

THE IMPACT OF MEASURING ADULT FLEECE TRAITS WITH GENOMIC SELECTION ON ECONOMIC GAIN IN MERINO SELECTION INDEXES

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SUMMARY

Stochastic simulation of a Merino sheep breeding program showed that measurement of adult fleece weight and fibre diameter, the two key adult production traits in Merino sheep, increased economic gain compared to measuring yearling expressions of the traits alone. Comparing three different selection indexes, gain increased in fleece weight by up to \$1.10 per ewe per year over 10 years of selection, depending on the importance of the trait in the selection index. For fibre diameter the increase in gain was lower, to a maximum of \$0.70 per ewe per year, because genetic correlations between yearling and adult performance are higher for fibre diameter. There was little benefit in multiple adult measurements of these traits, and since the Australian sheep industry's evaluation system already accommodates one adult measurement, most of the gains possible can be realised by breeders. Genomic selection of young rams resulted in further increases in gain when combined with adult measurements, particularly for fleece weight.

INTRODUCTION

There are perceptions among Merino breeders in Australia that the industry's genetic evaluation service MERINOSELECT (Brown *et al.* 2007) places too much emphasis on the performance of young animals at the expense of lifetime productivity. These perceptions are related to the fact that although estimated breeding values (EBVs) are available for lifetime productivity traits and these are included in selection indexes, only small numbers of animals are measured at ages beyond one year of age.

A companion paper in these proceedings (Brown *et al.* 2013) estimates genetic parameters for lifetime wool production of the two key economic traits, fleece weight and fibre diameter. In this paper we use those parameter estimates to quantify the impact on economic gain of including varying amounts of information on lifetime production in selection indexes, both with and without genomic selection.

MATERIALS AND METHODS

Selection indexes. Predictions of economic gain were made from stochastic simulations of breeding programs with three Australian industry standard selection indexes with varying amounts of emphasis on fleece weight and fibre diameter: Index1 (M3.5) with high emphasis on increasing fleece weight while maintaining diameter, Index2 (M7SS) with balanced emphasis on increasing fleece weight and reducing fibre diameter, and Index3 (M14SS) with high emphasis on reducing fibre diameter while maintaining fleece weight. All three of these indexes separate wool traits into yearling and adult expressions, but treat all adult expressions as single traits. The indexes were modified to treat adult fleece weight or fibre diameter as separate traits between two and five years of age by multiplying the economic value for either trait by the proportion of wool harvested in each age class. Assuming equal fleece weights in each age class, these proportions were 0.28, 0.25, 0.24, and 0.23 for two, three, four and five year old ewes respectively. Other assumptions in deriving these economic values were that the price of wool is the same for all age classes, and there is no adult wether flock.

* AGBU is a joint venture of NSW Dept. of Primary Industry and the University of New England

Breeding program simulations. Breeding programs were simulated with 300 ewes mated annually to 10 rams. Age at first lambing was two years for both ewes and rams, and both sexes were given a maximum of eight mating opportunities (during the selection phase animals were culled on genetic merit). A realistic model of flock dynamics was used which included assumptions of mortality rates across ages in rams and ewes, and fertility, litter size, and lamb survival across ages in ewes. The average number of lambs weaned per ewe joined across ewe ages was 0.83 in the base flock.

True breeding values were simulated as the sum of mid-parent breeding values and Mendelian sampling random deviates drawn from the multivariate normal distribution defined by the genetic covariance matrix of all index traits, appropriately adjusted for inbreeding. Genetic covariances for adult fleece weight and fibre diameter between two and five years of age were as estimated by Brown *et al.* (2013). All other covariances were derived from the genetic covariance matrix used in MERINOSELECT. In addition to fleece weight and fibre diameter, the traits simulated included fibre diameter coefficient of variation, staple strength, body weight, and reproduction rate as defined in the selection indexes.

Phenotypes were simulated by summing true breeding values with random deviates sampled from the multivariate distribution based on a residual covariance matrix constructed by combining parameters estimated by Brown *et al.* with MERINOSELECT parameters as above.

Ten years of random selection were carried out to stabilise the flock, followed by fifteen years of selection on estimated index values. These were constructed from estimated breeding values calculated from multi-trait animal model BLUP analyses with varying amounts of phenotypic information: Y, including yearling measurements of clean fleece weight, fibre diameter, CV of fibre diameter, and body weight measured on both sexes; A2, adding adult clean fleece weight measured on ewes at two years to Y; A3 adding clean fleece weight on ewes at three years to A2; A4 adding clean fleece weight on ewes at four years to A3; and A5 adding clean fleece weight on ewes at five years to A4.

Genomic selection was added to the breeding program by including GBV “phenotypes” for all young ram selection candidates to BLUP analyses as an additional trait, as described by Swan *et al.* (2011). With this method, the genomic information contributes to increased accuracy of traits in the index during BLUP analyses via the genetic correlations between GBV and index traits. Modification of index values constructed from EBVs is not necessary. The accuracy of the GBV as a predictor of the target trait (either adult fleece weight or fibre diameter) was assumed to be 0.5.

The five measurement scenarios described above form the basis for comparisons in this study. They were run both with and without genomic selection, and repeated separately for adult fleece weight and fibre diameter at each age i.e., A2 adds adult fibre diameter at 2 years of age to Y etc.

Selection was by truncation on estimated index value across age classes, allowing the development of optimal age structures of males and females. The BLUP analyses were performed “annually” including all phenotypes available at the time. This means that animals were regularly selected before they had adult trait measurements. The ability of this method to match the timing of trait expressions with selection decisions is the reason why stochastic simulation was used in this study.

Equilibrium economic gains. One hundred replicates of each scenario were simulated, and mean true breeding values saved for all traits by year of birth. Annual rates of gain for each trait at equilibrium were then calculated as the slope of the regression of mean true breeding value on year of birth for the last ten years of the breeding program. Economic gains were then calculated by multiplying economic values by trait gains. Individual economic gains for each age class were summed to calculate total adult gains, weighted by the proportion of wool harvested in each age class as described above.

RESULTS

Economic and genetic gains for total adult fleece weight over ten years of selection are shown in Tables 1 and 2 respectively. Adding adult measurements of fleece weight increased economic gain by \$1.10 per ewe per year for Index1 (a 41% increase), \$0.50 for Index2 (a 33% increase), and by \$0.50 for Index3, compared to the industry standard of measuring only at the yearling stage. Most of the gain was captured with a single adult measurement (A2), although there was some additional benefit in recording at later ages, in particular for Index2. Genomic selection with yearling only measurement increased economic gain by up to \$0.40 for Index1, \$0.30 for Index2 and \$0.20 for Index3, lower than adding adult measurements. The highest economic gains were realised when combining adult measurements with genomic selection (up to \$1.50 per ewe for A3 with Index1). Genetic gains in Table 2 demonstrate the basis for economic gains, with similar increasing patterns of gain.

Table 1. Economic gain (\$/ewe/year) over 10 years for adult clean fleece weight under different selection scenarios with (+) and without (-) genomic selection (GS)

Index	Emphasis	GS	Y	A2	A3	A4	A5
1	(FW↑ FD↔)	-	2.70	3.80	3.60	3.70	3.60
		+	3.10	3.70	4.20	4.10	4.00
2	(FW↑ FD↓)	-	1.50	2.00	2.20	2.30	2.30
		+	1.80	2.60	2.70	2.60	2.70
3	(FW↔ FD↓)	-	-0.30	0.20	0.00	0.10	0.50
		+	-0.10	0.60	0.60	0.50	0.40

Table 2. Genetic gain (%) over 10 years for adult clean fleece weight under different selection scenarios with (+) and without (-) genomic selection (GS)

Index	Emphasis	GS	Y	A2	A3	A4	A5
1	(FW↑ FD↔)	-	9.4	12.3	12.3	12.2	12.6
		+	10.5	12.5	14.1	13.8	13.3
2	(FW↑ FD↓)	-	5.1	6.9	8.0	8.4	8.3
		+	6.4	9.1	9.7	9.1	9.6
3	(FW↔ FD↓)	-	-0.9	0.7	0.3	0.5	1.4
		+	-0.2	2.2	1.9	1.7	1.5

Economic and genetic gains for adult fibre diameter are shown in Tables 3 and 4 respectively. Adding adult measurements of fibre diameter had less impact on economic gain than fleece weight in absolute terms, with a maximum increase relative to yearling only measurement of \$0.70 per ewe per year when fibre diameter was most important in Index3 (a 14% increase).

Gain increased by \$0.40 per ewe per year for Index2 (a 50% increase), but was unchanged for Index1. Likewise, genomic selection was only beneficial for Index3, in which yearling only measurement with genomic selection was as effective as the adult measurement strategies. In the majority of cases, there was no benefit in measuring adult fibre diameter more than once, with the exception of Index3 with genomic selection.

Table 3: Economic gain (\$/ewe/year) over 10 years for adult fibre diameter under different selection scenarios with (+) and without (-) genomic selection (GS)

Index	Emphasis	GS	Y	A2	A3	A4	A5
1	(FW↑ FD↔)	-	-0.10	0.00	-0.10	0.00	0.00
		+	-0.10	-0.10	-0.10	0.00	0.00
2	(FW↑ FD↓)	-	0.80	1.20	1.20	1.20	1.10
		+	0.80	1.20	1.10	1.40	1.40
3	(FW↔ FD↓)	-	5.00	5.70	5.70	5.70	5.60
		+	5.70	5.60	6.20	6.30	6.40

Table 4: Genetic gain (microns) over 10 years for adult fibre diameter under different selection scenarios with (+) and without (-) genomic selection (GS)

Index	Emphasis	GS	Y	A2	A3	A4	A5
1	(FW↑ FD↔)	-	0.1	0.0	0.1	0.0	0.0
		+	0.1	0.1	0.1	0.0	0.0
2	(FW↑ FD↓)	-	-0.4	-0.6	-0.6	-0.6	-0.6
		+	-0.4	-0.6	-0.6	-0.7	-0.7
3	(FW↔ FD↓)	-	-1.2	-1.4	-1.4	-1.4	-1.3
		+	-1.4	-1.3	-1.5	-1.5	-1.5

DISCUSSION

For the genetic correlations estimated by Brown *et al.* (2013), adding adult wool measurements to the breeding program increases economic and genetic gain, more so for fleece weight than fibre diameter. This is because the genetic correlations between ages are lower for fleece weight than fibre diameter. However, there was little benefit in measuring more than one adult expression, especially for fibre diameter. Consequently, because the Merino genetic evaluation system already accommodates one adult expression of these traits, breeders can already capture most of the benefits possible. Genetic gains would be increased throughout MERINOSELECT if more breeders recorded these traits.

A limitation on the genetic gain which can be made in adult wool traits is that measurement takes place after the most intense selection point (selection of young rams), and only on females selected for breeding. Genetic gains shown in Tables 2 and 4 are in fact lower than gains in equivalent yearling traits (results not shown), despite the fact that the adult measurements have higher heritabilities and phenotypic variances (Brown *et al.* 2013). This means that these traits are candidates for genomic selection, and the results of this study confirm that genomic selection for adult wool traits has benefits even when the traits are measured in the breeding program. These results support the findings of Van der Werf (2009) that the main benefit of genomic selection in Merinos is increased genetic gain in adult wool traits.

ACKNOWLEDGEMENTS

This work was funded by MLA Project B.SGN.0127.

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