SNP PREDICTORS TO ACCELERATE THE RATE OF GENETIC PROGRESS IN SHEEP

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SUMMARY

A selection index model was used to calculate the benefit of using SNP panels in a ram breeding program for 5 different target traits including growth, carcass yield, reproduction, survival and parasite resistance. Breeding programs using either a mixture of young, emerging and mature rams (based on industry average ram ages) or the use of predominantly young untested rams were considered. Using an index with modest emphasis on litter size, response to selection without markers was higher (111 index cents per annum) in the young ram program than that observed with an industry average program (106 index cents per annum). Whilst more information on mature rams leads to better selection decisions, the reduced generation interval achieved through use of young rams leads to a higher overall response. When SNP markers were included as selection criteria with a prediction accuracy of 0.5, the increase in overall breeding program response ranged from 2-10 cents of index per animal per year, with the largest gains observed in markers for growth and carcass yield. Proportionately greater increments of response are expected as the accuracy of the genomic scores increases beyond 0.5.

INTRODUCTION

In breeding programs, an index of economic merit is commonly used to assist in selection decisions. Recorded trait and pedigree information is used to estimate breeding values, which are combined into an index according to their relative economic weightings. Over the last 5 years, much research has gone into the development of high density DNA marker chips, containing hundreds or even thousands of single nucleotide polymorphisms (SNPs), which are linked to traits of economic importance. Associations of large numbers of markers spread across the genome with phenotypes linked to economic traits, has allowed development of marker assisted selection methods, used to predict breeding values for individuals using their combined marker genotypes (Meuwissen *et.al* .2001).

This paper uses a selection index model to predict the response to genomic selection in dual purpose sheep breeding flocks. Parameters and assumptions are based around selection indexes widely used within the New Zealand sheep industry (http://www.sil.co.nz/). Ages of candidates at selection were based on Amer (2009). Selection index methods can be used to determine the potential benefits of recorded trait and DNA marker information in selection decisions for young animals (Dekkers 2007). Results are presented as the breeding program response with and without genomic markers.

MATERIALS and METHODS

A selection index model was used to predict the response to conventional and marker assisted selection in dual purpose sheep breeding flocks. The total merit index was comprised of prolificacy, growth, carcase, wool, lamb survival and internal parasite resistance traits of direct economic performance. Selection criteria included, lamb survival observations, 2 live weights, recorded at weaning (WWT) and as the estimated weight at slaughter age (CW), a hogget fleece weight (HFW), ultrasonic fat depth (FD), eye muscle area (EMA), and faecal egg count measurements (FEC2).

Within a breeding program, animals available for selection include young rams and ewes with no progeny at the time of selection, and older rams with recorded progeny. The amount of data available for use in the selection process varies according to the age and sex of animals. Rams are split into 3 different ram types according to their age.

1. Young untested "new" rams have no progeny information available, but do have their own trait records along with WWT and SUR records from up to 120 paternal half sibs. Other trait records available include CW, EMA and FD on 100 paternal half sibs, 80 FEC2 and 60 HFW paternal half sib records. Information is also derived from their mother and 15 paternal aunts, who each have 2 performance records for NLB.
2. Emerging rams have been used once either as a hogget or a two tooth ram and have progeny information, including 100 records for WWT and SUR, 80 for CW, 60 for FEC2 and 50 for HFW, EMA and FD but have no daughter lambing records, so NLB information is still derived from their mothers and paternal aunts.
3. Mature rams have a complete set of progeny data, including 120 progeny records for WWT, SUR, CWT, and HFW. They also have 100 progeny records for both EMA and FD, and 80 FEC2 progeny records. NLB information is available from performance records of 40 female progeny and an additional 40 paternal half sibs.

Ewes are assumed to have the same records as those of young rams, with the exception that they have no HFW records for themselves or on their half sibs. Genetic and phenotypic correlation matrices are incorporated into the selection index calculation to account for known positive and negative associations between correlated traits.

Five genomic scores have been modeled, where each genomic score has a heritability of 0.95 (allowing for genotype error) and a correlation of 0.25, 0.5, or 0.75 with the corresponding breeding objective traits; litter size, carcase weight, meat yield, lamb survival and internal parasite resistance.

Selection index calculations are made specifically for each candidate type, where the superiority of the top 5% of rams selected for mating and the top 60% of ewe lambs going into the flock as replacement ewes each year is estimated (based on index). Results are reported for each specific target trait individually and as an overall economic index response from all target traits. Results have then been aggregated into an overall annual breeding program response (cents) taking into account the generation interval associated with each candidate type.

The generation interval of the ewes was fixed based on an average age of 3.3 years when their lambs are born. Rams in the average industry breeding program design had an average age of 2.28 years, comprising 44% young untested rams (aged 1 and 2) , 40% emerging rams (aged 2 and 3) and 16% mature rams (aged 3 and 4). In comparison the predominantly young ram program had an average ram age of 1.5 years, with 75% being untested rams (aged 1 and 2) and 25% emerging rams (aged 2 and 3).

RESULTS AND DISCUSSION

Response with conventional selection criteria. Responses for individual traits by candidate type and for the two industry breeding programs were estimated. The overall superiority of the top 5% of untested young rams over the total group of young rams available for selection is 381 cents. This increases to 574 cents for the top 5% of mature rams which have progeny information available for selection decisions. The selection intensity on ewe hogget replacements is much weaker with the top 60% of ewes valued at 109 cents above the average for all candidates. When the breeding program response is calculated taking into account the effect of generation interval, the overall response for the industry average breeding program was 106 cents, compared to 111 cents for the predominantly young ram breeding program. These modest differences reflect the trade-off between the increased information available when making decisions on mature rams versus the reduced generation interval that can be obtained by selection of young rams. These rates of progress are slightly above the average rates of progress for dual purpose flocks reported by Amer (2009).

Response with genetic markers. Single or multiple genomic scores may be used alongside the production trait information to assist in the selection of young animals. If multiple genomic scores are used, then the additional gains made by use of genomic scores for a single objective trait are diluted by the competing objective traits which also have additional genomic information. Table 1 shows the breeding program response for the objective traits, when no genomic scores are used, a single genomic score is used for each objective trait, and all 5 genomic scores are used simultaneously.

Table 1. Annual breeding program response using production traits and genomic scores (cents)

	Industry average ram program			Young ram program		
	Traits only scores	SingleGS score	MultipleGS	Traits only scores	SingleGS score	MultipleGS
NLB	3.0	6.2	5.3	2.2	6.8	5.5
Growth	58.8	67.3	60.1	63.1	76.8	67.0
Disease	17.2	24.1	20.8	17.5	28.0	23.3
Survival	4.1	10.9	9.4	3.7	12.8	10.6
Yield	11.7	22.4	20.4	12.4	25.8	22.5
Fleece	10.6	10.2[1]	8.8	11.8	11.2[1]	9.3
Total	105.5	109.7[2]	124.8	110.7	116.8[2]	138.2

[1] Average response to fleece weight when a genomic score for other target traits was applied

[2] Average increase in overall response due to selection using a single genomic score

Results are shown for industry average and young ram breeding programs. When any single genomic score is used, the breeding program response to that target trait increases, resulting in selection being diverted away from other traits. When all five genomic scores are used, selection pressure is applied to all traits affected by the genomic scores resulting in an increased response for all affected traits, which is only marginally smaller than that seen when a single genomic score is applied. No genomic score was modeled for fleece weight resulting in a reduction in its response, for all situations when one or more genomic scores were included as selection criteria.

Effect of genomic score accuracy on response. Figure 1 shows the overall breeding program response to use of individual genomic scores, as the accuracy of prediction for the genomic scores is increased. As the correlation between the genomic score and the objective trait increases, non linear gains were observed in both individual trait and overall responses. Largest gains were observed using markers for growth and carcass yield with lesser gains observed in disease, survival and NLB.

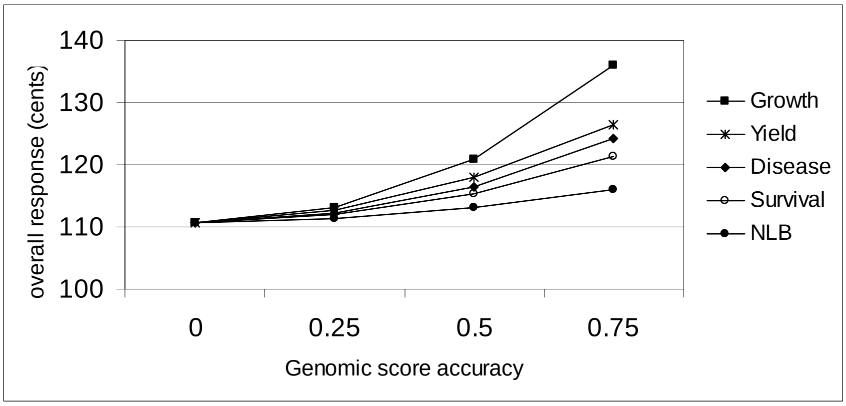

Figure 1. Annual response to selection at varying accuracies for genomic scores

CONCLUSIONS

Response to selection predicted using selection index theory was found to be relatively robust to the balance of ages of male selection candidates. However, additional response to selection when genomic scores were added as additional selection criteria were higher in the breeding program with a greater use of young rams. With genomic score accuracies of 0.5 for key breeding objective traits, rates of genetic progress are expected to increase by approximately 5% per annum. Proportionately greater increments of response are expected as the accuracy of the genomic scores increases beyond 0.5.

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