

## **THE IMPACT OF GENOMIC SELECTION ON GENETIC GAIN IN THE NEW ZEALAND SHEEP DUAL PURPOSE SELECTION INDEX**

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### **SUMMARY**

To identify the impact of using molecular breeding values (mBVs) on the New Zealand sheep dual-purpose (DP) index, genomic selection (GS) accuracies were estimated using a training and validation data set consisting of 4,237 genotyped and pedigree recorded Romney animals. Molecular BVs and their accuracies for a range of DP production traits including live weight, fleece weight, faecal egg count, dagginess, reproduction and survival were estimated. The Romney mBV accuracies ranged from 0.16 to 0.52. For the majority of production traits the accuracies of the mBVs contributed information equivalent to having 1 to 8 measured progeny. For the traits: number of lambs born, lamb survival and lamb survival maternal the mBVs contributed between 11 to 145 measured progeny, albeit lamb survival maternal had a large error estimate. Combined with reducing the generation interval of rams used, from 2 years to 1 year, the potential increase in genetic gain in using mBVs in a New Zealand DP index was estimated to be 84%.

### **INTRODUCTION**

The development of high density single nucleotide polymorphism (SNP) chips has allowed the development of GS which enables prediction of an animal's worth (via mBVs) from their genomic information at birth. In the dairy industry, GS has been implemented in many countries (Hayes *et al.* 2009). In the sheep industry, genomic information has been successfully implemented for many traits and breeds in New Zealand (Auvray *et al.* 2011). However, the impact of genomic selection on the New Zealand sheep industry has not been examined. The aim of this paper is to estimate the increase in genetic gain attainable for the Romney breed using the Sheep Improvement Limited (SIL) DP selection index plus resistance to internal parasites, dagginess and lamb survival.

### **MATERIALS AND METHODS**

**Data.** Phenotypes (as estimated breeding values, eBVs) and pedigree data were downloaded from SIL; the export consisted of 3,535,557 animals born between 1990 and 2010 for 233 SIL flocks. Traits included in this analysis were direct and maternal weaning weight at 3 months (WWT, WWTm), carcass weight (CW), live weight at 8 months (LW8), adult ewe weight (EWT), lamb fleece weight (LFW), fleece weight at 12 months (FW12), adult ewe fleece weight (AFW), dag score at 3 and 8 months (DAG3, DAG8), number of lambs born (NLB), direct and maternal lamb survival (SURV, SURVm) and faecal egg count in summer (FEC1) and autumn (FEC2) and as an adult (AFEC).

There were 4,237 SIL recorded animals, mainly sires at least 70% Romney that were genotyped on the Illumina Ovine SNP50BeadChip (50K). Genotyping results were put through a quality control pipeline before analysis (Dodds *et al.* 2009); including removal of SNPs not retained as part of the Ovine HapMap study (Kijas *et al.* 2012). There were 48,327 SNPs which passed quality control. The animals were split into training and validation sets for each trait. Cut off years were chosen so at least 200 animals were used for validation.

**Statistical analysis.** Molecular breeding values (mBV) were calculated for each trait using genomic BLUP (gBLUP) model using the methods of Garrick *et al.* (2009) and VanRaden (2008), fitting the G1 (VanRaden 2008) matrix. The first 6 principal components (PC), using G1 as a similarity matrix, were also fitted to adjust for breed effects.

The accuracies of the mBVs were derived from the validation animals using 2 different methods. For the first method (using G1);  $r_A = \text{cor}(y, \text{mBV})/h_g$  calculated using weights:  $1/(1-r^2)$ . The effective heritability from the GS analysis ( $h_g^2$ ) was used and is equal to the average reliability ( $r^2$ ) of the parent-average-removed, deregressed eBV,  $y$ . The second method uses the prediction error variance (PEV, Mrode 2005) from a gBLUP analysis (using a relationship matrix calculated using breed-specific allele frequencies) giving;  $r_I = \sqrt{1-(\text{PEV}_i/\sigma_u^2)}$ , where  $\sigma_u^2$  is the genetic variance. This was calculated for all validation animals and averaged (weighted by  $1/(1-r^2)$ ). The 'combined-accuracy' ( $r_C$ ) was taken as the average of  $r_A$  and the  $r_I$ .

**Comparison of genetic gain.** The multiple trait selection index worksheet (van der Werf 2006a) was used to estimate the response per selection round for a given breeding scheme scenario in a DP Romney flock. The breeding scheme was simulated and assumed; a flock of 631 ewes; rams used once at a ratio of 1:90; number of lambs weaned/ewes mated was 141% (NLB: 1.71, lambs weaned/lambs born: 0.86 and ewes present at lambing/ewes mated: 0.98 (McEwan *et al.* 1992, Jopson *et al.* 2000, Pickering *et al.* 2012)); ewes lambed first at 2 years of age and retained to 5 years of age, with a 10% death and culling rate each year.

Selection was on a DP index with emphasis on increase kg of lamb, fleece weight, number of lambs, disease resistance, lamb survival and decrease dag score per ewe per ha. Heritability, repeatabilities and genetic and phenotypic correlations were from Pickering *et al.* (2012) or were those used for SIL breeding value analysis (S. A. Newman, pers. comm.). This paper utilises the breeders equation: Genetic gain ( $\Delta G$ ) =  $i r \sigma_a / L$ , where  $i$  is the selection intensity,  $r$  is the accuracy,  $\sigma_a$  is the genetic standard deviation and  $L$  is the generation interval. The paper examines changes to  $r$  and  $L$  under the following scenarios:

- Scenario 1 assumed selection was on animal measurements either for a ram hogget (Scenario 1-A) or a 2 year old ram (Scenario 1-B) which is used only once.
- Scenario 2: Romney ram hoggets were genotyped with a 50K SNP chip, the number of equivalent progeny was estimated using  $r_C$  (van der Werf 2006b). This method assumes that the information of the mBVs and traditional eBVs are independent and this approach is equivalent to simple blending as outlined by Mrode (2005).

Dual-purpose economic weights for the traits were taken from Byrne *et al.* (2012). The FEC1, FEC2 and AFEC economic weights were converted from % to loge by multiplying by 100.

The maximum number of measurements available were; 1 measurement on the individual and sire, 2 on the dam (for NLB) and 126 on half sibs. For CW, LFW, AFW, FEC2 and AFEC no measurements were taken; these traits were estimated from their correlations with the other traits. Results were converted from selection response per 'selection round' ( $r \sigma_a$ ) to selection response 'per year' ( $\Delta G$ ) by multiplying by  $i/L$ . For scenario 1-B:  $i/L$  equalled  $1.73/2.68 = 0.64$  and for scenario 1-A and 2:  $i/L$  equalled  $1.73/2.18 = 0.79$ .

## RESULTS AND DISCUSSION

The accuracies ( $r_C$ ) ranged between 0.16 and 0.52, equivalent to between 1 and 145 progeny (Table 1). For traits with low heritability the number of equivalent progeny equal to the accuracy of the SNP chip is large e.g. SURV and SURVm. For traits that are easy to measure and have moderate heritabilities, the SNP chip is equal to 1 or 2 equivalent progeny e.g. AFW and EWT.

The selection response per 'selection round' and 'per year' for each selection scenario is shown in Table 1. Scenario 1-B, resembling a farmer's normal decision using 2 year old rams and no SNP chip, had a genetic response of \$1.43 per year (accuracy 0.34). Reducing the generation interval, by using ram hoggets (scenario 1-A) increased genetic response to \$1.72 per year (accuracy 0.33). Scenario 2, selection of a hogget ram with SNP chip information had a genetic response of \$2.63 (accuracy 0.51), an 84% increase compared to scenario 1-B.

**Table 1. The response to each selection scenario as the unit change in trait ( $\Delta$  units), the overall response per selection round (Response \$) and accuracy, conversion factor (i/L, selection intensity/generation interval), and rate of genetic gain ( $\Delta G$ ), for each scenario<sup>1</sup>. Economic weighting (EW, \$) for each trait and the accuracy of the SNP chip ( $r_c$ ) and as equivalent progeny (E prog).**

Trait	EW	1-A	1-B	SNP chip		2
		$\Delta$ units	$\Delta$ units	$r_c$	E prog	$\Delta$ units
Weaning weight	0.95	0.49	0.48	0.48	8	0.42
WWT maternal	0.84	0.25	0.26	0.34	3	0.32
Carcass weight	2.60	0.2	0.18	0.48	4	0.12
Live weight 8 months	0.00	0.56	0.54	0.50	3	0.45
Adult ewe weight	-1.04	0.12	0.04	0.48	2	-0.30
Lamb fleece weight	1.82	0.01	0.01	0.29	2	0.01
Fleece weight 12 months	0.79	0.02	0.04	0.50	3	0.02
Adult fleece weight	2.28	0.06	0.08	0.32	1	0.06
Number of lambs born	15.55	0.01	0.01	0.52	16	0.05
Survival	64.45	0.003	0.003	0.16	11	0.003
Survival maternal	58.40	0.0001	0.0001	0.48	145	0.005
Dag score 3 months	-0.34	-0.11	-0.11	0.40	2	-0.08
Dag score 8 months	-0.35	-0.09	-0.09	0.44	3	-0.07
Faecal egg count summer	-3.00	-0.07	-0.06	0.46	6	-0.07
Faecal egg count autumn	-3.00	-0.04	-0.04	0.50	7	-0.06
Adult faecal egg count	-2.00	-0.07	-0.07	0.41	2	-0.09
Response \$		2.18	2.22			3.32
Accuracy		0.33	0.34			0.51
i/L		0.79	0.64			0.79
$\Delta G$ (\$)		1.72	1.43			2.63

<sup>1</sup> selected on individual, dam, sire and half sib records as ram hogget (1-A), 2 year old ram (1-B), or ram hogget plus SNP chip based on breed combined-accuracies from genomic selection (2).

The majority of the gain was seen in the lowly heritable traits, or sex limited traits measured late in life. Also a proportion of the gain resulted from reducing the generation interval by using ram hoggets rather than 2 year old rams. The annual response in an Australian terminal index and a fine wool index after including genomic selection increased by 32% and 38% increase respectively (van der Werf, 2009). The results calculated here for scenario 2 are considerably larger than that presented by van der Werf (2009). They reflect differences in the economic weighting and accuracy of the genomic mBVs for the traits in the respective New Zealand and Australian breeding objectives. The example presented assumes that all animals in a flock are genotyped and that rams used are all of the same age. In practice, the actual response will vary by flock depending on the composition of the flock, breeding strategy and cost of SNP chips. Rams used will be a mixture of new untested rams, emerging rams used once before and mature tested rams. The current comparison also does not take into account the cost of genotyping. To maximise discounted financial returns, 2-stage selection would be used and only a proportion (10-20%) of ram lambs would be genotyped (Sise *et al.* 2011). This would effect a slight reduction on the

average mBV accuracies of the flock. In addition, costs would be reduced further by use of lower density chips, such as the 5K Ovine SNP chip, coupled with imputation. This would have minimal impact on the estimated mBV accuracies as shown by Berry and Kearney (2011) who estimated an average 97% correlation between mBVs estimated from imputed or real genotypes.

## **CONCLUSIONS**

Genomic selection can provide a significant increase in the rate of genetic gain per year when selecting on the New Zealand dual purpose index. The majority of the benefit comes from the increased accuracy of breeding value for sex-limited and measurements recorded later in life. Additional benefits can be derived by reducing the generation interval via use of ram hoggets. This comparison did not include facial eczema, flystrike or adult ewe longevity which will also greatly benefit from use of genomic selection.

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