

Selection Response in UK Sheep Breeding Program with the Application of Genomic Selection and Inclusion of Production Efficiency Traits

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Introduction

BLUP genetic evaluation combined with an economic index approach have been shown to be effective genetic improvement tools in different UK sheep breeding sectors (Amer et al. (2007); Haresign et al. (2007); and Conington et al. (2008)). Recent developments in marker and genotyping technology have made it possible to genotype dense SNP marker panels at commercially affordable prices. Such genome wide marker panels can be used to establish associations between markers and trait phenotypes in order to make predictions of breeding values based only on genotyping. Establishing the associations requires a training population (TP) in which animals have phenotypes and genotypes recorded. This method has been called Genomic Selection (GS) and enables the estimation of moderate to high accuracy EBVs for young animals and also provides an opportunity to introduce breeding values for new traits that are expensive or impractical to record in all selection candidates, such as residual feed intake.

The objective of this study is to explore the potential of including genomic information and its effect on selection response in the three main UK sheep breeding sectors; hill, longwool, and terminal sheep breeds. Different training and effective population sizes were simulated and the inclusion of new production efficiency traits was also tested.

Material and methods

Selection index methodology was utilised to investigate the impact of GS on selection response. Genetic parameter estimates that were used in the index were based on the estimates used in UK national genetic evaluations for the current index traits. Table 1 presents the current and new traits included in the index along with their estimates of heritability and economic weights. Estimates of genetic parameters for RFI were based on the few published results in this area (François et al. (2002); Snowden and Van Vleck (2003); and Cammack et al. (2005)). For lamb survival and ewe longevity, the estimates were based on reported values by Haresign et al. (2007), Sawalha et al. (2007), and Riggio, Finocchiaro, and Bishop (2008). Estimates of genetic parameters for footrot were based on the reviews published by Safari and Fogarty (2003) and Safari et al. (2005).

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Table 1: Current Index and new traits with heritability estimates (h^2) and economic values (EV) in GBP (£) used in the index.

Trait	Hill		Longwool		Terminal sire	
	h^2	EV	h^2	EV	h^2	EV
Current profit traits						
Carcass fat (mm)	0.25	-0.14			0.29	-1.76
Carcass muscle (mm)	0.35	0.55	0.36	5.87	0.28	2.66
Slaughter age (days)			0.23	-0.07		
Conformation score			0.12	0.55		
Mature size (kg)	0.43	-0.05	0.45	-0.5		
Litter wt weaned (kg)	0.1	0.19				
Litter size (count)	0.05	0.10	0.05	4.7		
Eight week wt (kg)	0.12	0.38				
New profit traits						
RFI-Lambs (kg/head/finishing period)	0.3	-0.04	0.3	0.07	0.30	0.06
RFI-Ewes (kg/breeding ewe/year)	0.3	-0.02	0.3	0.05		
Ewe longevity (years)	0.27	0.001	0.3	11.2		
Footrot (incidence)	0.045	-0.01	0.05	-0.20		
Lamb survival (yes/no)	0.03	0.46	0.03	38.8	0.03	15.6

The economic values for the current traits and for lamb survival were based on those reported by Conington et al. (2008) for hill sheep, Haresign et al. (2007) for longwool sheep, and Amer et al (2007) and Jones et al. (2004) for terminal sire sheep. The economic values for RFI were calculated accounting for feed requirements during the finishing period for growing lambs and for one year feed requirements for ewes assuming 5 to 7 pence per kilo of DMI (Amer, personal communications). For footrot, economic values were derived by Amer (personal communications).

Sources of information (relatives recorded for each trait) were estimated for each sex using UK pedigree and performance data. The selection intensity and generation interval of male and female candidates selected were also estimated from the pedigree data. Three main scenarios of selection were simulated.

- I- Base index: this is the current breeding programme with no new traits added.
- II- Base index with up to five new traits.
- III- Base index with up to five new traits and with genomic information (GEBVs). Four scenarios of genomic selection were simulated:
 - A- TP = 2000 and Ne = 200,
 - B- TP = 5000 and Ne = 200,
 - C- TP = 2000 and Ne = 500, and
 - D- TP = 5000 and Ne = 500.

The accuracy of the GEBVs (r_{MG1}) was calculated following (Daetwyler *et al.*, 2008;

Goddard, 2009): $r_{MG1} = \sqrt{\frac{\lambda h_o^2}{\lambda h_o^2 + 1}}$, where h_o^2 is the heritability of the trait and λ is the

number of phenotypes recorded in the training population/number of QTL underlying the trait. The number of QTL affecting the trait was approximated by the effective number of chromosome segments defined by Goddard (2009) as $Me = (2N_e L) / \ln(4N_e L)$; where N_e is the effective population size and L is the chromosome length. Genetic and phenotypic correlation matrices including EBVs and GEBVs were calculated based on the approach proposed by Dekkers (2007).

Results and discussion

The overall annual economic responses of different scenarios relative to the BLUP selection with new traits (Index II) are shown in Figure 1 for hill, longwool, and terminal sheep breeds.

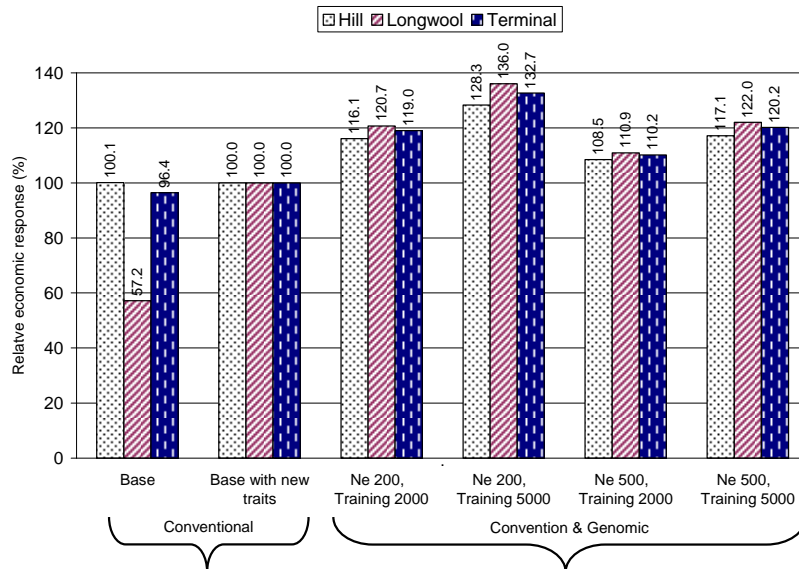


Figure 1. Overall annual economic response of different selection scenarios relative to the base index (base index including new traits, Index II) in hill, longwool, and terminal sire sheep.

Results show that the expected annual economic response is the same for the first two scenarios using BLUP for hill sheep. Similar results can be seen for terminal sire sheep where the inclusion of the new traits improved the current breeding program by just 4%.

However, for longwool, adding the new traits to the index improved the overall response by more than 40%. This was mainly due to the substantial contribution of longevity to the overall response in longwool sheep.

The inclusion of genomic information resulted in a substantial increase in economic response to selection ranging from about 8 to 28% increase in hill sheep, 10 to 36% increase in longwool sheep, and 10 to 32% increase in terminal sire sheep relative to the conventional breeding programme. The training population size has large effect on expected economic response (the larger the training population, the higher the expected response) and its effect is more apparent when the effective population size was smaller. Comparing the two effective population sizes at fixed training population sizes, there would be about 7 to 12% more gain for breeds with effective population size of 200 compared with those with effective population size of 500). Larger training population (5000 versus 2000 has more effect on selection response than smaller effective population size (200 versus 500).

When examining the response in traits individually, including genomic information along with conventional breeding resulted in higher favourable rate of response in most traits compared with conventional selection alone. Using genomic information with conventional breeding can reduce RFI by up to 606 g in growing lambs and by up to 1,336 g in breeding ewes compared with conventional breeding.

Conclusion

These results clearly show that inclusion of genomic information can have a favorable substantial effect on expected response to selection. New efficiency traits can be included in the index and improved through both conventional and genomic selection. It can also be concluded that it is possible to genetically improve traits that are difficult to record under commercial setting such as residual feed intake. However, phenotypes for the new traits will still be required for TP and that might still be too expensive to implement in practice.

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