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Wool and meat genetics - the joint possibilities

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Wool and meat genetics—the joint possibilities

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Abstract

Wool and meat contribute to profit in sheep enterprises and both need to be considered in breeding programs. The relative responses expected from selection for a range of traits are presented and the realised responses that have been achieved in Merinos and variation in maternal breeds are illustrated. Knowledge of genetic parameters is required for the development of complex breeding objectives and selection indexes, comprehensive genetic evaluation of animals and the design of effective breeding programs. A review of world literature has highlighted the lack of accurate estimates of genetic parameters, especially for genetic correlations between trait groups. Analyses of a combined dataset from seven Australian Merino resource flocks comprising over 2000 sires and up to 100,000 records for each of various traits have provided accurate estimates of parameters to fill these gaps in current knowledge. The results show that there are no major genetic antagonisms between wool and meat traits and that improvement of both can be achieved by using appropriate selection indexes. Sheep Genetics Australia now provides a common system for genetic evaluation of Australian sheep, including across-flock estimated breeding values for a comprehensive range of traits and several standard indexes for various wool and meat breeding objectives.

Introduction

Sheep breeders are increasingly interested in making profits from both wool and meat. To achieve this aim, superior management and the optimum combination of genetics is required. In Merino flocks, the major production traits for wool and meat include fleece weight, fibre diameter, liveweight and reproduction. Other traits, including those associated with product quality (wool staple strength; carcass and meat fat and muscle depth) and disease (worm resistance and fleece rot), may also contribute to profit. This paper deals with the joint opportunities for genetic improvement of the major wool and meat traits and discusses genetic variation among maternal breeds.

Current knowledge of genetic parameters

Breeding programs for sheep enterprises are becoming more complex. Knowledge of genetic variation of traits and covariation between traits is required to make accurate predictions of the responses that can be achieved by selection, genetically evaluate animals and design effective breeding programs.

The Australian Sheep Industry CRC compiled estimates of genetic parameters for sheep from data published in the world literature over the last decade (Safari and Fogarty, 2003) and summarised

these in a recent review (Safari et al., 2005a). The study revealed that there are more than 20 independent estimates of heritability for the major wool and growth traits, but there are considerably fewer estimates of heritability for reproduction, carcass and disease traits. The review highlighted the dearth of estimates of genetic correlations, particularly those between trait groups, and showed that those that were available were of very low accuracy. To remedy this paucity of information, the Sheep CRC quantitative genetics project analysed data that was compiled from seven Australian Merino research resource flocks. The combined dataset comprised over 2000 sires and up to 100,000 records for each of a comprehensive range of traits from animals with extensive pedigree records. The analyses provided very accurate estimates of genetic parameters for Australian Merino sheep, especially for genetic correlations between traits (Safari et al., 2005b).

How important are accurate genetic correlations?

The sensitivity of response to index selection for a range of genetic correlations between major traits was examined by Safari et al. (2006). The study involved simulation of selection for three breeding objectives (fine wool, dual-purpose wool/meat, and meat) relevant to Australian sheep enterprises using several traits in the indexes (growth, wool and carcass traits, reproduction and worm resistance). The sensitivity of responses to selection over the range of correlations varied according to the breeding objective. Selection responses were sensitive for the range of correlations between reproduction and wool traits under all objectives, and for the correlations between reproduction and growth, worm resistance and carcass muscling under some objectives. Selection responses for the fine-wool objective were highly sensitive to the correlation between growth and fibre diameter. The study highlighted the need for accurate estimates of these genetic correlations.

Expected responses to selection

Estimates of heritability derived from the combined data analyses revealed genetic variation and considerable potential response to selection for all the major traits (Table 1). The relative response was estimated from the product of heritability and the coefficient of variation of the trait assuming equal selection intensity, which may not be the case for all traits. Even though the heritability of reproduction was lower than that of other traits, it had high variation, which means that a moderate response can be achieved with an effective selection program.

Table 1. Estimates of heritability (\pm standard error), coefficient of variation (CV) and expected relative response to selection for major sheep traits.

Trait	Heritability	CV (%)	Relative response
Clean fleece weight	0.42 \pm 0.01	16.3	100
Fibre diameter	0.68 \pm 0.01	7.5	75
Hogget weight	0.38 \pm 0.01	11.8	66
Lambs born per ewe joined	0.054 \pm 0.005	63.2	50

Genetic correlations

Genetic correlations between traits were estimated with a very high level of accuracy (Table 2). There were no major antagonisms between the traits. The most important genetic correlations were between clean fleece weight (CFW) and fibre diameter (FD) ($r_g = 0.29$) and between FD and hogget weight ($r_g = 0.17$). Although selection for CFW or hogget weight will result in a small correlated increase in FD, maintenance or reduction of FD can be achieved using an index that includes FD,

as the correlations are only moderate in extent even though they are positive. The genetic correlation between reproduction (lambs born per ewe joined (LB/EJ) and FD was negligible and that between LB/EJ and CFW was small and negative ($r_g = -0.12$), whereas there was a positive correlation between LB/EJ and hogget weight ($r_g = 0.38$).

Table 2. Estimates of genetic correlations (\pm standard error) between major sheep traits.

Trait	Clean fleece weight	Fibre diameter	Hogget weight
Fibre diameter	0.29 \pm 0.02		
Body weight	0.27 \pm 0.02	0.17 \pm 0.02	
Lambs born per ewe joined	-0.12 \pm 0.04	0.02 \pm 0.04	0.38 \pm 0.04

Realised responses to selection

There are many examples of realised responses to selection in sheep flocks that clearly demonstrate that genetic selection is effective. Flocks selected for traits or combinations of traits have achieved predicted responses. The realised responses in the QPLU\$ lines after eight years of selection for indexes of CFW and FD in the three major Merino bloodlines have been close to 10-year predictions (Fig. 1. S. Mortimer, pers. comm.).

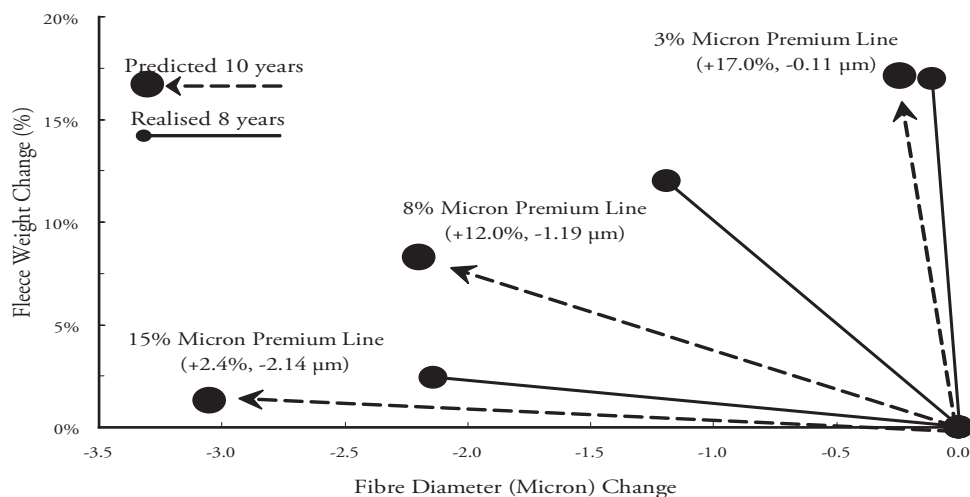


Fig. 1. Predicted and realised responses in QPLU\$ sheep lines.

Divergent selection of Merinos for high or low maternal multiple rearing ability (effectively, lambs weaned per ewe joined LW/EJ) over 16 years resulted in large, significant differences between the high and low lines in LB/EJ (1.50 vs. 1.32, respectively), LW/EJ (1.16 vs. 0.91, respectively) and litter weight of lamb weaned per ewe joined (23.9 vs. 18.0 kg, respectively). There were no differences between lines in fleece weight or ewe liveweight (Cloete et al., 2004). Fig. 2 shows genetic trends in average predicted breeding values (PBV) for the high and low lines.

The average annual response to selection for litter weight of lamb weaned per ewe joined over 12 years was 0.692 kg for nine lines of sheep in a study conducted in the USA (Ercanbrack and Knight, 1998). The traits contributing to the annual response included LW/EJ (1.81%, $P < 0.01$), fertility (0.23%, $P > 0.05$), prolificacy (1.44%, $P < 0.01$) and lamb survival (lambs weaned per lamb born alive; 0.45%, $P < 0.05$).

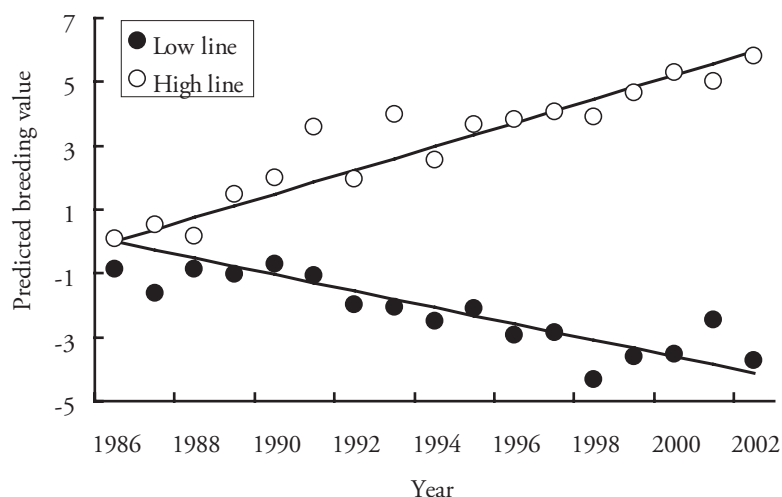


Fig. 2. Genetic trends for lines of Merinos selected for high or low maternal multiple-rearing ability.

Other traits

Several other traits are important or potentially important for breeding objectives that encompass both wool and meat production because of their likely impact on profitability. Estimates of heritabilities for these traits and responses relative to those for CFW are shown in Table 3.

Table 3. Heritability, genetic variation and response for various traits relative to that for CFW, which was assigned a value of 100.

Trait	h^2 ^A	CV (%) ^A	Relative response
Staple strength	0.34	29	184
Fat depth of the live animal	0.26	20	97
Muscle depth of the live animal	0.24	10	45
Carcass muscle pH	0.18	6	20
Worm resistance (faecal worm egg count)	0.27	31	156
Incidence of fleece rot	0.17	149	474
Feed intake at maintenance	0.13 0.42 ^B	20	49 158 ^B
Maternal lambing behaviour score	0.13	26	63
Ewe rearing ability	0.06	40	45
Lamb survival	0.03	47	26

^ASafari et al. (2005a), ^BFogarty et al., unpublished data.

Recent results from the national maternal-sire progeny test demonstrated that there is considerable variation among sires within maternal breeds for a range of traits (Fogarty et al., 2005a). The progeny test evaluated the performance of first-cross ewes sired by 91 industry-nominated rams of several maternal breeds. There was a range of \$19 gross margin/ewe/year among the means for the various sire breeds of the first-cross ewes, with a range of over \$40 gross margin/ewe/year among the 18 Border Leicester sired crossbred ewe groups and considerable overlap of the sire breeds (Fig. 3). Lamb turn-off was the major profit driver; lamb growth rate and carcass fat level also contributed to profit.

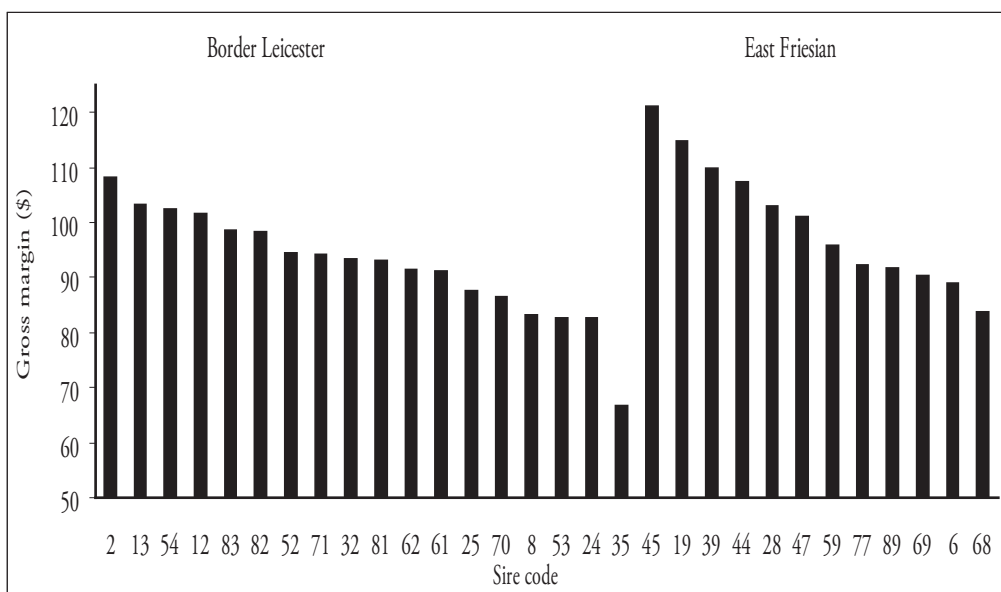


Fig. 3. Annual gross margin of first-cross ewes by various sires.

Outcomes for breeding programs

Accurate estimates of genetic correlations that were not previously available were provided by Sheep CRC project 1.1.1. These estimates facilitate improved accuracy of genetic evaluation and development of more complex breeding objectives that better reflect the future industry needs for genetic improvement. The results show there are no major genetic antagonisms between wool and meat traits and that improvement can be achieved in both traits using an appropriate selection index. Further research is required to examine sensitivities to price fluctuations and risk. The importance of genotype \times environment interactions should also be assessed, as there is evidence they may be important for some wool and growth traits (Carrick, 2005), worm resistance (Pollott and Greeff, 2004) and, in particular, reproduction in crossbred ewes (Fogarty et al., 2005b).

Following the launch of Sheep Genetics Australia (SGA) in October 2005, there is now a common system for genetic evaluation of all sheep in Australia. SGA provides across-flock estimated breeding values (EBVs) and some across-breed EBVs for a comprehensive range of traits and several standard indexes for a range of breeding objectives including wool and meat. The EBVs and indexes can be used to assist in selection of superior animals for various traits to enhance the rate of genetic improvement. EBVs for sires are correlated with the performance of their progeny (Ingham et al., 2005). The availability of accurate genetic parameters (especially genetic correlations) allows seedstock breeders to develop more complex breeding objectives that combine wool, meat and disease traits and

to be confident of the outcomes. In addition, commercial breeders can use the information provided by the EBVs and the various indexes to select rams that will make predictable changes to improve profitability and better meet market requirements.

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