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Breeding for bovine tuberculosis resistance in Irish cattle

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Introduction

Despite sustained national eradication efforts, bovine tuberculosis (bTB) remains a major animal health challenge in Ireland (Ryan *et al.,* 2023). The national bTB eradication program in the Republic of Ireland was initiated in the 1950s with the long-term objective of eliminating the disease. This goal has not yet been achieved. According to the Department of Agriculture, Food and the Marine (2025), disease herd prevalence has increased from 4.38% in 2020 to 6.08% in 2025, resulting in an additional 2,228 bTB-positive animals when comparing Q3 2020 with Q3 2025. This increase has occurred alongside substantial public investment, with government expenditure reaching €79.4 million between Q1 and Q3 2025, highlighting the ongoing economic burden of eradicating bTB. These trends highlight persistent difficulties in achieving effective bTB disease control within the national herd. Current control measures are based on routine on-farm herd testing, with identification and removal of infected animals, identified via the Single Intradermal Comparative Cervical Test (SICCT). These measures are supplemented by abattoir surveillance and the use of interferon-gamma blood diagnostic testing. While these approaches have previously contributed to reductions in disease prevalence, recent increases in herd incidence have renewed interest in complementary strategies to enhance existing control frameworks. Within the Irish national herd, bTB susceptibility has an estimated heritability of 0.12 with a genetic standard deviation of 0.09 (Ring *et al.,* 2019), exceeding that of most fertility traits in cattle, thereby highlighting the substantial potential for genetic improvement of bTB resistance through selection. As a result of this, the Irish Cattle Breeding Federation (ICBF) introduced a bTB resistance trait as a standalone trait in 2019, and further incorporated this in 2021 into its main breeding indexes for dairy and beef animals (Irish Cattle Breeding Federation, 2025). This initiative represents a strategic effort to integrate genetic resistance to bTB into national eradication efforts, supporting long-term, cumulative, and sustainable disease control within the Irish cattle population. The aim of this paper is to translate analyses of bTB heritability and genetic architecture into implementable breeding strategies to curtail and reverse the rising prevalence of bTB in Ireland which has thus far resisted systematic eradication efforts.

Materials & Methods

Within the ICBF genetic evaluations, estimated breeding values (EBVs) for bTB resistance are expressed as the expected percentage of an animal's offspring likely to test positive for bTB. Lower EBVs are more favourable, indicating reduced risk of infection in progeny. As an example, a bull with an EBV of 10% is predicted to produce offspring in which, one in ten are expected to test positive for bTB following exposure. The methodologies used to compute bTB EBVs are described in Ring *et al.* (2019). Within each evaluation bTB status is treated as a binary trait (0= not infected, 1=infected). Cattle are grouped by age, sex, and reproductive status prior to each herd-level positive bTB breakdown, and only animals present for at least 42 days before breakdown onset were included. Herd-level exposure was defined based on confirmed reactors from the SICCT, interferon-gamma blood diagnostic testing or lesions detected at slaughter. Pedigree information was used to assign animals to breed-based genetic groups, and genotype data from Irish dairy and beef breeds were included for genomic analysis.

Genetic parameters were estimated using an animal linear mixed model that included fixed data edits, as well as genetic and environmental influences.

Results

Validation of the ICBF bTB EBVs shows differences in infection outcomes based on an animals bTB EBV. Cattle with the least favourable EBVs for bTB showed a 26% higher number of reactors compared with animals in the same herds that had the most favourable EBVs. Analysis of 1,262 sires with at least 50 progeny across a minimum of 10 infected herds revealed substantial variation in progeny infection rates. As seen in figure one, there is substantial variation among sires mean prevalence of bTB observed in their progeny within high-risk herds. Some sires sired no bTB infected progeny despite exposure within high-risk herds that have an increased level of exposure to bTB, whereas other sires produced up to 40% bTB positive progeny under similar conditions. These between-sire differences in progeny infection outcomes reflect underlying genetic variation in susceptibility to bTB, which is captured though the bTB EBVs. Reducing even a single bTB infection can have wider benefits, as each prevented case may avoid an estimated 1.5 to 4.9 secondary infections arising from animal-to-animal transmission (Conlan *et al.*, 2012). These results show that selection for bTB resistance can meaningfully support national eradication efforts.

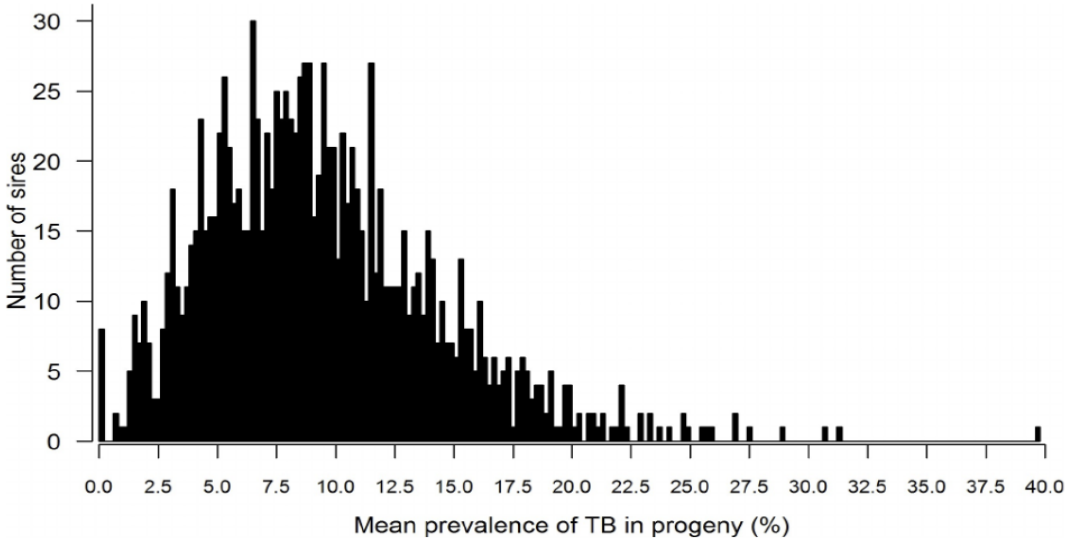

Figure 1. Distribution of the mean prevalence of bovine tuberculosis in the progeny of 1,262 sires that produced at least 50 progeny in 10 bovine tuberculosis-breakdowns.

When animals were grouped into bTB EBV risk categories based on percentile-ranked EBVs (low: lowest 20%, intermediate: 21st–79th%, high: highest 20%), differences in infection outcomes were observed. Animals in the highest bTB EBV risk group had 1.44 times greater odds of returning a positive bTB result compared with animals in the lowest risk group while animals in the intermediate risk group had 1.20 times greater odds (Ring *et al.*, 2019). This corresponded to a mean bTB prevalence of 9.3% in the high-risk category, compared with 7.5% in the intermediate group and 6.9% in the low-risk group, this shows a clear difference in infection risk based on an animals bTB EBV. To facilitate knowledge transfer to improve farmer engagement and understanding of the bTB EBVs, a traffic light classification system was introduced (Figure 2). This system uses a colour coding scheme to highlight the predicted genetic risk of bTB in an animals progeny.

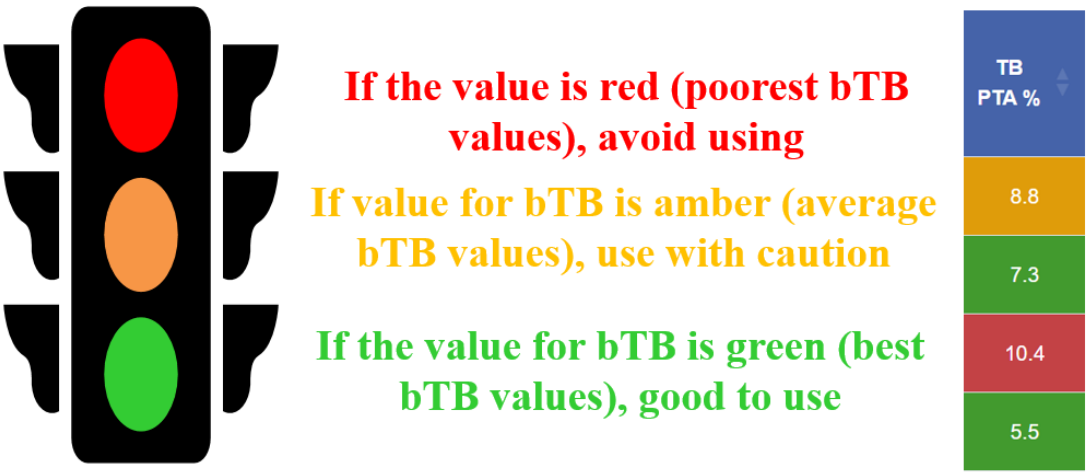

Figure 2. Traffic light system used to communicate genetic risk of bovine tuberculosis (bTB) to farmers. Animals are categorised by bTB EBV ranking, where green indicates low predicted progeny infection risk, amber indicates intermediate risk, and red indicates animals that are at high risk. Within each colour category, multiple EBVs for individual animals are displayed, reflecting the range of PTA values that fall within that risk category, consistent with how results are presented to farmers in practice.

For herd improvement, farmers are advised to prioritise animals with a high overall breeding index with subsequent favourable (low) bTB EBVs. This combination ensures both enhanced productivity and reduced genetic susceptibility to infection. EBVs for bTB are ranked within each evaluation cohort using percentile-based thresholds. Animals ranked within the lowest proportion of bTB EBVs are classified as green, indicating high genetic resistance; intermediate animals are classified as amber; and those within the highest proportion are classified as red, reflecting increased genetic susceptibility. These bTB EBV percentile thresholds are recalculated at each genetic evaluation to account for ongoing population-level genetic change.

Table 1. Percentile distribution of bTB estimated breeding values (EBVs) expressed as predicted progeny infection risk (%) across animal cohorts in the ICBF November 2025 routine national genetic evaluation.

November 2025 Evaluation Cohort	Trait	1st pctl	5th pctl	10th pctl	20th pctl	50th pctl	90th pctl	95th pctl	99th pctl
Herd-level Statistic	TB (% progeny infected)	6.7	7.12	7.32	7.53	7.88	8.32	8.43	8.63
All Cows	TB (% progeny infected)	4.42	5.64	6.27	6.92	7.86	9.41	9.92	11
AI Bulls born in last 10 years	TB (% progeny infected)	4.79	5.92	6.42	7.06	8.41	10.62	11.21	12.49
Heifer Calves	TB (% progeny infected)	4.28	5.49	6.09	6.81	7.99	9.63	10.16	11.22

Table 1 summarises the distribution of bTB EBVs across multiple animal cohorts. Median bTB EBVs ranged from 7.86% in cows to 8.41% in AI bulls born within the last ten years. However, to support practical interpretation of the percentile thresholds shown in Table 1, the traffic-light

classification system was disseminated to farmers and other stakeholders. Animals classified within the green category typically exhibit predicted progeny infection levels below approximately 6.5–7.0%, while animals in the red category exceed approximately 10–12%. These thresholds provide a ranking within the national population and allow farmers to quickly and easily select for bTB resistance when making mating decisions. Advice to farmers during breeding season is to use bulls with bTB EBVs classified as green within the traffic light, and subsequently choose the lowest possible EBVs in order to accelerate genetic progress. Analysis of the November 2025 evaluation highlights substantial variation in predicted progeny infection risk across herds and animal types, with herd-level risk varying from 6.7% to 8.63%, and AI Bulls ranging from 4.79% to 12.49%. Therefore, prioritising animals with favourable bTB EBVs alongside strong overall production index values enables permanent and cumulative improvement in both individual herd and population-level resistance to bTB without sacrificing main production traits. This information is readily available for farmers within their individual herd profile screens on the ICBF platform.

Conclusion

Despite decades of eradication efforts, bTB still presents a significant challenge in Ireland, which underpins the need for complementary approaches alongside existing strategies. Within the Irish national herd there is considerable genetic variation in cattle susceptibility to bTB. This suggests that selective breeding for genetic improvement in bTB susceptibility can support national efforts to reduce disease incidence and progress toward eradication of bTB. Integrating bTB resistance into national breeding indexes and providing user-friendly tools such as the Traffic Light system enables farmers to select animals with enhanced resilience while maintaining strong production performance.

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