1. Introduction

Context: Bovine paratuberculosis, caused by Mycobacterium avium subsp. paratuberculosis (Map), is a worldwide enzootic disease of considerable economic importance for dairy cattle producers, mainly introduce into herds by purchasing infected animals.

Objective: use the information present in epidemiological data to provide additional knowledge on uncertain key parameters for Map spread. This study focuses on dairy cattle herds located in Brittany (Northwestern France), region with a high density of cattle (85% of cows are dairy cows; Fig. 1).

2. Multiscale model and data overview

Stochastic mechanistic multiscale model of Map spread between dairy cattle herds \(\Rightarrow\) coupling of within-farm epidemiological models through cattle trade movements (Fig. 2).

- Stochastic within-herd demography (herd-specific size and management) (Fig. 2).
- Infection dynamics including all known transmission routes (Fig. 2).
- Animal trade (Fig. 3) and farming management, based on observed data.

Simulations and estimation process based on 2,030 dairy herds:
- 1044 herds with one single screening point, used to set their respective initial state
- 986 herds with at least 2 screening points: first point used to define the initial state and final screening point for inference (Fig. 5, Fig. 6).

3. Parameters estimation

Method used: Approximate Bayesian computation based on sequential Monte Carlo (ABC-SMC) (see Fig. 5 for a summary of the main steps).

Parameters estimated: the probability of purchasing infected cattle (\(p\)), the indirect local transmission rate (\(\beta_g\)), and the sensitivity of the diagnostic test (\(S_e\)).

Summary statistics: number of positive samples observed at the last screening point (for 986 herds)

Initial herd states (size and prevalence) based on data \(\Rightarrow\) desynchronized entry of herds in the simulation (Fig. 6).

Control measures implemented in herds: intensity level and coverage in agreement with expert opinion.

4. Results

- Estimation of the probability of purchasing infected cattle (\(p\)) not very accurate: the regional Map prevalence is probably high (40-60%) \(\Rightarrow\) in agreement with current knowledge.
- The indirect local transmission rate (\(\beta_g\)): estimated to be smaller (\(\cong 3.7 \times 10^{-10}\)) than the one used in previous study (\(9.3 \times 10^{-10}\)), but did not account for external introductions.
- Estimating the sensitivity of the diagnostic test (\(S_e\)): narrow distribution \(\Rightarrow\) very low average sensitivity (\(\cong 0.09\)).

5. Conclusion and perspectives

Our model is flexible, allowing incorporation of various sources of data, and provides data-driven predictions of infection dynamics and impact of regional control strategies.

This study provides additional information on key parameters difficult to observe in the field, at a scale still little studied.

- Inference results need to be validated based on identifiability-related investigations.
- Some uncertainty exists regarding control measures adopted by farmers: consider model selection in the estimation process by comparing different scenarios of realistic interventions.

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References