x 2)	6 samples (manure pit x 2, gutter x 2, other site of manure acumulation x 2)
Positive MAP herd status	≥ 1 positive sample (either IFC or ES)	≥ 1 positive sample (either IFC or ES)

Bacterial culture: MGIT Para TB culture liquid media and the BACTEC MGIT 960 system (Becton, Dickinson and Company).

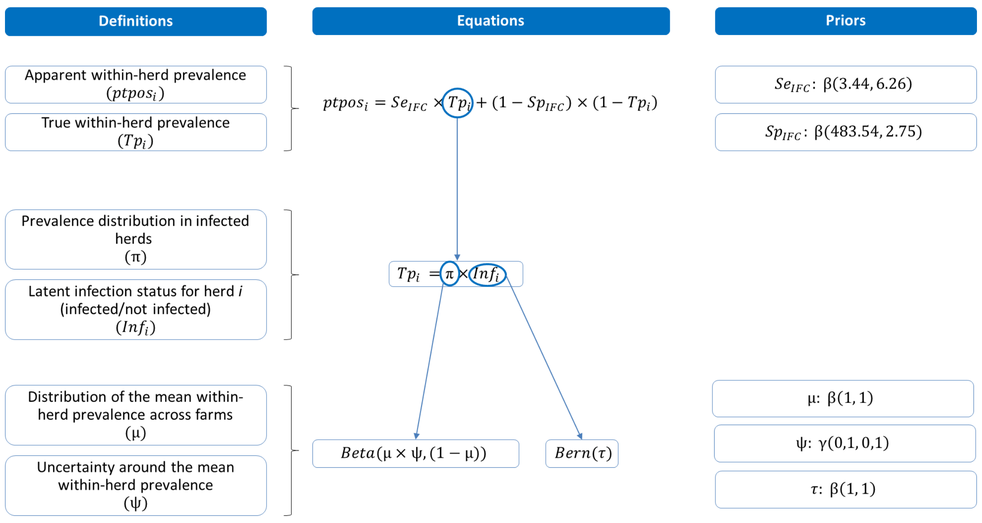
Statistical analyses:

Objective 1 (Se and Sp of ES): A one-test-one-population BLCM. Informative prior information for ES Se and Sp, and MAP herd-level prevalence in Québec (Corbett et al., 2018).

Objective 2:

a. Apparent and true within-herd prevalence

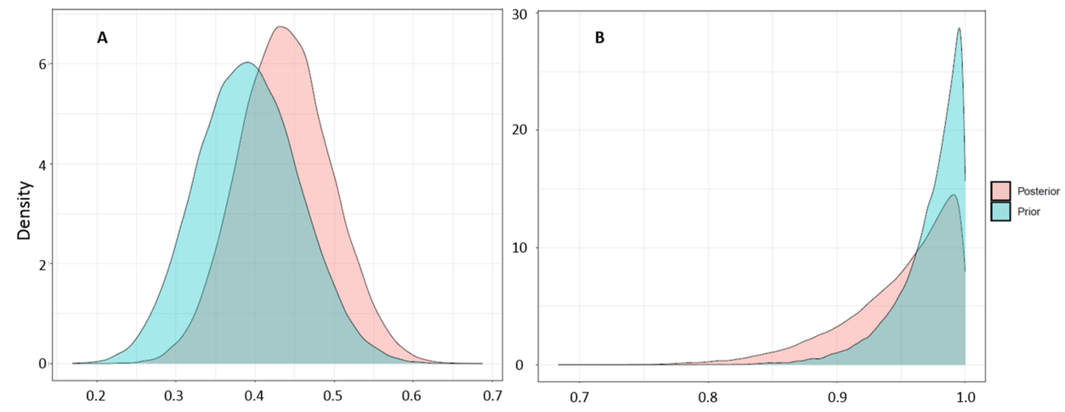
Model and priors: Two-stage cluster BLCM. Informative priors for IFC Se (median = 34.4%; 97.5th percentile = 66.1%) and Sp (median = 99.5%; 2.5th percentile = 98.6%) (Arango-Sabogal et al., 2018).



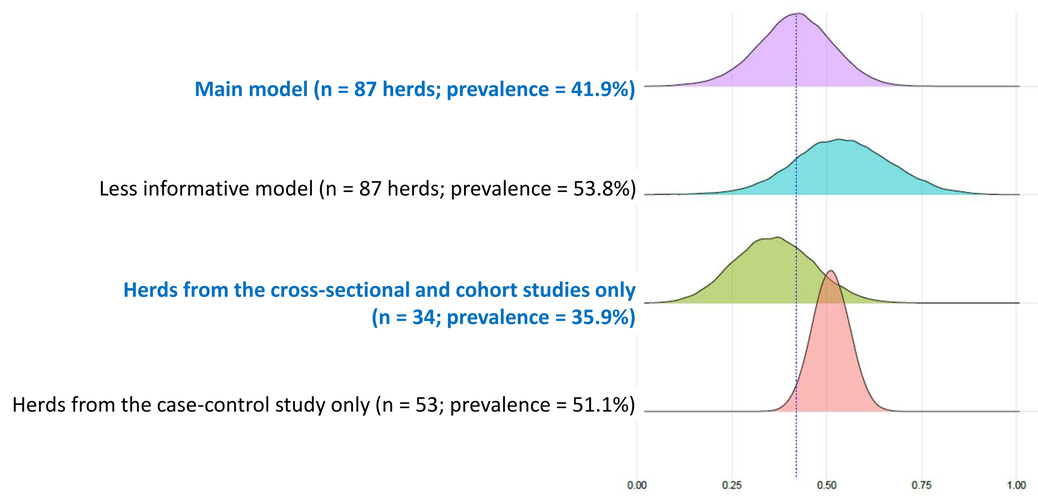
b. Association between withing-herd prevalence and ES: Zero-inflated negative binomial (ZINB) model.

RESULTS

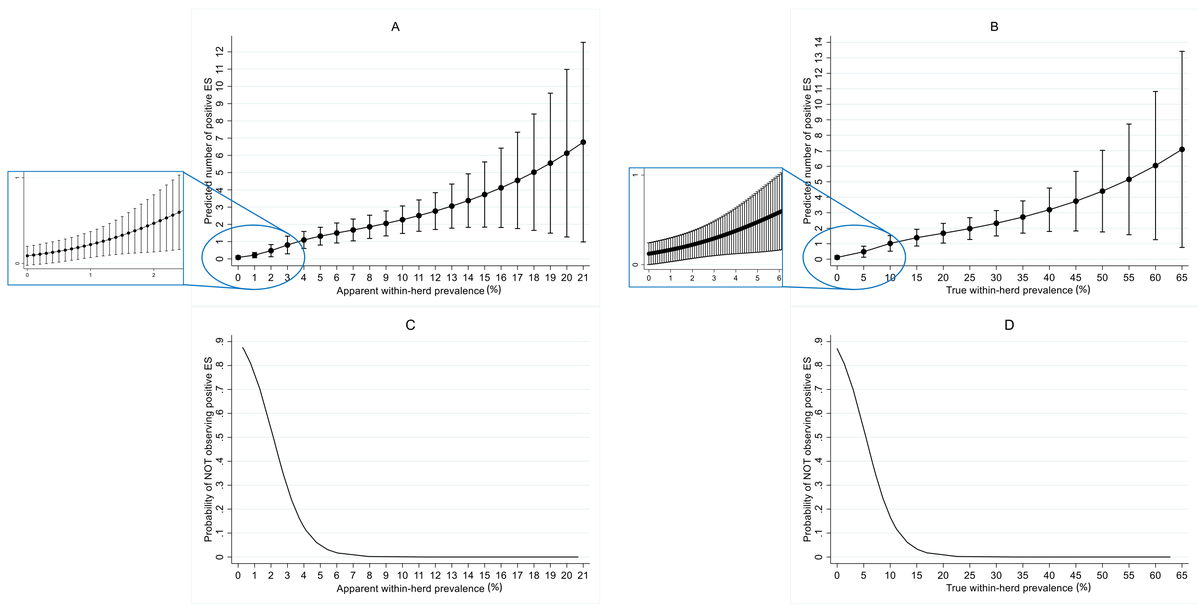
Prior and posterior densities for **Se** (A) and **Sp** (B) of ES.



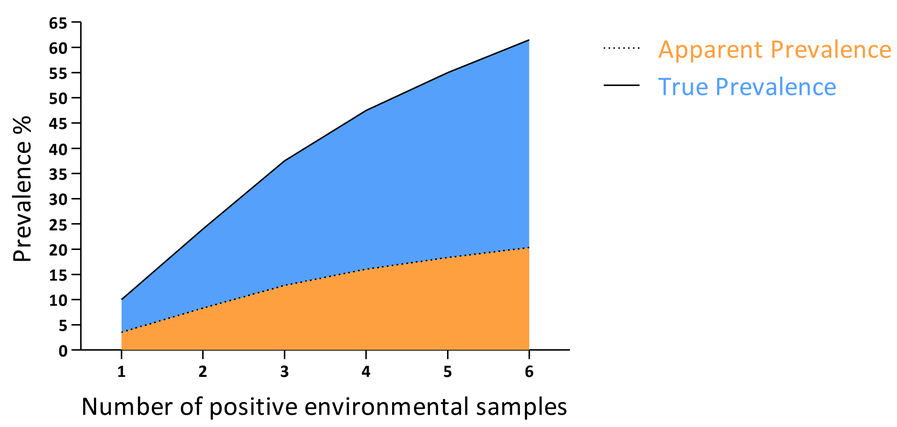
Posterior densities for **MAP herd-level prevalence** determined using ES.



Predicted number of positive ES (A, B) **and predicted probability of not observing positive ES** (C, D) as a function of the apparent (A, C) and true (B, D) within-herd prevalence.



Apparent (orange) **and true** (blue) **within-herd prevalence for a given number of positive ES.**



CONCLUSIONS

- Number of positive ES increased with the within-herd prevalence.
- Herds with no positive ES are likely to have a true within-herd prevalence lower than 5.9% but not necessarily MAP exempt.
- Despite its lower Se, ES is an inexpensive and non-invasive method to determine herd status and can be used as a proxy to estimate the true within-herd MAP prevalence.

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