Bayesian estimation of true herd-level prevalence of *Salmonella* Dublin and factors associated with its positivity in dairy herds in Alberta, Canada

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Background

Salmonella enterica subsp. *enterica* serovar Dublin (*Salmonella* Dublin) is a multidrug resistant pathogen adapted to cattle. Up-to-date prevalence is essential for designing and monitoring control programs.

Bulk tank milk has been used as a tool for surveillance of *Salmonella* Dublin, but imperfect test sensitivity and specificity require estimation of true prevalence. Bayesian latent class analysis accounts for test imperfection and uncertainty.

Objective

The objectives of this study were to:

- Estimate true herd-level prevalence of *Salmonella* Dublin in Alberta dairy herds

- Determine association of *Salmonella* Dublin positivity with herd characteristics

Methods

- Bulk tank milk samples were collected from all active dairy producers in Alberta twice (Jun and Dec 2024) and tested for antibodies against *Salmonella* Dublin, using PrioCheck ELISA with cut-off ≥35%

- Bayesian latent class model implemented to estimate true prevalence using JAGs via `R2JAGS` package in R assuming that observed test positivity (AP) was a function of sensitivity (Se), specificity (Sp) and true prevalence (TP) as follows:

$$AP = (Se \times TP) + [(1 - Sp)(1 - TP)]$$

Priors were assigned as follows: [a, b]

$Se \sim dBeta(\alpha_{Se}, \beta_{Se})$ where α and β parameters
$Sp \sim dBeta(\alpha_{Sp}, \beta_{Sp})$ were derived by specifying prior mode and 95% CI
$P \sim dBeta(\alpha_{P}, \beta_{P})$ using `epi.betabuster` function

Markov Chain Monte Carlo (MCMC) simulations with 4 chains using 55,000 iterations per chain with 5,000 burn-in was used, convergence assessed via traceplots and sensitivity analysis was performed using alternate priors

- Associations of herd positivity (2024) with herd characteristics and with prior *Salmonella* Dublin status (2021-22) were assessed by computing prevalence ratios (PR) using log binomial regression models
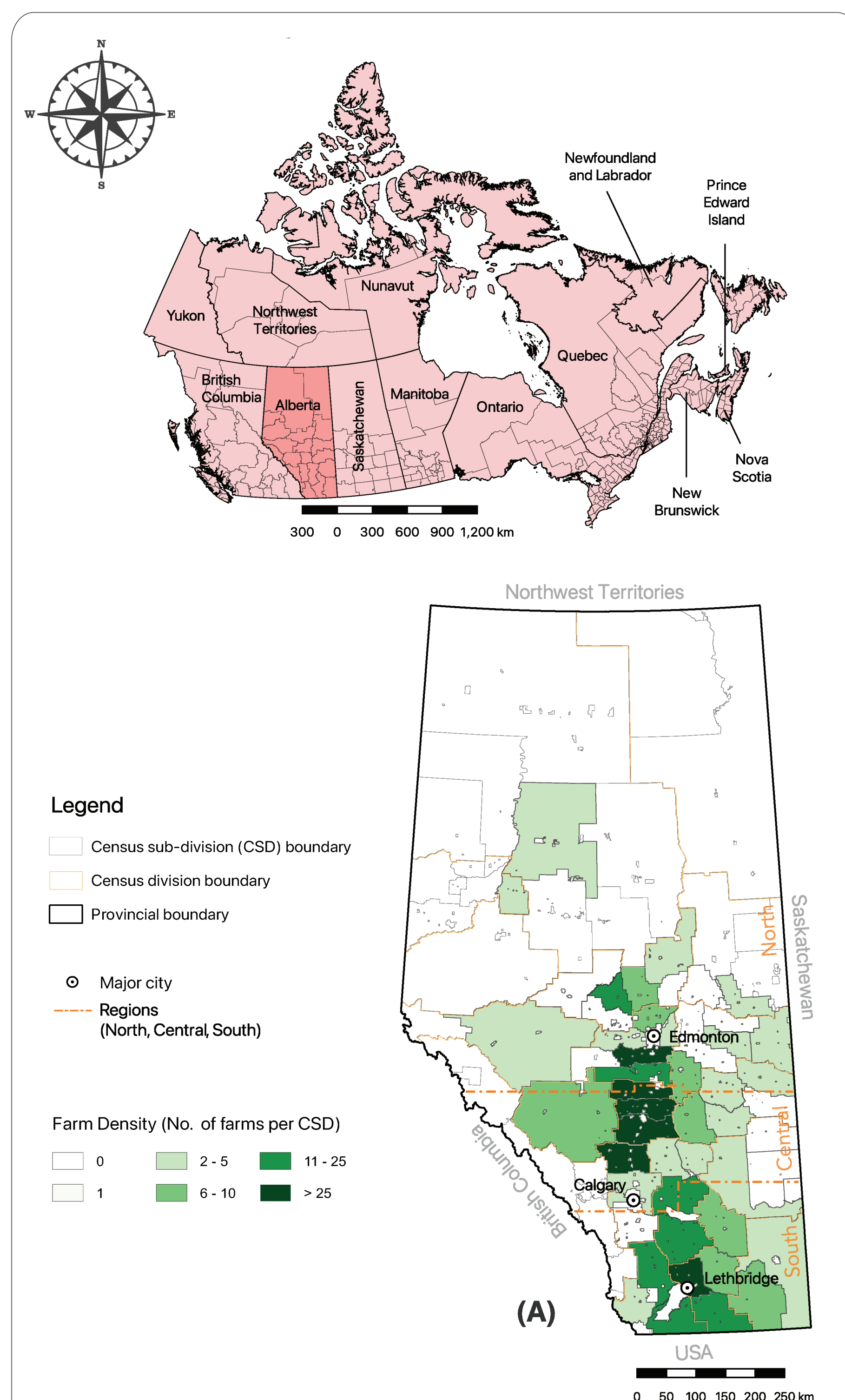

Figure 1. Spatial distribution of dairy farms in 3 regions across Alberta, Canada

Results

Farm density varied across census subdivisions of Alberta (Figure 1).

True herd-level prevalence was 9.2% (95% BCI: 6.7 - 12.1) in June 2024 and 11.8% (95% BCI: 9.1 - 14.9) in December 2024 (Figure 2).

South-region herds and non-Hutterite colony herds were more frequently positive. Herds that were more frequently positive in 2021-22 were more likely to test positive in 2024 (Figure 3).
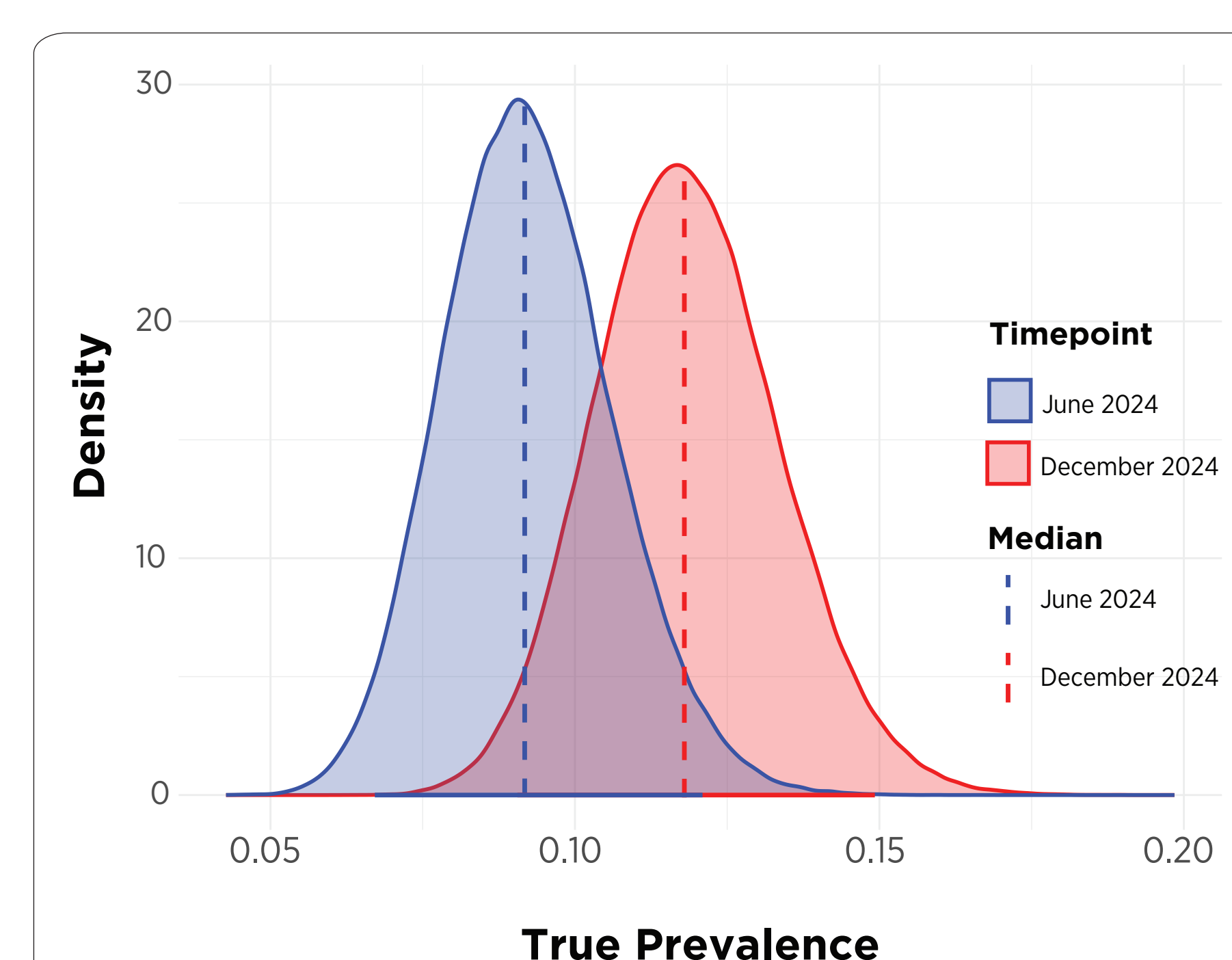

Figure 2. Posterior density of the true prevalence of *Salmonella* Dublin in Jun and Dec 2024
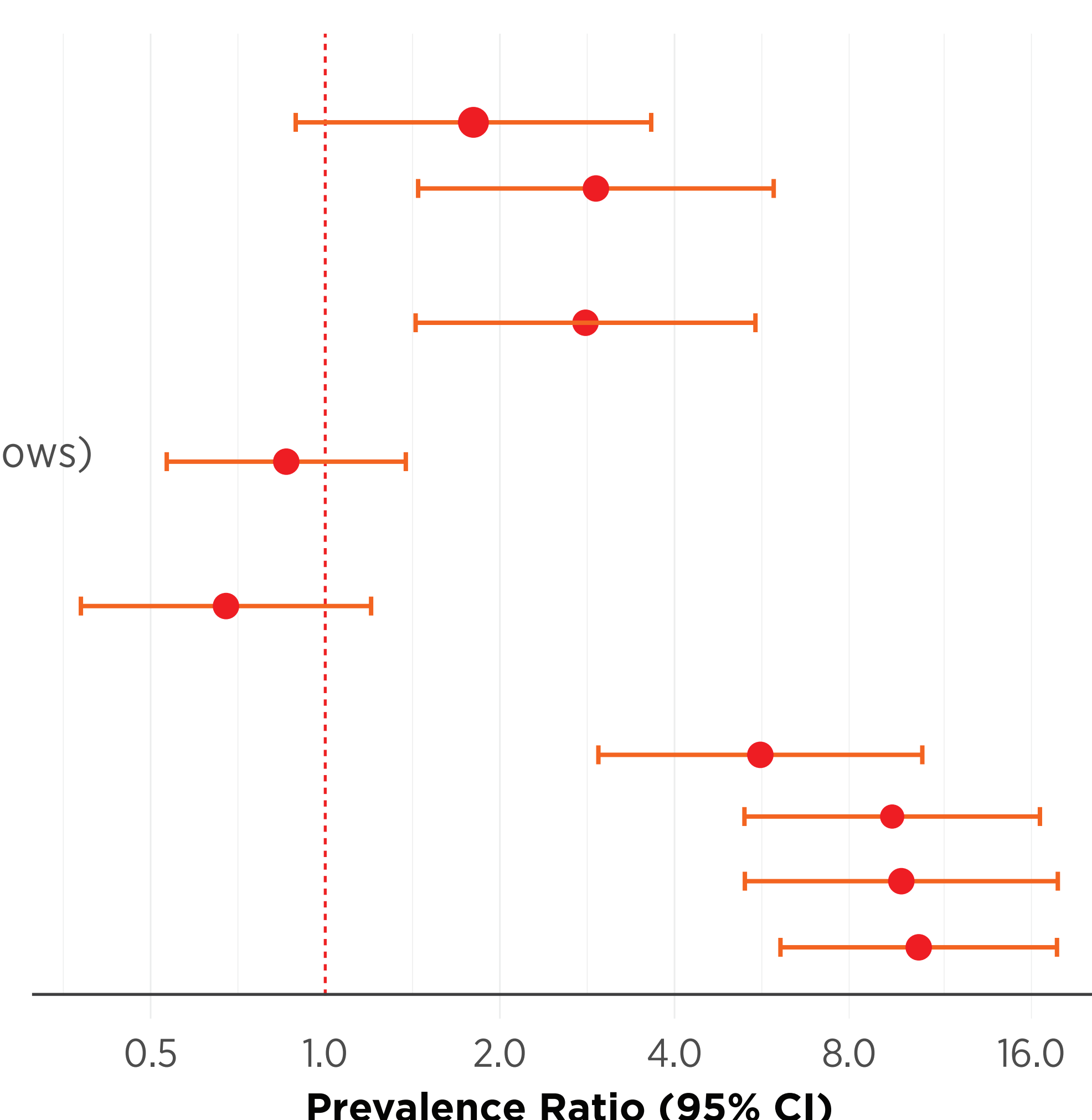

Figure 3. Prevalence ratios and 95% confidence intervals for associations between herd characteristics and *Salmonella* Dublin postivity, and between past *Salmonella* Dublin status and 2024 positivity

References

[a] Um et al. (2023). Accuracy of testing strategies using antibody-ELISA tests on repeated bulk tank milk samples and/or sera of individual animals for predicting herd status for *Salmonella* dublin in dairy cattle. Prev. Vet. Med. 220:106048.

[b] Shaukat et al. (2024). Herd-level prevalence of bovine leukemia virus, *Salmonella* Dublin, and *Neospora caninum* in Alberta dairy herds using ELISA on bulk tank milk samples. J. Dairy Sci. 107:8313–8328.

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