Targeting phenotypic traits to improve resistance to paratuberculosis in dairy cattle: a modelling approach

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Introduction

Paratuberculosis is an infectious disease caused by *Mycobacterium avium* subsp. *paratuberculosis* (Map). Control strategies of the disease in infected herds are currently based on hygiene improvement and test-and-cull of infected animals. These actions are difficult to implement by farmers and lack effectiveness. Genetic selection could enhance disease control if focused on phenotypic traits of animals which influence the disease dynamics in a population. However, there is a lack of knowledge on which traits contribute the most to the disease dynamics.

Objective

To assess the effect of changes in different phenotypic traits on the dynamics of paratuberculosis in dairy herds .

Used model

- Stochastic within herd model (Marcé et al. 2011, Beaunée et al. 2015)
- Population dynamics: herd structured in age groups
- Infection dynamics:
  - Mutually exclusive health states (Fig 1)
  - Transmission routes: in utero, indirect transmission, from local and general environments, milk, colostrum
  - Heterogeneity in shedding levels (T < Is << Ic)
  - Resistance acquisition at 1 year of age

Approach

- Comparing the disease dynamics between situations (1 scenario = 1 set of values of parameters defining traits):
  - With current phenotypic traits: 1 reference scenario
  - Assuming that the whole population is composed of more resistant animals: 390,624 tested scenarios (Fig 1)

Outcomes of interest and data analysis

- Disease dynamics 25 years after infection first introduction:
  - Infection persistence in the herd
  - Within-herd prevalence of infected animals
  - Within-herd prevalence of clinically affected animals
  - Cumulated number of newly infected animals over 25 years
- Cluster analyses on the 4 outcome variables to identify the most influential phenotypic traits

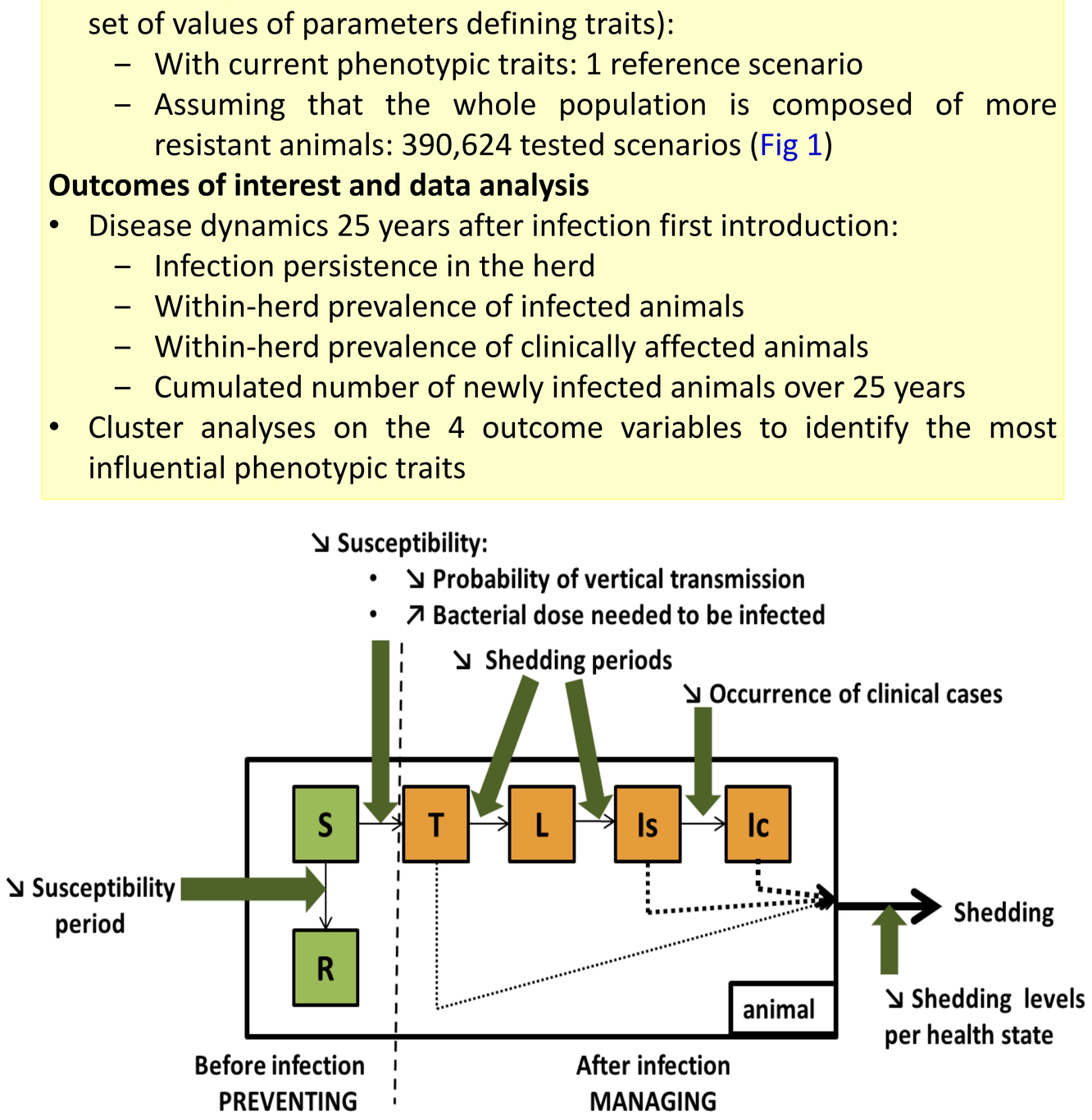

Fig 1: Phenotypic traits of interest to better control paratuberculosis dynamics, with *S*: susceptible, *R*: resistant, *T*: transiently infectious, *L*: latent, *Is*: subclinically infectious, *Ic*: clinically affected (and infectious).

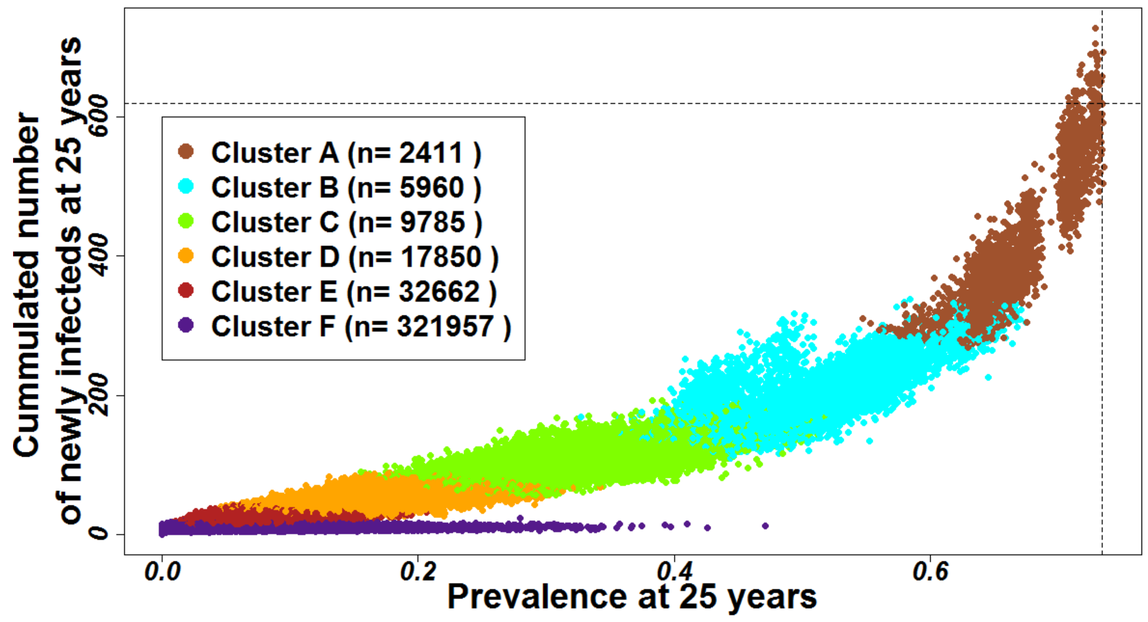

Fig 2: Clusters of scenarios by outcomes and distribution on two outputs of interest. Dotted lines correspond to the initial levels of both outputs.

Highlights

- 6 clusters on the 4 outputs with a gradient in improvement (Fig 2)
- Most effective phenotypic traits (Fig 3)
  - Earlier resistance acquisition
  - Increased dose needed to be infected
  - Increased duration before Ic state
  - Decreased fecal shedding level in Ic state (not shown)
- Phenotypic trait with slight influence on disease dynamics
  - Decreased probability of in utero transmission

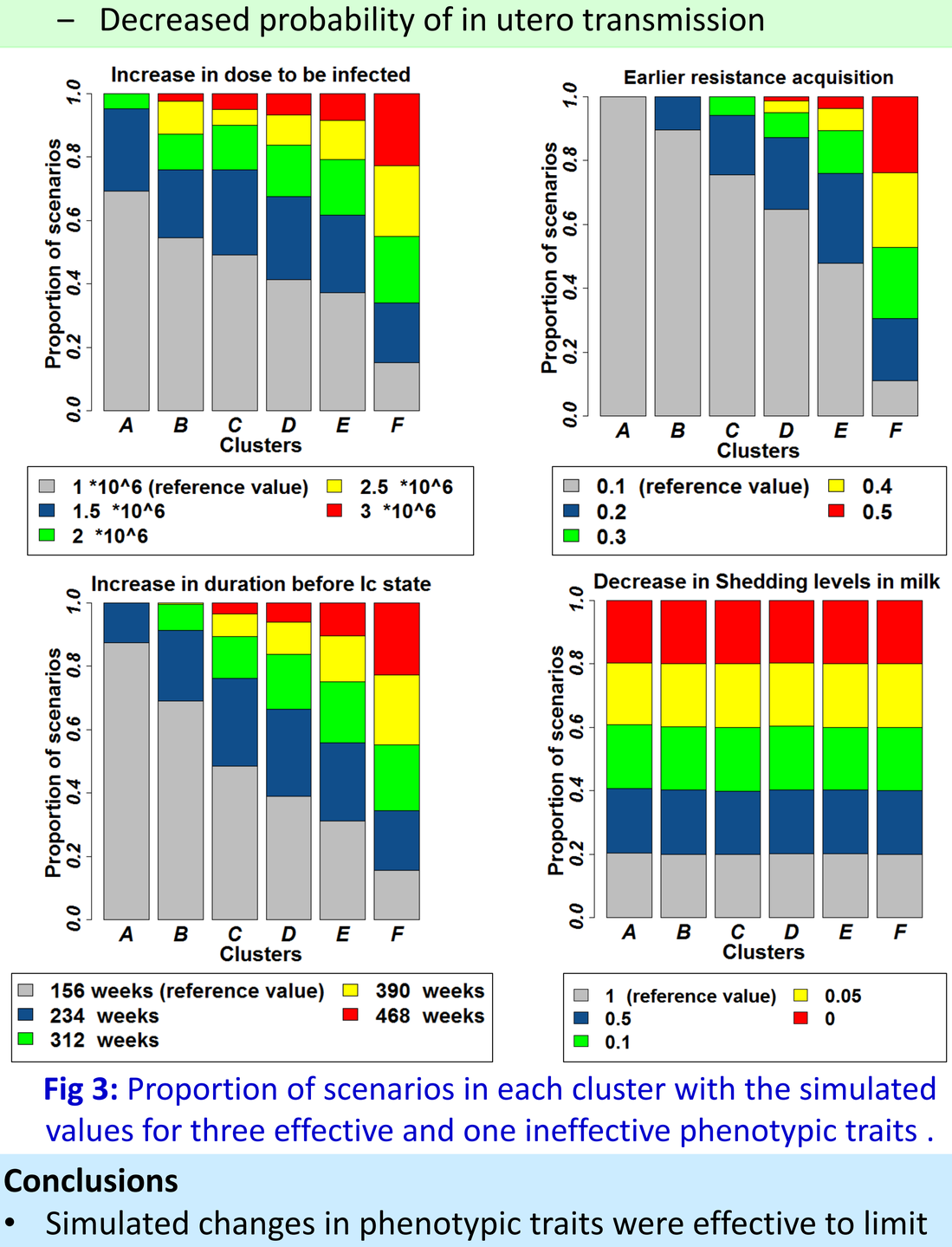

Fig 3: Proportion of scenarios in each cluster with the simulated values for three effective and one ineffective phenotypic traits .

Conclusions

- Simulated changes in phenotypic traits were effective to limit paratuberculosis dynamics in dairy herds
- 5 relevant phenotypic traits of resistance to paratuberculosis have been identified → orientation for future genetic selection

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