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Using Commercial Data and Genomics to Improve Female Fertility and Calf Survival of Limousin beef cattle in the UK

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Summary

Improving female fertility (FF) and calf survival (CS) in the beef suckler herd will result in more calves reared, increased beef production and a reduction in greenhouse gas emissions per output. To date there has been little improvement in these traits with the industry focused primarily on terminal traits coupled with inadequate or absent selection tools available for fertility and survival. This has been to due to the low accuracy at the time of bull selection of conventional FF estimated breeding values (EBVs) and that previously there have been no CS selection tools. National UK data was used to produce genomic EBVs (GEBVs) for CS and FF traits; age at first calf, calving interval and lifespan. The data showed that on a national level the largest number of heifers calved as three year olds, average first calving interval was 424 days, only 47% of cows had more than three calves in a lifetime and 5% of calves do not survive past 10 months of age. These findings were common across a number of different UK beef breeds. The traits were found to be lowly heritable with heritabilities ranging from 0.04 for CS to 0.13 for age at first calf. The resulting genetic trends showed that there has been no genetic improvement in these traits across the beef industry. Comparing the fertility and survival trait GEBVs with existing video image analysis (VIA) abattoir carcass trait GEBVs showed small to moderate antagonistic relationships between the carcass and fertility traits.

Keywords: female fertility, calf survival, genomics, breeding value, national data, beef

Introduction

Fertile suckler beef cows and low calf mortality are essential for profitable beef production systems. Current UK beef production is 847,000 tonnes and represents only 77% of beef consumed (EBLEX, 2014a). There is significant opportunity to sustainably increase UK production and efficiency. There are ~1.6M beef cows in the UK and British Cattle Movement Service (BCMS) national records show 31% are sired by Limousin bulls. Improving Limousin genetics for female fertility (FF) such that a Limousin sired cow produces an extra calf in her life will result in 496,000 extra calves and, assuming a 300kg carcase and 84% weaning rate, an extra 125,000 tonnes of beef (15% of current production levels). Calf loss from birth to weaning has been shown to be ~4% (EBLEX, 2014b). If genetic improvement resulted in 1% more calves surviving in the suckler herds, this would result in a further 1,500 tonnes of beef produced per annum. As these increases in production are assuming the same sized national herd, genetic improvement for fertility and survival could reduce greenhouse gas emissions by between 537,000 and 578,000 tonnes of CO_2e (Navajas *et al*, 2008).

The beef sector currently has estimated breeding values (EBVs) for a range of production and FF traits (Coffey *et al*, 2007). Signficiant genetic progress has been made for production traits, but little genetic improvement has been made for FF traits (Roughsedge *et*

al, 2005a). This is partly the result of the traits being sex-limited, lowly heritable and expressed late in life, resulting in low EBV accuracy at the time of bull selection. Animal selection decisions have often already been made by the time the EBVs reach effective levels of accuracy, this frustrates the rate of improvement a herd and the wider sector can achieve. It is these attributes, however, that make FF traits ideal for genomic selection and allow accurate selection decisions when the animal is young. Another reason for the poor genetic improvement for FF traits is that breeding goals tend to be focused on the terminal traits (Roughsedge *et al*, 2005b), which are often antagonistic with fertility traits. There is currently no genetic improvement for calf survival (CS) as death dates in the pedigree sector are often not provided and dead calves are generally not registered in the pedigree databases, this means a CS phenotype has not been possible to date.

The use of national data sets and genomic selection to genetically improve traits has already been undertaken in the UK with genomic EBVS (GEBV) for Video Image Analysis (VIA) abattoir carcass traits being available to UK Limousin cattle since 2016 (Moore *et al*, 2017). This approach has successfully allowed GEBVs to be provided for traits that are economically important but difficult to obtain accurate conventional pedigree based genetic evaluations. Changing the FF genetic evaluation to use national BCMS data will allow information from pedigree and commercial suckler cows to contribute, where previously only pedigree information was considered. For example, previously when a young bull was sold into the commercial sector there was no information known about the fertility of his daughters born in the commercial sector, but with BCMS data the fertility information of all descendents are included in the genetic evaluation. The significant increase in the number of records will increase the accuracy of evaluations, as will the implementation of genomic selection. As the BCMS data has both birth and death dates recorded for all beef animals surviving after 20 days, the first CS genetic evaluation is possible, with genomic selection also expected to benefit a survival genetic evaluation.

The aim of this work was to use the national BCMS data and genomic selection to produce GEBVs for FF and CS for Limousin's. It was anticipated that these selection tools will be used by the Limousin pedigree breeders to make genetic progress for the FF and CS.

Material and Methods

Data Extraction from BCMS

Recording basic animal information into BCMS has been compulsory since 1998. For each animal, dates of birth and death, sex, breed, dam and movement information is recorded with sire optional. An accurate breed make up of animals was obtained from a 'super-pedigree' which combines BCMS information with UK milk recording organisations and both beef and dairy herd books and calculates breed make up as a percentage. In total, 8,718,721 animals that were 45+% Limousin and born 2003+ were extracted from the BCMS database. Animals were removed if an invalid birth date (i.e. before parents born), the herd of birth was missing or had fewer than 5 animals in the birth year of their herd, the animal was listed as a dam but was male in sex, cows with calves without a valid birth date, cows where their age at first calf was not between 1.5 and 4 years of age and cows where calving intervals were not between 270 and 913 days. The edited dataset contained 8,139,121 animals (4,117,013 males and 4,022,108 females) born in 41,073 different herds. This dataset was used to summarise the FF and CS traits in the Limousin commercial population.
Trait definitions

Examination of the raw data helped to define the FF and CS trait definitions. Only the calving interval trait definition is the same as those currently applied to the pedigree evaluation. Three FF traits and one CS trait were defined as follows; Age at first calf (AFC) - Age (days) of the cow at her first parity, Calving Interval (CI) - Time (days) between parity's 1 and 2, Lifespan (LS) - Number of parities before 6.5 years and Calf Survival (CS) - Survival (1=died, 2=survived) to 10 months of age. Beef calves dying before 20 days of age are not compulsory to be recorded in BCMS. For LS the age of 6.5 was chosen as approximately only a third of cows are still producing calves after this age and it allows a LS phenotype to be generated before the cow actually dies.

Genetic Parameter Estimation

For genetic parameter estimation the dataset described above was further edited removing animals born after 2009 to ensure an animal's reproductive life was complete, animals with unknown dam and animals where sire and maternal grandsire were unknown. This resulted in 1,770,600 animals. Trait specific edits were then undertaken. The AFC and CS contemporary groups (CG) were based on the heifer's birth herd and birth year and season. For all CG the season was formed by splitting the year into two six month seasons (Spring and Winter). The CI and LS CG were the same and formed using the birth herd and birth year/season of the heifer's first calf.

AFC records were only used where, the heifer was aged between 548 and 1,460 days, the calf was not the result of ET, the calf birth date was before the heifer death date, the AFC record was not greater than 3 standard deviations from the CG mean record and the heifer was not part of a single sire or small (n<5) AFC CG. CI records were only used where the cow had a valid AFC record, the CI was greater than 270 days, the CI record was not greater than 3 standard deviations from the CG mean record and the cow was not part of a single sire or small (n<5) CI CG. Cows with a CI record greater than 913 days received a penalty value of 930 days. LS records were only valid when the cow had a valid AFC record and the cow was not part of a single sire or small (n<5) LS CG. This resulted in 58,148, 27,861 and 34,307 records respectively for AFC, CI and LS. CS records were set to missing if the animal was from a birth where more than 2 calves were born, if all animals in a CS CG had the same phenotype, were sired by a single sire or had fewer than 5 animals. In addition, whole CGs were removed where the death rate of the whole CG was less than 2% or the death rate within each sex was outside 3 standard deviations from the population (within sex) mean death rate. This resulted in 140,309 survival records which were further reduced to those born between 2007 and 2009 resulting in 55,149 records.

A 3 generation pedigree was built and genetic parameters estimated using ASReml (Gilmour *et al*, 2009). Statistical models for FF traits were adapted from those used in conventional genetic evaluations. All three FF traits fitted CG as a fixed class effect, heterosis and recombination coefficients as covariates and animal as a random effect. As fixed class effects, AFC fitted dam parity and CI fitted the month of calving. Both CI and LS fitted as covariates the linear and quadratic effects of age at first calf. With no prior model available for CS the PROC MIXED function in SAS (SAS institute, 2007) was used to determine significant fixed effects by backwards elimination fitting sire as random. The final model fitted was fixed class effects CG, dam parity, sex and number of calves in the parity. As covariate effects dam age (days), heterosis and recombination coefficients were fitted with animal fitted as a random effect. Details of the heterosis and recombination coefficients for all

four traits can be found in Moore *et al*, (2017). Univariate models estimated variances and heritabilities with bi-variate models estimating co-variance components.

Genomic Estimated Breeding Values (GEBVs)

To produce GEBVs 5,487 Limousin genotypes of varying densities were available; 1,889 Illumina 800k HD chip, 2,106 Illumina 50k V2 chip, 641 Illumina IDB 50k chip and 1, 253 and 597 Illumina IDB LD V1, V2 and V3 chip, respectively. The genotypes were sourced from research projects (n=3,562), international swapping (n=977) and Limousin genotyping service, (n=948). Duplicate genotypes (n=110) and those with a call rate <0.90 (n=252) were removed. Almost half of the genotypes (n=2,693) could be parentage verified with 3% failing (n=90) and being excluded from the analysis. This failure rate is very low as a result of the breed society's policy on parentage testing. After edits, 5,023 genotypes remained. Using Findhap version 4 (Van Raden, 2017) genotypes were imputed to a standard subset of 38,905 SNPs from the Illumina 50k chip preselected for UK genetic evaluations after previous analysis removed SNPs with poor call rates and minor allele frequency. Single-Step approach using Mix99 (Lidauer and Stranden, 1999) was employed to produce GEBVs based on the imputed genotypes and the models described for genetic parameter estimation. Breeding values were produced for 5,905,249 animals based on the genotypes described above and 101,376, 43,969, 36,101 and 246,654 records for AFC, CI, LS and CS, respectively. The data extraction rules are similar to those described for genetic parameter estimation but without the end year cut-off to allow modern animals into the evaluation. The requirement for sire or maternal grand sire to be known is the major reason why the number of phenotypes was lower than the number of animals in the national database.

Results and Discussion

Description of female fertility and calf survival in the UK Limousin population

Examination of FF and CS in our dataset reflects the whole industry rather than a single subset, i.e. pedigree only data. Although only Limousin results are reported, all major beef breeds were considered and showed similar results and trends.

Analysis of 559,832 dams in the dataset for AFC showed a distribution with two peaks at 25 and 36 months of age. This reflects variation in calving policies with some herds aiming to calve as 2 year olds and others as 3 year olds. Approximately twice as many cows calved at 36 months compared to 25 months, showing that industry can make significant gains decreasing the AFC to 2 years of age. Average AFC has remained unchanged across the years (results not shown) demonstrating a lack of improvement for the reasons outlined in the introduction. Subsequent CI showed that as cows have more calves the CI decreases, most likely as the less fertile cows are culled and don't remain in the herd. The average 1st-2nd, 2nd-3rd, 3rd-4th and 4th-5th CI was 424, 402, 394 and 390 days, respectively. Table 1 show that less than half of the breeding cows have more than 3 calves. The average age of cows that do, indicate that these cows on average calved as a 2 year old and then produced a calf every 365 days.

Table 1. Lifetime productivity of Limousin sired cows, showing the number and age of cows with different number of lifetime parities, and the percentage of cows progressing to future parities.

Number	Number	Average dam age	Percentage of all	Percent of dams from

parities	cows	(days/years)	dams	previous parity
1	559,832	961/2.6	100.0	-
2	435,001	1,396/3.8	77.7	77.7
3	341,358	1,798/4.9	61.0	78.5
4	263,169	2,185/6.0	47.0	77.1
5	196,876	2,560/7.0	35.2	74.8

Most calf mortality occurs early in life (results not shown) and from 409,941 calving records it was shown that 5% of calves did not survive to 10 months of age with higher mortality amongst males (results not shown). A closer look at the deaths in the first 30 days (results not shown) show a large peak at 1 day of age suggesting that although not compulsory, a large number of deaths immediately post calving are being recorded in BCMS, and this is when the largest number of calf deaths occur.

Genetic Parameter Estimates

All traits were heritable with sufficient variation for selection (Table 2). Heritabilities were low ranging from 0.04 for CS to 0.13 to AFC. Genetic correlations between fertility traits all had high standard errors resulting in non-significant estimates close to 0, except a moderate negative genetic correlation estimated between CI and LS. This correlation indicates that as the calving interval increases, the number of calves that a cow will produce by the time she is 6.5 years will decrease. The phenotypic correlation estimates showed the same. These estimates are similar to those reported by Roughsedge *et al*, (2005a) from purebred pedigree phenotypes. Bi-variates between CS and the fertility traits were not investigated.

Table 2. Phenotypic variances (Vp), heritability (on diagonal) and genetic (above diagonal) and phenotypic (below diagonal) correlations for female fertility and calf survival traits (standard errors).

Trait[1]	Number	Vp	AFC	CI	LS	CS
AFC	58,148	15057 (99.40)	0.13 (0.01)	-0.04 (0.18)	-0.03 (0.14)	-
CI	27,861	10448 (96.05)	-0.03 (0.01)	0.05 (0.02)	-0.46 (0.19)	-
LS	34,307	1.19 (0.01)	0.01 (0.01)	-0.30 (0.01)	0.05 (0.01)	-
CS	55,149	0.075 (0.001)	-	-	-	0.04 (0.01)

[1] AFC=Age at first calf, CI=Calving interval, LS=Lifespan and CS=Calf survival

Genomic Estimated Breeding Values (GEBVs)

Breeding values from single step methodology were produced for 5,905,249 animals, of which 510,554 were pedigree Limousin cattle. These results will consider only pedigree Limousin cattle. Despite being low heritability traits, the EBVs of sires with accuracy greater than 50% and more than 10 phenotyped progeny showed reasonable of progeny performance. For AFC there were 1,853 sires and the correlation and regression between sire EBV and average progeny performance was 0.20 and 0.96, respectively. For CI the correlation and regression was 0.37 and 1.38 from 522 sires, and for LS the correlation and regression was 0.41 and 1.34 from 474 sires. The correlation and regression for CS was 0.43 and 1.12 from 3,582 sires. This indicates that selecting sires with EBVs increasing will on average increase the performance of progeny, however correlations tend to be lower reflecting the large impact that management also has on the phenotypes. The regression coefficients indicate that for

AFC and CS the EBVs are unbiased but there is a small positive bias for LS and CI with EBVs tending to be overestimated for this small number of sires.

Genetic trends from 2000 were computed from EBVs with accuracy greater than 50%. There was effectively no change over time; for AFC, CI, LS and CS there was an average change of 0.09 days/year, -0.001 days/year, 0.0006 calves/year and 0.00008 %survival/year, respectively.

To avoid industry confusion the FF GEBVs produced will replace conventional pedigree FF EBVs. Despite trait definitions changing significantly between the evaluations, correlations between the 2 sets of EBVs were moderately positive indicating that while there will be re-ranking, high EBV sires from the pedigree only based evaluation will also tend to be the high GEBV sires from the new evaluation based on industry data. Correlations of 0.33, 0.33 and 0.43 were found for AFC, CI and LS EBVs, respectively for animals with EBV accuracy greater than 50%. Reasons for re-ranking could be due to the addition of new data, the new trait definitions and/or the introduction of genomics.

Data structure did not allow for correlation estimates between FF and CS traits and abattoir carcass traits provided to industry in 2016. However, correlations between GEBVs showed that there was no relationship between carcass weight and FF/CS GEBVs with correlations ranging from -0.05 with CS to 0.03 with LS. This was unexpected as Roughsedge *et al*, (2005a) reported moderate correlations between 400 day live weight and FF traits. Slaughter age also had very small correlations ranging from -0.03 with CS to 0.03 for AFC. In general, small positive correlations were observed between AFC and the six VIA primal cuts (0.11 with fillet to 0.16 with topside) and between CI and the same primal cuts (-0.01 with striploin to 0.20 with topside). Small negative correlations were found between the LS GEBV and the primal cuts (-0.22 with fillet to -0.04 with striploin). The relationship between the primal cuts and CS was very slightly negative, but close to 0 with correlations ranging from -0.10 with fillet to -0.04 with topside. These are the first known attempt to investigate the correlation between VIA primal cut and FF and CS traits. AFC and EUROP conformation were moderately positively correlated with r=0.19, but the correlation between conformation and the other traits were very small (-0.08 with LS to 0.04 with CI). EUROP fat was positively correlated with LS (0.18) but negatively correlated with the remaining traits with-0.06 for CS to -0.23 for CI. Although based only on GEBVs, these correlations suggest that reducing AFC, reducing CI or increasing LS would all see a decrease in the primal cuts and EUROP conformation, but not the overall carcass weight, and would result in an increase in fat cover. The effects of improving CS would not have a big impact on the carcass traits based on these correlations.

Conclusions

GEBVs produced for FF and CS traits provide to the industry, for the first time, accurate selection tools from birth. Using these tools breeders will be able to breed for improved fertility and survival as well as improved carcass attributes resulting in increased production, efficiency and profitability for the UK beef sector.

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