Impact of Genomic Selection for Residual Feed Intake and Calf Survival in Beef Cattle on Profit and Greenhouse Gas Mitigation

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Introduction

Studies in the UK showed that beef breeding programmes increase farm profitability and contribute to greenhouse gas (GHG) mitigation (Moran *et al.* (2008)). Improving calf survival and decreasing residual feed intake (RFI) could lead to further increases in system efficiency and decreases of feed input resulting in further reductions in GHG emissions. The inclusion of RFI in breeding programmes has been limited due to difficulties of obtaining individual measurements of intake on selection candidates. However, genomic selection (GS) provides a possible opportunity to use a trait such as RFI more broadly in breeding programmes. The implementation of GS, based on the prediction of genomic merit, relies on establishing the associations between phenotypes and the dense marker panels in a training population (TP). The accuracy with which genomic breeding values can be estimated depends mainly on the effective population size (Ne) and the number of animals in the TP. The objective of this study was to investigate the effects of including RFI and calf survival in the breeding objective simultaneously with the implementation of genomic selection. This was quantified in the current UK maternal breeding programs and in an alternative young bull program in terms of the economic benefit and GHG emissions at the whole beef industry level.

Material and methods

Breeding programmes. Three scenarios were considered in this study: (1) CBP: the current UK maternal breeding programs in which selection indices are based on estimated breeding values (EBV). The current traits included in the breeding goal are weight at 200 days (WT200), carcass weight (CW), carcass fat score (CFS), carcass conformation score (CCS), gestation length (GL), calving difficulty (CD), calving interval (CI), age at first calving (AFC), lifespan (LS), mature weight of breeding animals (MW-m), and mature weight of replacements (MW-r); (2) CBP-GS: the breeding structure is similar to the CBP but survival and RFI were added to the breeding goal. EBV for survival traits were added to the current traits in females. In males, GS was integrated by combining genomic EBV (GEBV) to the EBV in the selection indices for the current traits and survival. Selection for RFI was based only on GEBV; (3) YBP-GS: goal traits and selection criteria were the same as in CBP-GS for males and females but the breeding population differed because only young bulls (YBP)

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were used as breeding program sires. Table 1 shows heritabilities, economic values and effects of GHG emissions on current and new goal traits (RFI for slaughter calves; RFI for breeding cows; birth and weaning survival (BSV, WSV)). In the CBP, the proportion of animals selected and generation intervals for females and males were 0.04 and 0.53, and 5.58 and 6.25 years, respectively. In the YBP the values for females remain the same, whilst the proportion of males selected was 0.06 and the generation interval decreased to 3 years.

Table 1: Heritabilities (h^2), phenotypic variances (σ_P^2), economic (EV) and GHG values of current and new goal traits

Traits[α]	h^2	σ_P^2	EV	GHG
WT200	0.07	807.44	0.65	-8.8
CW	0.44	859.60	0.73	-12.26
CFS	0.13	4.10		
CCS	0.11	9.83	7.00	
GL	0.29	23.81	-1.00	
CD-d	0.12	1.02	-2.47	
CD-m	0.05	1.02	-1.66	
CI	0.09	2367.54	-0.63	-7.46
AFC	0.20	0.22	-170.00	-3.85
LS	0.11	6.06	46.02	
MW-m	0.51	3779.25	-0.17	
MW-r	0.51	3779.25	-0.41	0.8776
RFI-g	0.30	95852.16	-0.069	0.3782
RFI-b	0.30	46915.56	-0.066	0.4253
BSV-d	0.10	0.03	230.00	
BSV-m	0.03	0.03	230.00	
WSV-d	0.11	0.01	230.00	
WSV-m	0.05	0.01	230.00	

[α] –d, direct component; -m, maternal component

Genetic responses. Selection index theory was applied to predict the genetic responses in the three scenarios. Genetic and phenotypic parameters used in the analysis are those used in the national beef genetic evaluations for the current traits. Further information for the goal traits was obtained from Roughsedge *et al.* (2005). Parameters for the new traits were based on a review of several sources (i.e., Nkrumah *et al.* (2007)). Ages of selection candidates and recorded trait information modeled in the selection index equations were based on average industry practice as determined from a summary analysis of the national database. Accuracies of GEBV were predicted based on trait heritability, number of phenotyped animals in the TP, the number of QTL underlying the trait and the Ne (Daetwyler *et al.* (2008); Goddard (2009)), as described by Sawalha *et al.* (2010). Genetic responses for CBP-GS and YBP-GS were calculated for Ne of 100 and 300 and TP of 2000 and 5000 animals. Correlated responses on RFI and survival were also predicted for the CBP

Economic evaluation at industry level. Cumulative marginal net discounted return from 10 years of selection with benefits considered over a 20-year horizon was the primary criterion for comparison of effects on farm profitability. Discounted incomes were calculated for each of the goal traits based on the annual genetic gain in the trait units and their economic values discounted by the specific genetic expression coefficients considering time and number of expressions of the genetic progress, and the number of bulls from the breeding programmes required to mate the industry females, assuming a 100% adoption of the technology. A discount rate of 7% was used when discounting genetic expressions of goal traits over time. The net returns of CBP-GS and YBP-GS were presented as proportionate increases relative to the net returns for CBP. The costs included were: (1) the cost of genotyping the selection candidates (£200 or £100/sample) during the 10 years of selection discounted at 7%, and (2) the costs associated with the TP, which included genotyping and RFI measurements (£1700/animal). No additional costs of recording survival were accounted for as the information is already available in the current databases. Other costs associated with the implementation were considered similar to the CBP and therefore not added to the total cost.

GHG emissions. The volumes of GHG emissions were calculated taking into account the genetic gains, discounted genetic expression coefficients and the estimates of emissions of CO_2 equivalent per unit of change per breeding animal (Wall *et al.*, (2010); table 1). These estimates, which considered methane and nitrous emissions, were obtained from the modeling of UK beef production system to calculate the GHG emissions when production traits were modified. Not all traits were considered due to modeling limitations and lack of information on the associations among traits (Wall *et al.* (2010)).

Results and discussion

Figures 1a and 1b shows the cumulative discounted income of CBP-GS and YBP-GS and the responses in GHG mitigation (reduction of GHG emissions). Both traits are expressed relative to the values observed in the CBP (economic response, £62.6 million; GHG mitigation, 1.5 million ton of CO_2 equivalent).

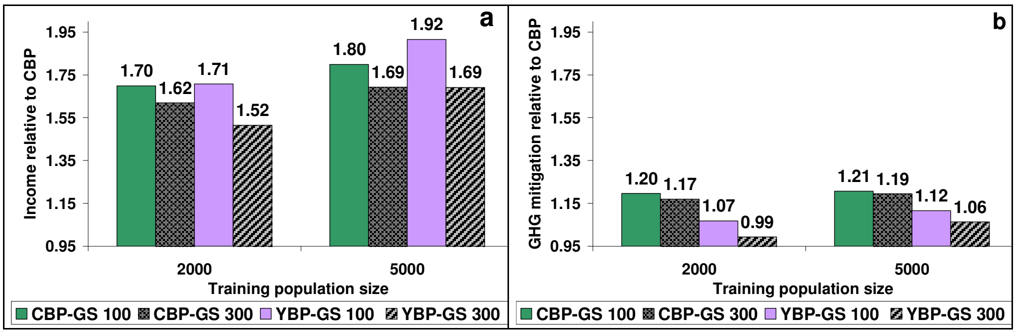

Figure 1: Cumulative economic discounted income (a) and GHG mitigation (b) in CBP-GS and YBP-GS where the Ne of the cattle population is 100 or 300. Results are expressed relative to values observed in the CBP

Improvements in both economic and environmental terms resulted from CBP-GS and YBP-GS, compared to CBP (values higher than 1 in figures 1a and 1b). The responses in income were higher in both alternative scenarios when smaller Ne were assumed. For a given Ne, larger TP sizes increase the economic response. This effect was proportionally larger for the young bull breeding program compared with the current breeding program. Lower effective population size resulted in a higher cumulative discounted income but the effects of Ne being 300 to Ne being 100 was less than increasing the TP size from 2000 to 5000. Proportional changes in GHG emissions were smaller than proportional changes in cumulative economic discounted income. The value of 0.99 for YBP-GS 300 with a TP of 2000 in Figure 1b indicated a small increase of 1% of kg of GHG emitted. All other options improved GHG mitigation. The CBP-GS showed a more significant contribution to GHG mitigation (reduction of GHG emitted) compared to the YBP-GS.

The net returns of all options were positive (data not presented) indicating that they were all cost-effective. To simplify comparisons the net returns of the options t are expressed relative to the value of the CBP-GS with Ne and TP of 100 and 2000, respectively (table 3). The lower net returns were obtained when Ne was of 300 animals. Although higher costs were associated with larger TP, the net return was 3% higher when the TP was of 5000 animals in the CBP-GS. This difference increased to 30% in the YBP-GS. Lower genotyping costs from £200 to £100 had an important impact on net returns which increased on average by 42%.

Table 3: Relative cumulative marginal net discount returns $^{\beta,\gamma}$

Alternative scenarios	Ne=100 TP=2000	Ne=100 TP=5000	Ne=300 TP=2000	Ne=300 TP=5000
CPB-GS	1.00	1.03	0.77	0.72
YBP-GS	1.02	1.35	0.48	0.72

[β] Relative to the value of the CBP-GS wit Ne=100 and TP=2000

[γ] Genotyping cost = £ 200/animal

Conclusion

The inclusion of RFI and survival traits and use of GEBVs had a large favorable impact on net economic returns and a more modest impact on reduced GHG emissions. Higher responses in GHG mitigation may be possible if GHG is directly incorporated into the breeding goal. Optimizing GS strategy in practice should consider the real undetermined beef cattle effective population sizes. Further analysis should include the sensitivity analysis for the main parameters assumed in this deterministic analysis.

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