

BREEDING FOR WOOL PROCESSING PERFORMANCE AND PRODUCT QUALITY IN MERINO SHEEP

I. W. Purvis and A. A. Swan

CSIRO Division of Animal Production, Armidale, Australia
and CRC for Premium Quality Wool, Armidale, Australia

SUMMARY

This paper discusses the issues confronting Merino breeders in developing selection programs based on raw wool measurements that are aimed at improving wool processing performance and final product quality. Two approaches to predicting the genetic consequences of selection for raw wool measurements on processing performance are shown. The first makes use of existing prediction formulae which have been developed from trials with no genetic structure. This was demonstrated using a formula which predicts hauteur (fibre length in top) as a linear combination of raw wool traits. Genetic relationships between predicted hauteur and these traits were derived and used to predict correlated responses to selection on clean fleece weight and fibre diameter. The results show a reduction (deterioration) in hauteur as the emphasis on fibre diameter increases in the index. The second approach involves direct estimation of the relevant genetic parameters from experiments based on sire processing batches, where batches are formed by pooling fleeces from individual progeny within sire progeny groups. Results are presented from such an experiment based on a fine-wool Merino flock, and show that the relationships expected from the prediction formula approach may not always be appropriate for individual Merino genotypes and production environments.

Keywords: Merino, wool, processing performance, selection

INTRODUCTION

This paper discusses the issues involved in acquiring information on the genetic relationships between raw wool attributes and processing outcomes, and presents results from experimental studies conducted to date. Traditionally, breeders of Merino sheep have defined their breeding objectives in terms of biological attributes that influence costs and returns and are expressed on a per animal basis. In practice, most breeders focus on returns when defining their goals. In part, this is because of the extensive nature of the industry, which makes the collection of cost of production data on an animal basis difficult. In most countries, the price information used in the calculation of the relative economic values for wool production and quality traits is taken from the public open cry auction system and thus represents data of industry relevance. There is an argument that these price data reflect the preferences of users of wool right through the processing sector, the garment manufacturer and finally to the consumer of apparel ware. However, many breeders are concerned that breeding objectives that are focussed on raw wool characteristics may not be appropriate for the delivery of preferred products in the processing sectors of the industry. This concern has been heightened in recent times because the processing industry has undergone a significant transformation.

The introduction of new technologies in this sector has been associated with faster processing speeds, greater automation, more focus on quality control and an increased capability of producing specialised products that highlight individual attributes of the wool fibre. This has led to a greater demand for predictability and objective specification. In turn, this had led to the development of prediction equations that turn the specifications of the outputs of one sector into predictions of processing performance of the next.

The process of converting a raw material into a product that then serves as the input material to the next sector is a feature of many manufacturing industries. This feature results in changing determinants of product value as one moves along processing pipelines. It also results in loss of identity of the original raw materials, be they based on animal, farm, sale lot, top, or yarn. Similar problems exist in most other livestock industries. Increasingly consumer preferences and manufacturing requirements are directly driving the agenda of livestock breeders, rather than simple price signals at the first point of sale post farm gate.

This situation raises the question of how best do animal breeders address these increasingly complex manufacturing and marketing systems. There are several ways of approaching the problem. One is to continue to define breeding objectives simply in terms of biological outputs using the logic that these are the traits by which the returns of wool producers are currently classified, and in the perhaps naive expectation that saleyard or raw material auction rooms will adequately reflect the signals from later stage processors and end point consumers. The great danger in this attitude is that, in the absence of fabrics and garments with desired properties, consumers will simply abandon wool products and change to another fibre. Perhaps the ideal outcome is to know what the prices/costs of inputs and outputs are for the downstream products and to estimate the genetic relationships between these "traits" and those biological traits of the animal. However, this presumes that the identity of animals or genetic groups can be followed through the processing pipeline, and that experimental programs can provide the data for estimation of the appropriate phenotypic and genetic parameters. A practical outcome lies somewhere in the middle of these two extreme positions. That is, by using experimental groups where the genetic unit can match the requirements of the downstream sector in terms of size and specification, but retain identity and give sufficient precision to make the exercise worthwhile.

RESULTS OF SAWTRI PROCESSING STUDIES

The South African Wool Textile Research Institute (SAWTRI) has been extremely innovative in the area of relating raw wool characteristics to processing performance (summarised in Hunter, 1980; and Hunter *et al*, 1982). A major focus of their work has been to understand the effect of fibre properties on processing efficiency and fabric properties with the goal of rationalising the conversion process into one that relies on objective specification and one that has a high degree of predictability. They have also endeavoured to establish what factors other than fibre properties may influence processing performance. One such factor is breed of sheep. Hunter *et al* (1982) processed more than 80 fleece lots that were selected so as to span the range of fibre characteristics (ie, length, diameter, and crimp) generally associated with a particular breed. Their consistent finding was that once the

measured differences in fibre properties was taken into consideration and corrected for, breed *per se*, played only small role in determining variation in hauteur (fibre length in top), noil (wastage in top), and spinning performance.

BREEDING STRATEGIES TO IMPROVE PROCESSING PERFORMANCE

There are two alternative methods which may be used to investigate the genetic consequences of selection for raw wool traits on downstream processing performance. The first involves the use of prediction equations currently used in the marketing of raw wool, while the second involves directly estimating the necessary genetic parameters from appropriately designed experiments.

Genetic parameters from prediction equations. CSIRO Division of Wool Technology has directed a considerable amount of research into prediction of processing performance from raw wool traits. Anon. (1988) describe the “TEAM” equations to predict hauteur (H: length in the top) and CV of hauteur (CVH) for mill consignments from staple length (SL), staple strength (SS), mean fibre diameter (MFD), percentage of mid-breaks adjusted to a minimum of 45% (M*), and vegetable matter (V). These equations were derived by multiple regression using data from 545 mill consignments from a very broad range of wool types, representing a variety of production environments and genotypes, ranging in fibre diameter from 17 to 31 micrometres. In this discussion, we will focus on the TEAM equation for hauteur:

$$H_p = 0.52SL + 0.47SS + 0.95MFD - 0.19M^* - 0.45V - 3.5$$

where H_p represents predicted hauteur. One way to approach a genetic analysis of H_p is to use the TEAM equation to calculate predicted values for individual animals, and include these in a multivariate genetic analysis with the raw wool traits of interest. Alternatively, the relevant genetic parameters involving H_p can be derived from existing knowledge of parameters for raw wool traits, following Lin and Allaire (1977). Firstly, we define a vector w containing the regression coefficients in the TEAM equation:

$$w' = [0.52 \quad 0.47 \quad 0.95 \quad -0.19 \quad -0.45]$$

Secondly, we define the phenotypic covariance matrix for the raw wool traits in the TEAM equation as P_{11} . The phenotypic variance for H_p may now be expressed as $w'P_{11}w$, and the covariances as $w'P_{11}$. Similarly, the genetic variance for H_p may be expressed as $w'G_{11}w$, where G_{11} is the genetic covariance matrix of the raw wool traits. The heritability for H_p is therefore:

$$\frac{w'G_{11}w}{w'P_{11}w}$$

Calculating the effect of a typical Merino selection program on H_p also requires knowledge of covariances between H_p and traits not included in the TEAM equation, most notably clean fleece weight (CFW). Defining the phenotypic covariance matrix for these traits as P_{10} , the required covariances are $w'P_{10}$. The complete phenotypic covariance matrix for traits defined either in the breeding objective or as selection criteria, TEAM predictors, and H_p is:

$$\begin{bmatrix} P_{00} & P_{01} & P_{01w} \\ P_{10} & P_{11} & P_{11w} \\ w'P_{10} & w'P_{11} & w'P_{11w} \end{bmatrix}$$

The equivalent genetic covariance matrix can be constructed in a similar fashion. From these two matrices, all genetic parameters of interest can be derived, including heritabilities and genetic and phenotypic correlations. The parameters may then be used to construct selection indices.

An example is given using parameter estimates from the CSIRO Fine Wool Project described by Swan *et al.* (1993), and from literature values. These are shown in Table 1. Parameters for CFW, MFD, SL, and SS were estimated from the Fine Wool flock using ASREML (Gilmour *et al.*, 1997). Parameters for V were as reported by Mortimer and Atkins (1993) with the following modifications: because the flock used by Mortimer and Atkins had a higher vegetable matter content than is observed in the Fine Wool flock, the phenotypic variance for V was adjusted downwards using the CV reported in their paper. Consequently, the variance assumed here was relative to a mean of 1% for V, compared to 1.66% reported by Mortimer and Atkins. In addition, none of the correlations involving V estimated by Mortimer and Atkins were significantly different to zero, and therefore have been set to zero in Table 1. Due to difficulties in estimating parameters for adjusted percentage of mid-breaks (M^*), this trait was ignored. This implies that percentage of mid-breaks is always less than 45%, and M^* is therefore invariant, which is an unrealistic assumption.

Table 1. Genetic and phenotypic parameters for breeding objective traits (CFW and MFD), hauteur predictor traits (MFD, SL, SS, and V), and predicted hauteur (H_p). Phenotypic standard deviations (SD_p), heritabilities (bold), genetic correlations (below diagonal), and phenotypic correlations (italics, above diagonal).

	CFW	MFD	SL	SS	V	H_p
SD_p	0.25	1.07	8.46	9.20	0.77	6.37
CFW	0.38	<i>0.21</i>	<i>0.36</i>	<i>0.19</i>	0	<i>0.41</i>
MFD	0.19	0.68	<i>0.17</i>	<i>0.15</i>	0	<i>0.38</i>
SL	0.43	0.12	0.52	<i>-0.04</i>	0	<i>0.69</i>
SS	0.17	0.24	-0.12	0.33	0	<i>0.67</i>
V	0	0	0	0	0.06	<i>-0.09</i>
H	0.48	0.45	0.73	0.56	-0.24	0.42

The parameters shown in Table 1 were used to construct a selection index with CFW and MFD used as both breeding objective traits and selection criteria. SL, SS, and H_p were included to predict correlated responses (due to zero correlations with other traits, V was not considered). Responses were predicted on a per year basis, assuming selection intensities of 1.985 and 0.798 for males and females respectively, and generation intervals of 2.5 and 4 respectively. Three micron premiums were tested: 2.5, 5, and 10%. These are defined as the

extra value realised from a one micron decrease in MFD, and so determine the emphasis placed on that trait in the index. Results are shown in Table 2.

Table 2. Predicted responses per year to selection on CFW and MFD for three micron premiums (2.5, 5, and 10%)

Premium	Obj(\$)	CFW(Kg)	MFD(μ)	SL(mm)	SS(N/Kt)	H _p (mm)
2.5%	2.27	0.03	-0.15	0.49	-0.05	0.09
5%	3.20	0.02	-0.24	0.25	-0.23	-0.21
10%	5.72	0.01	-0.29	0.03	-0.35	-0.43

Response in H_p is positive only for the lowest micron premium (2.5%). As the emphasis on MFD increases in the 5 and 10% indexes, response in H_p becomes more negative. The reasons for this may be seen both from the TEAM equation and from the parameters in Table 1: H_p is associated with higher MFD, both genetically and phenotypically, so selection to reduce MFD has a negative effect on the trait. CFW on the other hand is positively correlated with H_p, and also with all of the predictor traits. Consequently, the negative effect of selection on MFD is counteracted by selection on CFW. Positive correlations between MFD and SS are also worth noting: as the emphasis on MFD increases, response in SS becomes more negative. It may be possible to reduce the effect on SS by placing an economic value on the trait and including the CV of fibre diameter as an additional selection criterion, since the genetic correlation between these traits is quite strongly negative (Greeff *et al.*, 1995).

These results demonstrate that the effect of current Merino selection practices on processing performance are worthy of further research. However, there are several deficiencies of the analysis shown above. Most important is the question of the overall suitability of the TEAM prediction equation for fine Merino wools. As was stated above, the prediction was developed from a very broad range of mill consignments. It may be that the relationships are different within the more limited range of wool types found at the fine end of the Merino clip.

Direct estimation of genetic parameters. The use of prediction equations can be validated by designing experiments to estimate genetic parameters for processing. Designing such experiments is very challenging. The size of commercial processing batches in both the topmaking and spinning/weaving sectors is such that commercial trials at the breed level are the only practical possibilities. At the other extreme, CSIRO Division of Wool Technology has experimental processing facilities that can process fleeces of individual animals through to top. However, the cost of processing sufficient single animal batches to obtain parameter estimates of acceptable precision makes this option impractical. A compromise between these two approaches is to pool fleeces within progeny groups of individual sires. Swan (1998) has developed procedures that can be used for the estimation of variance components from pooled biological material from groups of animals. He shows that although pooling of samples leads to a reduction in the precision of estimates, when balanced against the reduced cost of processing, the outcome is acceptable.

Such an experiment has been initiated within the CSIRO Fine Wool Project flock. This breeding flock is maintained at Armidale, NSW, Australia, a major centre for fine-wool production. The flock includes 11 bloodlines, and is a representative sample of sheep available to commercial producers. Processing batches were formed by pooling skirted fleeces from individual animals within sire groups. These batches represent 69 individual sires mated in 1993 and 1994, and have been processed at the Geelong research facilities of CSIRO Division of Wool Technology. The batches have been processed into top, and measures of processing efficiency recorded, including top and noil yield, noil %, hauteur, CV of hauteur, evenness (uster), and mean fibre diameter in the top.

Currently, results are only available for one batch per sire, and it is therefore not possible to estimate sire and residual (co)variance components separately. However, analyses were performed to estimate batch (co)variances after adjusting for bloodline and year effects. With only one batch, the expectation of these components is the variance of half-sib family means:

$$\sigma_s^2 + \frac{\sigma^2}{n} \quad (1)$$

where σ_s^2 and σ^2 are the sire and residual variances respectively, and n is the number of progeny in each batch, assuming a balanced design. Estimates of these batch variances and correlations for achieved hauteur and the hauteur predictor traits are shown in Table 3. Measurements for the predictor traits MFD, SL, and SS were made on the sire batches prior to processing. For purposes of comparison, measurements of these traits made on the individual animals contributing to the batches were analysed by fitting a multivariate sire model in ASREML. Sire and residual component estimates from this analysis were used to calculate expected values for sire batch components using equation 1 above, with $n = 20$, the average number of progeny per batch. These values are also shown in Table 3.

Table 3. Sire batch variances (diagonals, in bold) and correlations for achieved hauteur (H_a) and predictor traits. Expected values in brackets.

	MFD	SL	SS	H_a
MFD	0.19 (0.21)			
SL	0.07 (0.05)	10.18 (11.99)		
SS	0.28 (0.27)	0.05 (-0.03)	9.93 (10.22)	
H_a	-0.13	-	0.12	7.24

The realised values for sire batch variances and correlations were similar to their expected values, although the variance estimates were consistently smaller. The sire batch correlations among MFD, SL, and SS were also of similar magnitude to the genetic correlations in Table 1, suggesting that such comparisons are not unreasonable. The correlation between achieved hauteur and SL was the identical to the genetic correlation between H_p and SL in Table 1 (0.73), demonstrating that SL has the greatest impact on achieved hauteur, as expected. However, the correlations for achieved hauteur with MFD (-0.13) and SS (0.12) were considerably lower than the corresponding genetic correlations involving H_p in Table 1 (0.45

and 0.56 respectively). These results show that in fine-wool Merinos managed in this environment, MFD and SS have a smaller phenotypic influence on hauteur than predicted by the TEAM equation. Whether this is also true at the genetic level is less clear at this stage of the experiment. However, in a sense, these results were not entirely unexpected. For example, MFD had a much lower range in the Fine Wool Project sire batches (15.5 to 19 micrometres) in comparison to the TEAM consignments (17 to 31 micrometers) Hence, the small correlation between MFD and hauteur in the sire batch data was not surprising.

Improvement of processing performance in industry breeding programs. The two approaches we have taken lead us to different conclusions about the importance of raw wool traits on processing performance in fine wool flocks. However, it is not entirely appropriate to place too much weight on such comparisons. The TEAM equation was based on mill consignments, which are formed by pooling sale lots. The sire batches from the Fine Wool Project are analogous to sale lots. Although forming consignments from sale lots is highly predictable from measurements on the latter, the first step in extending this work is to use sale lot prediction formulae in place of the TEAM equation.

New processing trials may also be warranted, perhaps conducted within the current across-flock genetic evaluation system of the Australian Merino industry, including both central test sire evaluations and wether comparisons. A robust set of equations developed from such work could then be used in within-flock selection programs by individual ram breeders. Further validation may be worthwhile in experiments designed to obtain genetic parameters for processing performance, within current experimental resource flocks and selection lines. This framework is likely to be highly beneficial as an extension tool, as it would focus breeders' attention on the traits of importance in their breeding programs. However, given that experimental processing resources are extremely scarce, it would require a coordinated effort to maximise the benefits to the whole industry.

CONCLUSIONS AND FUTURE RESEARCH NEEDS

The enormous changes that have occurred during the last 10 years in the wool processing industry worldwide, have aimed at producing increased output through greater machinery speeds and lower labour requirements through greater automation. Associated with these changes is an increased demand for predictability of processing performance (see Whiteley, 1994). These demands have seen an increase in the use of objective specification of raw wool traits and the imposition of tighter tolerances in the specification of sale contracts.

Increasingly the effects of these changes are being felt at the level of the woolgrower and the stud breeder. In order to satisfy their immediate and downstream customers, breeders will be required to produce more comprehensively specified animals. In order to remain competitive they also need the capacity to change the genotype of their animals to meet changing downstream requirements, or to position themselves to meet niche market specifications.

The major wool producing countries have adopted staple-based raw wool measurement systems and developed prediction equations for top characteristics based on these

measurements. These equations can be used to predict genetic changes in processing performance from selection programs based on raw wool measurements. The results in this paper show that this is a worthwhile exercise for Merino breeders, as the predicted changes are not always favourable.

Further studies are required to determine whether the current prediction systems are robust enough to be used to predict genetic change over the range of Merino bloodlines and production environments. The Merino industry, particularly in Australia, would benefit greatly by having access to the results of well designed studies focussed on this area.

ACKNOWLEDGMENTS

This production of this paper would not have been possible without the dedicated work of the Breeding for Wool Quality and Production team at CSIRO Division of Animal Production, Armidale, and the Physical Processing group at CSIRO Division of Wool Technology, Geelong. Support of Australian woolgrowers through the IWS and the Cooperative Research Centre for Premium Quality Wool is also gratefully acknowledged.

REFERENCES

- Anonymous (1988) Report on trials evaluating additional measurements 1981 - 1988. Australian Wool Corporation.
- Gilmour, A.R., Thompson, R., Cullis, B.R., and Welham, S.J. (1997) ASREML. Biometric Bulletin 3, NSW Agriculture, 92pp.
- Greeff, J.C., Lewer, R.P., Ponzoni, R.W., and Purvis, I.W., (1995) Proc. 11th Conf. Aust. Assoc. Anim. Breed. Genet. pp. 595-601.
- Hunter L, (1980). Proc. IWTO Conf. Vol 1. Pretoria, 1980. pp 133-193.
- Hunter, L., Turpie, D.W.F. and Gee, E. (1982) SAWTRI Technical Report No. 502.
- Lin, C.Y. and Allaire, F.R. (1977). Theor. Appl. Genet. 51:1.
- Mortimer, S.I. and Atkins, K.D. (1993) Aust. J. Agric. Res. 44: 1523-1539.
- Swan, A.A., Lax, J., Piper L.R. and Hansford, K. (1993) In "Merino Genetic Resource Flocks in Australia", pp 46-57, Editors R.W. Ponzoni and D.R. Gifford, AWC Melbourne.
- Swan, A.A. (1998) These proceedings.
- Whiteley, K.J. (1994). Proc. IVth Wld. Merino Conf. Editors Azzarini, M and Cardelino, R, Montevideo, Uruguay. pp 209-227.