

How do endemic infectious diseases affect culling rates and longevity of dairy cows?

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AIM was to estimate the herd prevalence of selected endemic bovine pathogens among large commercial dairy herds and to analyse their associations with herd culling rates and longevity.

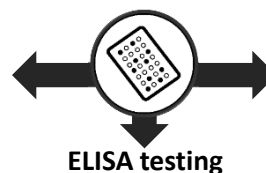
Materials & Methods

Data

- 120 large-scale dairy herds in Estonia
- Freestall farms with at least 100 cow-years
- 10 heifers' serum samples per herd + bulk tank milk sample (BTM) from each milk tank
- Samples collected between August 2019 and July 2020
- Data from Estonian Livestock Performance Recording Ltd (ELPR): herd size, milk yield, average age of the culled cows (MAofCC), yearly cow culling rate (CR)



Heifers

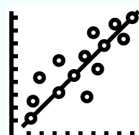


ELISA testing



Lactating cows

- **BHV-1** (bovine herpesvirus 1)
- **BVDV** (bovine viral diarrhoea virus)
- **BRSV** (bovine respiratory syncytial virus)
- **S. Dublin** (*Salmonella* Dublin)
- **M. bovis** (*Mycoplasma bovis*)
- **MAP** (*Mycobacterium avium* spp. *paratuberculosis*)



Multivariable linear regression models for analyzing the associations between herd pathogen status and CR and MAofCC.

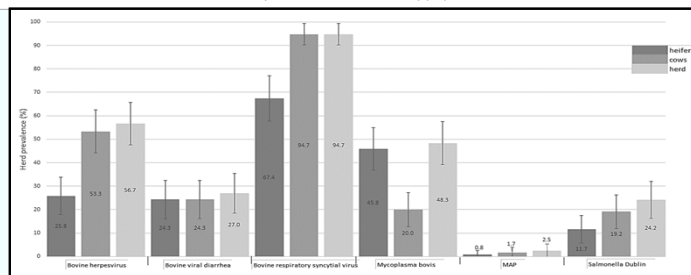
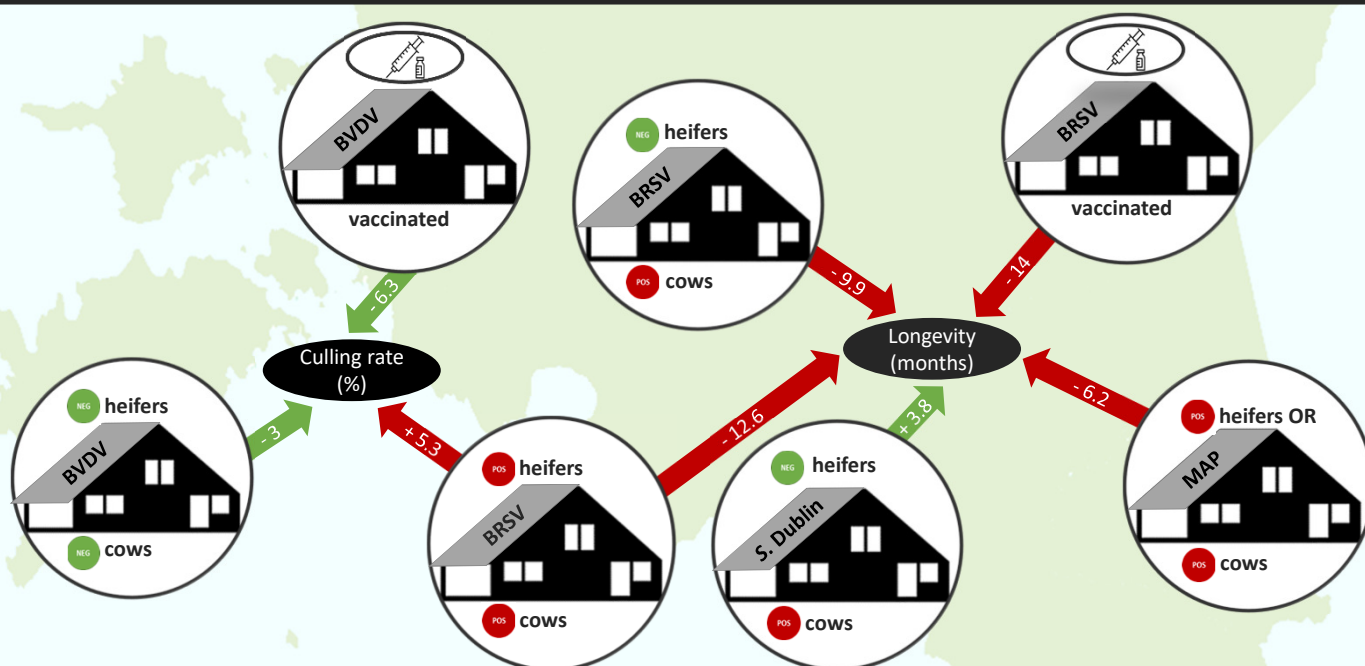


Figure 1. Herd seroprevalence of tested infectious diseases in 120 large-scale Estonian dairy herds.

Conclusions

- This study confirmed that Estonian large-scale dairy herds are endemically infected with BHV-1, BVDV, BRSV, *M. bovis* and *S. Dublin*. Also, low herd prevalence of MAP was identified.
- Due to the impacts of herd BVDV, BRSV, *S. Dublin* and MAP status on herd culling rates and cow longevity and zoonotic consequences of some of these pathogens, control and elimination of these infections should be encouraged.



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