POTENTIAL BENEFIT OF GENOMIC SELECTION IN SHEEP

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SUMMARY

The short term benefits of applying whole genome selection to sheep breeding programs are estimated. If breeding values of all objective traits can be predicted with accuracy equal to the square root of heritability, genomic selection could increase overall response for a terminal sire index by about 30%, and a fine wool merino index by about 40%. Response is relatively more increased for those traits that are normally not measured on breeding animals.

INTRODUCTION

Major research efforts are undertaken worldwide to attempt prediction of genetic merit from genomic information. This renewed effort is motivated by the idea of genomic selection (GS), i.e. selection based on the joint effects of very many genes linked to markers densely covering the whole genome. The first paper to propose the idea of predicting genetic merit from dense gene markers was published by Meuwissen *et al.* (2001), showing theoretically a potential accuracy of up to 80%. Developments in genotyping technology, along with the publication of genome sequences for human in 2001, and bovine in 2006, have allowed rapid detection of Single Nucleotide Polymorphisms (SNPs) and development of SNP-chips for rapid genotyping. A bovine SNP chip was initially developed for 10,000 (10k) markers and in 2007 a 56k chip was released by Illumina. Similarly, a 57k ovine chip was developed and released in August 2008, partly based on a *virtual ovine genome sequence* (Dalrymple *et al.* 2007).

First results of whole genome association studies in dairy cattle have shown some convincing results, with the ability to predict breeding values of young dairy bulls with an accuracy of around 60%. This is the correlation between a predicted breeding value based on genomic data and one based on the mean performance of a large number (~100) of progeny, i.e. genomic information can predict around 36% of the variation in true breeding value (additive genetic variance). The benefit of this to dairy breeding programs is large. As genetic change is largely based on selection of bulls, and since milk production is sex limited, breeders have to accept long generation intervals and wait for a progeny test, or select at a younger age based on less accurate EBVs. Genomic selection allows selection of bulls at a young age based on a much improved accuracy. Schaeffer (2006) suggested that dairy programs could possibly double their rate of genetic gain by using GS.

The benefit of GS might be smaller in sheep as 1) many traits under selection in sheep can be measured on both sexes an before selection of animals for first mating, 2) several important traits have a high heritability, and 3) there maybe less information available to derive accurate prediction equations as there are fewer progeny tested sires. However, some traits in sheep are also difficult to measure on breeding animals, e.g. female fertility, slaughter traits, wool traits when measured on adults and parasite resistance. Furthermore, the Australian sheep industry invests in an *Information Nucleus* (Fogarty *et al.* 2007) that allows measurements of those objective traits that are normally not measured in commercial stud flocks. The overall benefit of GS will depend on measurability of the various breeding objective traits, and their relative economic importance. The purpose of this paper is to give a ballpark figure of potential benefit of GS in sheep breeding programs.

MATERIALS AND METHODS

Selection index theory was used to predict selection accuracy of male and female selection candidates in different age classes. The genomic information is modelled as an additional information source known at birth, explaining a percentage of the additive genetic variation (V_{QTL}). This percentage will be larger if more animals are used in deriving prediction equations and when the heritability is higher (Goddard 2006). Selection index theory was used to predict the accuracy of selection on a breeding objective, assuming the usual sheep traits measured. BLUP selection was mimicked, with information available on 29 half sibs, and 30 progeny on sires, when the appropriate age is reached. The index accuracy increases with age, and can vary between sexes. The age structure of a breeding program was optimized by truncation selection across age classes for each sex. Therefore, if genomic information was available, it was more likely that younger animals had high enough accuracies to be selected, and the optimal generation interval was generally lower. Increased selection accuracy and decreased generation intervals were therefore modelled as contributing to the benefit of GS.

The annual response to selection was compared for scenarios with and without genomic selection. First, this comparison was made for single trait selection, where the trait heritability, the trait measurability and V_{QTL} were varied. Secondly, the benefit of GS was compared for indexes relevant to the industry and derived by *SHEEP OBJECT* (Andrew Swan, personal communication), both for fine wool merinos and for terminal sire breeds. The terminal sire index, which is not (yet) used by the industry, contains carcass traits in the objective and growth and ultrasound scan measures for fat and muscle as selection criteria traits (see Table 2 for detail on traits). Three carcass traits have all a similar dollar value per genetic standard deviation, except that the value for carcass fat is negative and about one third as large. The main objective traits in the fine wool index were adult weight, adult clean fleece weight, adult mean fibre diameter, adult staple strength and number of lambs weaned. Young breeding animals have measurements for none of these traits at first selection.

Two GS scenarios were compared: under GS1 it was assumed that V_{QTL} is equal to the trait heritability (h^2). This is not a functional relationship, but a reasonable approximation of expected predicted accuracy of GS when phenotypic information on about 2500 animals is used for deriving GS prediction equations. Alternatively, $V_{QTL} = \frac{1}{2} h^2$, which would be achievable in an experiment with about 1000 phenotypic measurements

RESULTS AND DISCUSSION

Results of single trait selection with and without GS are shown in Table 1. The benefit of GS is clearly highest for traits that are more difficult to measure and have low heritability. The maximum benefit is a doubling of genetic gain. It should be noted that in practice it is more difficult to achieve a high GS accuracy for traits with low h^2 as much more phenotypic data are needed to derive GS prediction equations of such accuracy. The benefit is obviously highest for traits that cannot be measured at all, unless such traits have very high correlations with measured traits. Table 1 gives a benchmark figure for the approach used here. The potential benefit for sheep will have to be evaluated for a combination of traits, each with benefits varying according to conditions outlined in Table 1.

Results in Table 2 show for terminal sire breeds a 32% increase in overall response with accurate genomic selection (GS2) and a 16% increase with less accurate genomic selection (GS1). Obviously, individual carcass traits benefit greatly from GS as these traits are not measured on breeding animals. As a consequence, the GS response for traits measured post weaning is lower than with no GS. Results for a selection index for fine wool merino show a 38% increase in overall response with accurate genomic selection (GS2) and a 19% increase with GS1. Although fine wool traits are highly heritable and can be measured, the adult expression of these traits is usually

not recorded. Moreover, number of lambs weaned has limited measurability and is much more improved whereas staple strength, being an unmeasured trait, declines much less under genomic selection.

Table 1 Increase of rate of genetic gain (%) for single trait genomic selection for various degrees of variance explained by genotype (V_{QTL}), heritability (h^2) and trait measurability conditions.

Trait Measurability	V_{QTL} = 10%			V_{QTL} = 30%		
	h^2=0.1	h^2=0.3	h^2=0.5	h^2=0.1	h^2=0.3	h^2=0.5
Measured < 1 year, males and female	13	4	2	37	13	6
Measured > 1 year, males and females	19	9	6	64	29	18
Measured >1 year, females only	38	17	13	109	54	39
Measured on Corr. Trait, r_g = 0.9	17	7	4	48	20	11
Measured on Corr. Trait, r_g = 0.5	61	33	24	143	83	62

Listed heritability values refer to trait under selection, i.e. to correlated trait if applicable

Table 2. Accuracy and annual response to selection for meat sheep and fine wool merino indexes in scenarios with no (no GS), less accurate (GS1) and more accurate (GS2) genomic selection.

Meat Sheep Index	Phen	h^2	Accuracy			Response (trait units)		
			no GS	GS1	GS2	no GS	GS1	GS2
Muscle conformation (mm)	0	0.25	0.58	0.63	0.68	0.36	0.34	0.34
Dressing %	0	0.30	0.37	0.47	0.59	0.16	0.27	0.37
Saleable meat yield %	0	0.30	0.35	0.46	0.59	0.36	0.46	0.55
Carcass fat depth (mm)	0	0.30	0.41	0.51	0.62	-0.05	-0.06	-0.07
Post weaning weight	1	0.30	0.68	0.72	0.76	0.39	0.36	0.34
PW fat depth US	1	0.20	0.58	0.62	0.66	0.01	0.01	0.01
PW eye muscle depth US	1	0.30	0.66	0.70	0.75	0.34	0.31	0.29
Overall Merit ($Index)			0.46	0.58	0.66	1.30	1.51	1.71

Wool Sheep Index	Phen	h^2	Accuracy			Response (trait units)		
			no GS	GS1	GS2	no GS	GS1	GS2
Adult body weight	0	0.40	0.57	0.67	0.75	0.17	0.10	0.03
Adult clean fleece weight	0	0.44	0.48	0.62	0.74	0.03	0.06	0.07
Adult mean fibre diameter	0	0.60	0.66	0.76	0.85	-0.26	-0.25	-0.26
Adult staple strength	0	0.30	0.41	0.53	0.63	-0.37	-0.16	-0.01
Number of lambs weaned	fem	0.06	0.25	0.30	0.34	0.001	0.004	0.006
Overall Merit ($Index)			0.43	0.52	0.60	3.30	3.94	4.54

Variance explained by genotypes as proportion of additive genetic variance is equal to the heritability (h^2) for GS2 and ½h^2 for GS1, Phen indicates whether or not a trait is measured.

DISCUSSION

The approach followed in this study gives an approximate estimate of the potential value of GS. The results point out the main findings, i.e. the magnitude of the relative additional benefit is similar for meat and wool sheep, being between 15% and 40 %, and the potential change in trait

emphasis, away from easy to measure traits towards economically important but hard to measure traits. This shift in trait response is an important outcome of GS, besides the overall additional gain in total merit. The selection index approach works from the basis of information sources and their explained variance, and in that sense should be a reasonably robust approach in predicting GS outcomes. The main shortcoming of the method used here is that the long term effect of selection is not modelled. In an ongoing population under directional selection, the genetic variance generally reduces to about 75% of the variance in unselected populations. More importantly, it is mainly the between family variance that decreases whereas the within family (WF) variance is much less affected by selection. It is not fully clear whether GS exploits between or WF selection. If GS is based on estimated QTL effects, it would be more likely to exploit WF variance. A simulation study by Daetwyler *et al.* (2007) showed that GS limits the decrease in effective population size, suggesting that it works more at the WF variance level. However, we currently know little about the true genetic model underlying GS. There could be a number of factors that cause GS to be overestimated with the current theoretical approach, e.g. in reality, the prediction equations might not be equally accurate in all environmental and genetic backgrounds. Experimental evidence is needed to support these theoretical predictions. In addition, more work is needed to find ways of practical implementation of GS in the sheep industry.

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