LINKING MERINO BREEDING TO WOOL PROCESSING

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SUMMARY

The relative importance of raw wool traits on predicted processing performance and the relationship between breeding objectives with different emphasis on CFW and FD (3, 6 or 12% micron premium) was examined for four studs representing superfine, fine, medium and broad wools. The stud itself was the major source of variation in predicted processing. The likelihood of studs having different relationships with predicted processing performance is small, regardless of their micron range or relative selection emphasis on fleece weight and fibre diameter. The addition of other factors, such as cv of fibre diameter and style, into the TEAM equations is unlikely to improve the prediction of sire processing performance. Merino breeders wanting to predict the processing performance of their sires should include staple length and strength measurements in their program.

Keywords: Merino breeding, wool processing, TEAM, predicted hauteur, CV(H), noil.

INTRODUCTION

The TEAM equations are the industry standard for predicting the processing performance of wool consignments. Although they have been successfully tailored to adjust for mill effects, no attempt has been made to modify them for sire group prediction. The relative importance of each wool trait currently in TEAM was derived from analysis of commercial consignments consisting of a number of sale lots. It is likely that the relative importance may differ for sire groups where the masking effects of blend engineering do not occur. It is essential to determine whether the TEAM equations are robust enough to apply to wools from different environments, if the prediction varies between fine, medium and broad micron wools and between differing selection emphasis placed on CFW and FD by studs.

MATERIALS AND METHODS

Four Merino studs, representing superfine, fine, medium and broad wools, were approached and agreed to participate in this study. During shearing, midside samples were taken from approximately 20 ewe hogget progeny of each young progeny tested sire and pooled for each sire. The pooled sample was subsampled to provide 60 staples for length and strength measurement and guidance tested at the Australian Wool Testing Authority. The measurements (airflow diameter - FD, vegetable matter % - VM, staple length - SL, staple strength - SS and per cent midbreaks - %M) were used to predict processing performance (hauteur, CV(H) and noil) using the TEAM equations (Australian Wool Corporation 1988).

The importance of stud effects on predicted processing performance was partitioned and the relative importance of each raw wool trait (those mentioned above and the coefficient of variation in fibre diameter - CVFD), within and across studs was analysed using REG (Gilmour 1993a). Three models were fitted (Model 1: mμ = Trait + Stud + Trait x Stud; Model 2: mμ = Trait + Stud; Model 3: mμ = Trait). A regression screening technique was used to determine which combination of traits along with their order, overcame the effect of stud and provided the best fit to the data. BVEST (Gilmour 1993b) was used to estimate within stud sire progeny values (within stud) from the performance data, clean fleece weight (CFW) and fibre diameter (FD), recorded on the ewe hogget progeny (with the exception of the broad wool group for which the data was unavailable) for 3, 6 and 12% micron premiums (MP). The significance of the EPVs and indexes at each MP was determined using REG by fitting models similar to those described above but with the 3, 6 and 12% MP CFW and FD progeny values and indexes in place of Trait.

RESULTS AND DISCUSSION

Stud effects and relative importance of traits. The effect of stud was the major source of variation accounting for over 85, 77 and 81 per cent of the total between sire variation in predicted hauteur, CV(H) and noil respectively (Table 1). This large stud effect was largely driven by environmental effects and differing management regimes in place at each stud rather than genetic differences between the studs.

Table 1. Least squares means (± se) for predicted processing performance at each stud, the percentage of variation due to stud and the number of progeny tested sires at each stud

	Sires	Hauteur	CV(H)	Noil
Stud A - Superfine	10	66.0 ± 1.8	45.4 ± 1.2	6.8 ± 0.4
Stud B - Fine	15	70.0 ± 1.6	58.0 ± 1.1	6.0 ± 0.4
Stud C - Medium	10	62.7 ± 1.8	53.0 ± 1.2	6.9 ± 0.4
Stud D - Broad	8	90.1 ± 1.9	49.6 ± 1.2	1.7 ± 0.4
r^2		85.20	77.39	81.55

The within stud ranking of traits as to their relative importance in explaining the variation in predicted processing performance was the same for hauteur and noil but varied substantially for CV(H) (Table 2). In addition the r^2 values for each trait were quite similar for the prediction of hauteur and noil but significantly different for predicting CV(H). Staple strength and cv of fibre diameter (CVFD) clearly were not important sources of variation in hauteur and noil, however the reverse was true for predicted CV(H) with SS explaining 82 per cent of the variation with CVFD the next most important trait (50%).

Given the nature of the TEAM equation, it is likely that combinations of traits (two or more) will provide a better fit to the data. This was certainly true for predicted hauteur and noil, where adding SS to SL increased the r^2 by more than 25% to 0.93 for hauteur and by nearly 30% to 0.93 for noil. In these two instances the residual stud effect was small, 0.006 and 0.01 for hauteur and noil respectively. However, addition of further traits to this combination for either hauteur or noil provided either little or no improvement in the prediction of these two parameters. As an example, including FD to the SL and SS combination for hauteur did not improve the data fit ($r^2 = 0.93$), while including %M provided only a small increase in fit ($r^2 = 0.94$). In fact, including all 6 traits gave less than a 1% improvement in r^2 (0.94) compared with the SL and SS combination. The situation for noil was almost identical to that for hauteur. In contrast, combining additional traits with SS ($r^2 = 0.82$) produced much smaller increases in the r^2 for CV(H). The best fit to the data, which totally overcame any residual effect of stud, was achieved by including SS, CVFD, %M and SL ($r^2 = 0.87$). As the traits included in this analysis accounted for a high proportion of the variation in predicted hauteur, CV(H) and noil, it is unlikely that including additional factors, such as CVFD or style for instance, into the TEAM equations will improve their predictive capability.

Table 2. The ranking of raw wool traits as to their relative importance in explaining variation in predicted processing performance with the residual stud effect (RSE)* after fitting each trait

Rank	Hauteur			CV(H)			Noil		
	Trait	r^2	RSE	Trait	r^2	RSE	Trait	r^2	RSE
1	SL	0.68	0.23	SS	0.82	0.03	SL	0.64	0.23
2	FD	0.48	0.38	CVFD	0.50	0.27	FD	0.56	0.26
3	VM	0.27	0.57	% M	0.28	0.50	VM	0.27	0.55
4	% M	0.27	0.58	SL	0.09	0.66	% M	0.17	0.63
5	SS	0.04	0.85	VM	0.05	0.71	SS	0.06	0.84
6	CVFD	-0.01	0.85	FD	-0.02	0.82	CVFD	0.00	0.80

* RSE is the different between the adjusted r^2 for the analysis including stud and that without stud.

Fleece weight and fibre diameter are the two traits which were ranked the highest in a survey of the breeding objectives of NSW Merino studs (Casey 1990). However, other wool quality measurements, such as staple length and staple strength, are not widely used. Merino breeders who wish to link their breeding programs to processing performance should incorporate staple length and strength measurements into their breeding plan. The challenge for breeders is to determine the most cost effective method of incorporating these measurements. A most likely scenario would be to include them during the second stage selection of progeny tested rams.

Selection emphasis. The likelihood for the various studs having different relationships with predicted processing performance is small. The only traits for which the interaction between the trait in question and stud was significant were staple strength and fibre diameter for predicted noil and % midbreaks for predicted hauteur and CV(H) ($P<0.05$). Despite this, little differences in the prediction of processing performance of superfine, fine, medium and broad wools are likely to occur due to the average fibre diameter of the wool. This study has shown that the TEAM equations can be used with confidence to predict the processing performance of sire groups from diverse flocks. This contrasts with work by Purvis and Swan (1998) who examined predicted and actual processing performance for fine Merino wools and suggested that the relationships may be different for the limited range of wool types found at the fine end of the clip. It is important that further comparisons with actual processing performance over a wider range of Merino genotypes and production environments are made.

The small differences between studs as identified by the significant interactions between stud and staple strength, fibre diameter and % midbreaks were apparently not related to the different breeding objectives of the studs included in this study. The analysis of variance which included progeny values for CFW and FD for a 3, 6 or 12% MP index found that, regardless of the relative selection emphasis on these two traits, neither CFW nor FD progeny values on their own were a substantial source of variation in predicted hauteur, CV(H) or noil. However, the index rank was a significant source of variation in each of the predicted processing performance parameters for all three micron premiums. The best fit to the data again occurred when stud effects were included into the model with the r^2 ranging from 73 to 79 for predicted hauteur, 83 to 87 for CV(H) and 48 to 59 for noil. The strength of the relationship between index values and predicted processing performance was similar.

For example, the regression coefficients for predicted hauteur were 0.52, 0.56 and 0.53 for the 3, 6 and 12% micron premiums respectively, representing a change of 0.5mm hauteur for every 1 unit change in index value. For predicted CV(H) and noil a similar pattern occurred with the regression coefficients for each of the micron premium indexes being remarkably alike. For every 1 unit change in index value, there was a change of 0.4% in CV(H) and 0.05% in noil. These relationships provide breeders, regardless of their relative selection emphasis on fleece weight and fibre diameter or micron range, with a means to link their breeding program to processing performance. This will enable them to monitor the impact of their breeding programs on the downstream performance of both their own and their client's wool clips.

It is interesting to note that for hauteur, the stud interaction term was significant ($P<0.05$) for each of the 3 MP indexes. Further analysis of the relationship between the 3 MP indexes and staple length and strength, the two most important determinants of predicted hauteur, showed that the relative importance of staple length and staple strength to each stud tended to differ. The regression coefficients for the stud C were always lower than those for both studs A and B, while those for stud A were higher than stud B except for the 12% MP index and staple length and the 3% MP index and staple strength where the situation was reversed. This finding clearly warrants further investigation.

In conclusion, the TEAM equation can be used by Merino breeders to predict the processing performance of their sires with confidence regardless of the micron range of their wool or the relative emphasis they place on fleece weight and fibre diameter in their breeding objective.

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REFERENCES

Australian Wool Corporation. (1988) "TEAM Report on trials evaluating additional measurements 1981 - 1988" Report to the Raw Wool Measurement Research Advisory Committee of the Australian Wool Corporation. December 1988. Australian Wool Corporation, Melbourne

Casey, A.E. (1990) *Proc. Aust. Assoc. Anim. Breed. Genet.* **8**: 231

Gilmour, A.R. (1993a) REG - A Generalised Linear Models Program. NSW Agriculture

Gilmour, A.R. (1993b) BVEST A multiple trait animal model Best Linear Unbiased Predictor breeding value estimation program. NSW Agriculture Biometric Bulletin No. 2

Purvis, I.W. and Swan A.A. (1998) *Proc. 6th Wld. Congr. Genet. Appl. Livest. Prod.* **24**:23