# Application

Selecting cattle with low infectivity, alongside enhanced disease resistance, can help eliminate bovine tuberculosis (bTB) in the UK.

# Introduction

bTB is an infectious cattle disease that continues to impose significant financial burden to the UK. Since 2016, genetic selection of cattle with enhanced genetic bTB resistance has been contributing to UK goal to achieve an officially tuberculosis free status by 2038. Recent studies have indicated that concurrently reducing infectivity in cattle while enhancing their resistance may accelerate the process of bTB eradication (Banos, 2023).

Our previous analyses of a subset of the data used in genetic evaluations for bTB resistance of dairy cattle has provided first empirical evidence that dairy cattle may vary genetically in their bTB infectivity (Madenci et al., 2023). However, the models used in that study could not properly account for genetic variation in bTB resistance, and the large extent of zero inflation and overdispersion observed in the infectivity phenotype. The main aim of the present study was to provide conclusive evidence for genetic variation in dairy cattle infectivity by applying generalized linear mixed models that can better handle the inherent complexities in the data.

# Material and methods

The dataset used was provided by Egenes and consists of the same data as used for the national genetic evaluation of bTB resistance (Banos et al., 2017), and the resulting estimates of genetic merit in bTB resistance. The dataset includes bTB records (date of first positive test) and pedigree data of dairy cattle (only Holstein Friesian) involved in all nationally recorded bTB breakdown herds in England and Wales between 2000 and 2022.

This study focuses on estimating genetic variation in the infectivity of index cases, defined as the first cows per breakdown that tested positive within first test period. Secondary cases were defined as those that tested positive in the subsequent testing period. Only breakdowns with a single index case (6,668 index cases) and pedigree data extracted for these cows spanning seven generations (2,931 sires) were considered, and infectivity was defined as the number of secondary cases per index case.

Generalized linear mixed models (implemented in MCMCglmm R-package (Hadfield, 2014)) that could handle both zero inflation and overdispersion, specifically the zero inflated poisson (ZIP), hurdle and geometric (GEO) model, were used to estimate genetic parameters for the above infectivity phenotype. All models included as fixed effects breakdown year, season (all four seasons), county, herd size, age of the index case, and the average estimated genetic bTB resistance of all herd members, and sire of the index case as random effect.

# Results

The distribution of the number of secondary cases showed that majority of the breakdowns (~73%) have zero secondary cases, and large over-dispersion, justifying the choice of the models considered in this study. Table 1 presents posterior means of variance components for each model. The ZIP and Hurdle models yielded similar estimates of sire variance (Poisson part of the models), and the 95% highest posterior density (HPD) intervals for both models do not encompass zero, indicating that index cases vary genetically in their infectivity. In contrast, the geometric model estimated a slightly higher sire variance although the range of the interval was wider, and with the lower bound closer to zero. Our results also suggest that average resistance EBV does not have direct effect on infectivity phenotype, indicating that cattle may be selected for lower infectivity without impacting selection for resistance.

Table 1: Posterior means of variance components and the 95% highest posterior density intervals (HPD95%)

|  |
| --- |
| Model |
|  |  Hurdle |  ZIP | Geometric |
| Variance1 | Binary2 | Poisson | Binary2 | Poisson |  |
| $$σ\_{s}^{2}$$ | <10-5 | 0.0242(0.0002, 0.0886) | <10-5 | 0.0148(0.0002, 0.0591) | 0.0332(<10-5,0.1177) |
| $$σ\_{e}^{2}$$ | 1.000 | 1.2990( 1.131, 1.475) | 1.000 | 3.9570( 3.556, 4.331) | 3.0610(2.695,3.393) |
| 1 $σ\_{s}^{2}$=sire variance, $σ\_{e}^{2}$=residual variance 2 The residual variance, $σ\_{e}^{2}$, for the zero-part in both ZIP and Hurdle models fixed at 1 |

# Conclusion

The study provides more conclusive evidence that UK dairy cattle vary genetically in bTB infectivity, implying that genetic selection for lower cattle infectivity may be feasible to help bTB eradication. Detection of genetic variance in index case infectivity in current models is encouraging as index cases represent only a small proportion of the cattle population. Future studies that account for genetic differences in infectivity of all dairy cattle involved in bTB breakdowns are expected to uncover more genetic variation in infectivity. In addition, further investigation is ongoing to identify best model to use for future analysis which remains as a future work.

# Acknowledgements

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# References

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