Genetic Evaluation for bTB Resistance in Beef Cattle

Final Report

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Acronyms

APHA	Animal and Plant Health Agency
bTB	Bovine (*Mycobacterium bovis*) Tuberculosis
PTA	Predicted Transmitting Ability
BCMS	British Cattle Movement Service
EGENES	Edinburgh Genetic Evaluation Services

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1. Executive summary

- Previous reports included results from the first three pilot genetic evaluations based on bTB breakdown data collected up to December 2017, August 2018 and April 2019, respectively.
- The current report includes results from a fourth (final) pilot genetic evaluation run using all breakdown data available up to August 2019 and a genomic evaluation run.
- The present report also summarises the key project results.
- With regards to the fourth pilot genetic evaluation:
    - As before, two datasets were formed, one consisting of herds with 100% beef cattle (Dataset 1) and one of herds with at least 10% beef cattle (Dataset 2).
    - Following edits, 577,495 and 1,067,125 records of 325,867and 618,640 animals, respectively, were kept in Datasets 1 and 2. These animals were progeny of 29,941 and 47,217 sires, respectively.
    - Proportions of infected individuals were 7.4% and 7.1% in Datasets 1 and 2, respectively, consistently with previous runs.
    - Heritability of the trait was 0.1063 and repeatability 0.6352, very close to and within the confidence interval of estimates from the previous runs.
    - Correlations of sire Predicted Transmitting Abilities PTA between the present and previous runs were 0.97 (April 2019), 0.94 (August 2018) and 0.91 (December 2017) attesting to the stability of the genetic evaluation.
    - Correlations with sire PTAs for other traits were also estimated and were generally lower than 0.12 (absolute value).
    - A genomic evaluation has been produced but insufficient genotyped sires with PTA exist as yet to make this a feasible proposition.
- In all cases, sire PTA were expressed so that positive values denote resistance.
- The project has demonstrated the feasibility of calculating genetic evaluations for bTB resistance. The amount of genetic variance observed in the trait warrants selection aiming to reduce incidence of disease. The impact of said selection on other beef traits is expected to be minimal.

2. Background

National bTB surveillance data were received from the Animal and Plant Health Agency (APHA). The latest genetic evaluation was the fourth pilot run and considered all bTB breakdown data collected until August 2019 (inclusive). The previous three pilot genetic evaluation runs were based on data collected until December 2017, August 2018 and April 2019, respectively. In all cases, herds with at least 1% beef cattle were first maintained. Subsequently, two datasets were formed for the purposes of the genetic evaluation: one including herds that had only beef animals (50% of herds) and another including herds with at least 10% beef cattle (93% of herds). Separate genetic evaluations were conducted for each dataset.

3. Trait definition and data edits

As before, individual animals had repeated skin test result records within a given breakdown in the APHA file. Following the same protocol as in the dairy bTB genetic evaluation, a single skin test record was derived for each animal per breakdown based on the sequence of its skin test results:

1. Non-Reactor: if the last or only skin test was a non-reactor and there were no reactor tests in the breakdown sequence for the particular animal.
2. Reactor: if the last or only skin test was a reactor or at least two consecutive tests were inconclusive, and no non-reactor tests were present in the sequence.
3. Unclassified: records not fitting any of the above two definitions.

Subsequently, skin test records and available post-mortem examination results (presence/absence of visible lesions and an *M. bovis* culture) were combined to determine the health status of each individual animal per breakdown as follows:

1. Healthy: live non-reactor or slaughtered non-reactor with negative post-mortem examination results (i.e. absence of lesions and negative *M. bovis* culture).
2. Infected: reactor regardless of post-mortem examination result or positive post-mortem result regardless of skin test.
3. Unconfirmed: all other cases; unconfirmed records were not included in further analyses.

Finally, breakdowns were split into 2-mo intervals. Intervals with at least one infected individual and a minimum of five animals were kept for further analyses. Healthy animals were assigned a record of zero in each breakdown interval kept. Infected animals received a record of 1 in the interval where they were infected and a record equal to 0.40^n in previous intervals where n is the distance from the infection interval; that is, the record would be 0.4 in the immediately previous interval, 0.16 in the one before the latter, 0.0624 in the one before etc. This definition is fully described in the dairy genetic evaluation manuscript.[1]

[1]Banos G, M Winters, R Mrode, AP Mitchell, SC Bishop, JA Woolliams and MP Coffey. 2017. J Dairy Sci. 100(2):1272–1281 https://doi.org/10.3168/jds.2016-11897.

Afterwards, data were edited as summarised in Table 1, including all data edit steps and the corresponding percentage of records removed.

Table 1. Data edits and percentage of records lost (all genetic evaluation runs).

Edit	% records lost; dataset 1*	% records lost; dataset 2*
Animal more than 87.5% dairy	<1%	37%-38%
Breakdown less than 60 days	1-2%	3-4%
Stock bulls >36 months old	<1%	<1%
Calves born during breakdown	18-19%	21-22%
Unconfirmed records	<1%	<1%
Missing sire identity	58-59%	64-66%
Breakdown intervals with <5 records	2-3%	2-3%

*dataset 1: herds with 100% beef cattle; dataset 2: herds with at least 10% beef cattle

4. Data description

Tables 2 and 3 describe the final data used in all four pilot genetic evaluations (after edits).

Table 2. Data used in each pilot genetic evaluation (herds with 100% beef cattle).

	Dec 2017	Aug 2018	Apr 2019	Aug 2019
Number of records	487,153	513,627	555,915	577,495
Number of animals with records	276,331	286,147	311,014	325,867
…. of which females	182,107	189,732	206,153	214,027
…. of which males	94,224	96,415	104,861	111,840
Number of sires of animals with records	26,485	27,532	29,142	29,941
Number of breakdowns	5,804	6,101	6,589	6,734
Number of breeds	50	50	51	52
Percentage of infected individuals	7.5%	7.7%	7.6%	7.4%
….. infected females	8.4%	8.7%	8.6%	8.4%
….. infected males	5.6%	5.8%	5.8%	5.5%

Table 3. Data used in each genetic evaluation (herds with at least 10% beef cattle).

	Dec 2017	Aug 2018	Apr 2019	Aug 2019
Number of records	860,284	919,237	1,017,237	1,067,125
Number of animals with records	499,206	525,095	584,799	618,640
…. of which females	307,962	325,271	360,770	378,786
…. of which males	191,244	199,824	224,029	239,854
Number of sires of animals with records	41,496	43,278	45,835	47,217
Number of breakdowns	10,602	11,238	12,327	12,721
Number of breeds	61	61	61	61
Percentage of infected individuals	7.3%	7.5%	7.3%	7.1%
….. infected females	8.4%	8.6%	8.5%	8.3%
….. infected males	5.4%	5.6%	5.5%	5.3%

5. Model of genetic evaluation

The following model was used in all genetic evaluations:

Y = μ + bi + bid + ym + age + sx + calvno + het + rec + gen + pe + re

where: Y=health status record; μ=population mean; bi=breakdown interval; bid=breakdown interval duration (1: 2-month, 2: shorter last interval); ym=year-month interaction of breakdown onset; age=linear regression on age of animal at breakdown onset; sx=sex of animal; calvno=calving number (females only); het=linear regression on heterosis; rec=linear regression on recombination; gen=random animal genetic effect (incl. pedigree); pe=random permanent environment effect; re=random residual.

This model was used for the estimation of the trait variance components and genetic parameters, and the derivation of predicted transmitting abilities of individual animals.

6. Variance component and genetic parameter estimation

Table 4 summarises these estimates from all four pilot genetic evaluation runs.

Table 4. Variance component and genetic parameter estimation in all genetic evaluation runs

	Dec 2017		Aug 2018		Apr 2019		Aug 2019	
	Estimate	*s.e.*	Estimate	*s.e.*	Estimate	*s.e.*	Estimate	*s.e.*
Phenotypic variance	0.0567	*0.0003*	0.0580	*0.0003*	0.0580	*0.0003*	0.0568	*0.0003*
Genetic variance	0.0044	*0.0005*	0.0056	*0.0005*	0.0060	*0.0005*	0.0060	*0.0005*
Permanent environment var	0.0317	*0.0005*	0.0317	*0.0005*	0.0314	*0.0005*	0.0301	*0.0005*
Residual variance	0.0206	*0.0002*	0.0207	*0.0002*	0.0206	*0.0002*	0.0207	*0.0002*
Heritability	0.0777	*0.0084*	0.0967	*0.0088*	0.1032	*0.0084*	0.1063	*0.0083*
Repeatability	0.6373	*0.0039*	0.6437	*0.0037*	0.6441	*0.0035*	0.6352	*0.0035*

In each case, estimates were within the 95% confidence interval of the estimates from the previous run.

7. Derivation of Predicted Transmitting Ability (PTA)

Given the trait definition, negative animal solutions indicated low percentage of infection. However, the sign was reversed in the post-process so high values indicated desirable PTAs.

Sire PTA correlations between consecutive genetic evaluations are summarised in Table 5. These pertain to sires with a minimum PTA reliability of 0.30 and attest to consistency of results across runs.

Table 5. Correlations between sire PTAs from consecutive genetic evaluation runs; dataset 1 above diagonal, dataset 2 below diagonal*

	December 2017	August 2018	April 2019	August 2019
December 2017		0.93	0.90	0.90
August 2018	0.95		0.95	0.94
April 2019	0.91	0.95		0.97
August 2019	0.91	0.94	0.97	

*dataset 1: herds with 100% beef cattle; dataset 2: herds with at least 10% beef cattle

8. PTA correlation between bTB resistance and other traits

Table 6 summarises the sire PTA correlation between bTB and other animal traits in the beef genetic evaluation. Two thresholds of PTA accuracy were considered: minimum PTA reliability of 0.30 and progeny in at least 10 herds. Correlations were generally very low, with the absolute value reaching 0.12; this is a positive correlation with lifespan, suggesting that bTB resistant sires have progeny with enhanced longevity. However, the magnitude of the estimate means that only a very small proportion of variance is common to the two traits.

Table 6. Sire PTA correlation (r) between bTB and other traits; D1=dataset 1 (100% Beef); D2=dataset 2 (>10% Beef); sires with minimum reliability of 0.30 or progeny in at least 10 herds.

	Rel. ≥ 0.30				≥ 10 herds			
Trait	D1		D2		D1		D2	
	r	*s.e.*	r	*s.e.*	r	*s.e.*	r	*s.e.*
Age at slaughter (days)	0.05	*0.01*	0.03	*0.01*	0.04	*0.07*	-0.02	*0.03*
Net carcass weight (kg)	-0.05	*0.01*	-0.02	*0.01*	0.02	*0.07*	0.05	*0.03*
Carcass conformation (EUROP)	0.03	*0.01*	0.03	*0.01*	0.09	*0.07*	0.11	*0.03*
Carcass fat class (EUROP)	-0.01	*0.01*	-0.02	*0.01*	-0.11	*0.06*	-0.11	*0.03*
Average daily gain (kg/day)	-0.07	*0.01*	-0.03	*0.01*	-0.02	*0.07*	0.05	*0.03*
Lifespan (no. parities)	0.08	*0.01*	0.03	*0.01*	0.12	*0.04*	0.01	*0.04*

9. Genomic predictions

The existing genomic evaluation system for dairy “TB Advantage” was adapted to utilise beef bTB evaluations. The procedures have been successfully changed to incorporate the different animal identifier standards applied in beef versus dairy. These differences are primarily related to eartag vs herdbook numbers but also a number of non-pedigree beef bulls are used on farm and their identifier used in the system is the BCMS internal database number that has no outside meaning.

Until now, dairy genotypes have been stored separately from beef genotypes. In addition, the super pedigree used in bTB evaluations utilises data from a range of sources and the animal identities in each source are different (UK eartag, herdbook number, internal BCMS number). The system worked all the way through when pointed at the dairy genotypes file. The next step was to merge the dairy and beef genotypes file and point the system to that merged file to determine genomic breeding values for all genotyped animals.

The timing of the decision to merge beef and dairy genotypes into one file for use in the beef bTB genomic evaluation was preceded by the dairy system moving up from 50k SNP panel to a new 80k SNP panel. In theory this should make beef bTB genomic evaluations more accurate but we were unable to test this effect because we could not easily recreate a 50k dairy genotype file at this point. The decision was made to construct a single genotype file containing 80k dairy genotypes and 80k beef genotypes and accept any increase in accuracy. A further complication was that the beef genotypes were mapped using a slightly older SNP map than the dairy genotypes and had to be transformed on to the later SNP map before merging.

The combined file had 12,529 beef and 342,403 dairy genotypes (combined male and female) to be used by the evaluation system. There were 139,337 bulls with a PTA for bTB resistance of which 73,569 were bulls with only a BCMS ID (eartag). This effectively meant these were stock bulls that had not been registered in a herdbook and were likely bulls bred by the owner for use simply on the owner's farm. This is an important point of note because to be included in the genomic evaluation process a bull must have usable information in the form of effective daughter counts (EDC) and needs to be used across more than 1 herd. All of these bulls failed that criteria. Furthermore, out of the 139,337 bulls considered, only 12,416 had a PTA and at least 1.0 EDC and a minimum reliability of 0.20. These formed the basis of the genomic evaluation run.

Unfortunately, only 97 bulls had a PTA of sufficient accuracy and a genotype to be included in the SNP key creation. The addition of the Limousin beef genotypes resulted in 1 additional bull being added to the reference population.

When more beef cattle are genotyped, the system will be adapted to become a single step process using the new CIEL platform but as yet that has not been undertaken due to very few genotyped bulls having a PTA for bTB resistance. This mismatch between bulls having a PTA and being genotyped is due primarily to the fact that all of the genotyped beef bulls are Limousin breed and very few of those are used predominantly in the bTB area. This is expected and is a major source of information loss in the dairy evaluations as well. The UK is the first country in the world to publish dairy bTB evaluations and so there are no international proofs to add to the system. Thus, only the passage of time will create sufficiently large datasets of UK evaluated and genotyped beef bulls for useful genomic evaluations.

10. Genetic evaluation system transfer to EGENES

The suite of algorithms developed within this project for the genetic evaluation of beef cattle for bTB resistance has been transitioned and integrated into the current genetic evaluation system at EGENES (Edinburgh Genetic Evaluation Service) and is ready for routine implementation. At the moment the system is set up to accommodate both evaluations based on 100% beef herds or herds with at least 10% beef, as outlined above.

11. Conclusions

This project demonstrated the feasibility of calculating genetic evaluations for beef bTB in the UK. The amount of genetic variance observed in the trait warrants selection aiming to enhance animal

resistance and reduce incidence of disease. The impact of said selection on other beef traits currently in genetic evaluation is expected to be minimal.

Data quality is more of a challenge in beef compared to dairy and would benefit from some extension work to improve data quality such that bTB evaluations (and other potential traits) are of higher quality and can therefore be of more use to the beef industry.