PREDICTING GENETIC CHANGE IN STAPLE STRENGTH – HOW MUCH GAIN CAN WE EXPECT?

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SUMMARY

Genetic change in staple strength (SS) was predicted using phenotypic and genetic parameters and approaches from two independent studies [South Australian (SAp&g) and Western Australian (WAp&g)]. The SAp&g treat trait expressions in the two sexes and at different ages (hogget or adult) as different traits, whereas the WAp&g treat them as a single trait. Clean fleece weight (CFW), fibre diameter (FD), coefficient of variation of fibre diameter (CV) and SS were included in the breeding objective, and a range of selection indices and economic values for FD, CV and SS were investigated. Based on the more elaborate model provided by the SAp&g it was concluded that although genetic gain in SS was possible, it would be smaller and harder to achieve than earlier suggested by Western Australian studies.

Keywords : Staple strength, genetic change, breeding objective, Merino sheep

INTRODUCTION

To date the message to ram breeders and woolgrowers regarding the prospects of genetic improvement of staple strength (SS) in Merino sheep has been mainly based on information derived from Western Australian studies (Lewer and Li 1994; Greeff *et al.* 1995; Greeff *et al.* 1997). The message has been one of high expectations with important gains in SS achieved relatively easily using the coefficient of variation of fibre diameter (CV) as a selection criterion.

Here we conduct a selection index study to predict and compare the genetic change in staple strength when CV and SS are included in the breeding objective and in the selection index. This is done using South Australian parameters (SAp&g) as well as those derived from the Western Australian program (WAp&g) (Greeff 1997 and Greeff pers. comm.).

MATERIALS AND METHODS

The data used in the estimation of the SAp&g were from the ram and ewe progeny of the Turretfield Merino Resource Flock (Ponzoni *et al.* 1995). The ram records were taken at 16 months of age and the ewe records were taken at 16, 28 and 40 months of age. The rams and ewes had 6 and 12 months of wool growth, respectively. Wool samples were taken from the mid-side of each fleece for measurement of the wool characters (Table 1).

Heritabilities and phenotypic and genetic correlations were estimated using ASREML (Gilmour *et al.* 1998). An animal model was fitted, including the fixed effects of year, stud, age of dam, type of birth and rearing class (ram and ewe data) and lambing and rearing status (ewe data only). Day of birth was fitted as a linear covariate. Parameters for 28 and 40 month old ewes were averaged to

generate 'adult' (a) ewe parameters, whereas female (f) and male (m) 16 month old parameters were called 'hogget' (h) parameters (Table 1). The WAp&g were taken from Greeff (1997) and Greeff (pers. comm.). The 'permissibility' of the resulting phenotypic and genetic variance-covariance matrices was tested (Hill and Thompson 1978; Foulley and Olivier 1986) and the necessary conditions were satisfied for both SAp&g and WAp&g.

Table 1. SA (bold) and WA parameters : phenotypic standard deviations (σ_P), heritabilities (along diagonal) and phenotypic (above) and genetic (below) correlations

	hCFWm	hCFWf	aCFWf	hFDm	hFDf	aFDf	hCVm	hCVf	aCVf	hSSm	hSSf	aSSf
σ_P	**15.00**	**15.00**	**16.00**	**1.50**	**1.50**	**1.76**	**2.40**	**2.40**	**2.40**	**11.5**	**9.10**	**10.5**
	15.53			1.75			2.57			8.91		
hCFW m	**0.57**			**0.35**			**-0.01**			**0.24**		
	0.40[A]			0.20			0.00			0.06		
hCFWf	**0.75**	**0.42**	**0.59**		**0.27**	**0.24**		**-0.01**	**-0.06**		**0.10**	**0.07**
aCFWf	**0.73**	**0.80**	**0.45**		**0.10**	**0.23**		**-0.03**	**0.03**		**0.11**	**0.15**
hFDm	**0.38**	**0.07**	**0.13**	**0.62**			**-0.16**			**0.33**		
	0.25			0.50			-0.09			0.16		
hFDf	**0.21**	**0.30**	**0.10**	**0.96**	**0.72**	**0.75**		**-0.17**	**-0.11**		**0.27**	**0.20**
aFDf	**0.21**	**0.37**	**0.26**	**0.93**	**0.92**	**0.70**		**-0.01**	**-0.21**		**0.23**	**0.20**
hCVm	**-0.08**	**-0.03**	**0.15**	**-0.24**	**-0.15**	**-0.04**	**0.60**			**-0.35**		
	0.16			-0.04			0.51			-0.49		
hCVf	**0.00**	**-0.08**	**0.10**	**-0.16**	**-0.20**	**-0.08**	**0.97**	**0.71**	**0.65**		**-0.31**	**-0.24**
aCVf	**-0.05**	**-0.17**	**0.04**	**-0.24**	**-0.19**	**-0.03**	**0.83**	**0.84**	**0.66**		**-0.33**	**-0.49**
hSSm	**0.44**	**0.10**	**0.10**	**0.50**	**0.27**	**0.30**	**-0.42**	**-0.48**	**-0.45**	**0.45**		
	0.21			0.24			-0.72			0.41		
hSSf	**0.13**	**0.09**	**0.05**	**0.50**	**0.43**	**0.33**	**-0.40**	**-0.56**	**-0.50**	**0.59**	**0.42**	**0.45**
aSSf	**0.14**	**0.16**	**0.16**	**0.43**	**0.53**	**0.45**	**-0.55**	**-0.52**	**-0.52**	**0.65**	**0.40**	**0.35**

[A] The WAp&g do not distinguish between the sheep classes, however for convenience the parameters are placed in the hogget sections of this Table.

A base breeding objective (BASE) was defined which included CFW and FD. The breeding objective was then expanded to include CV and SS. The SAp&g distinguish between the hogget male, the hogget female and the adult female expressions of these traits. The expanded genetic model was used because the genetic correlation between trait expressions in the two sexes or at different ages was not equal to one (Table 1). By contrast, the WAp&g (and reports on genetic change based on these parameters) treat the expression of these traits in the different sexes and ages as if they were the same trait. The economic values were calculated (Ponzoni 1988) for two different micron premiums (3 and 12 %), and for three different price differentials of staple strength ($0.03, 0.06 and 0.12 per Newton per kilotex per kg of clean wool), assuming the price of 1 kg of clean wool was $4.50. Genetic change was calculated for a standard selection index which included hCFWm and hFDm, and then for indices which included hCVm and hSSm. The genetic change was calculated for a period of 10 years, assuming the ratio of average selection intensity to generation intervals (in males and females) was 0.4.

RESULTS AND DISCUSSION

Table 2 shows that with the WA approach the inclusion of CV in the breeding objective and in the selection index was enough to stop the deterioration of SS at all micron premiums. That was not the case when SAp&g and a more elaborate genetic model were used. At a micron premium of 12 % there was a reduction in SS with the SAp&g even when SS was in the breeding objective (with low and medium economic values) but not as a selection criterion. When SS was a selection criterion the decline still occurred at low and medium economic values for SS, but was somewhat attenuated.

Table 2. Predicted genetic changes from the use of SAp&g (bold) and WAp&g

B.Obj.	Sel. Ind.	CFW (%)		FD (μm)		CV (%)		SS (N/ktex)	
		Hogget	Adult	Hogget	Adult	Hogget	Adult	Hogget	Adult
3 % micron premium									
BASE	BASE	**20.10**	**20.07**	**-2.02**	**-2.24**	**0.75**	**0.79**	**-4.52**	**-3.57**
		22.01[A]		-0.64		0.83		1.46	
BASE + CV	BASE	**20.44**	**19.76**	**-1.93**	**-2.19**	**0.04**	**0.20**	**-3.61**	**-2.29**
	+CV	22.12		-0.63		0.95		1.19	
BASE + CV	BASE +	**21.52**	**19.97**	**-1.00**	**-1.26**	**-1.55**	**-1.25**	**-0.03**	**1.88**
+ SS_L	CV	20.74		-0.23		-0.85		5.46	
BASE +CV	BASE +	**20.36**	**18.15**	**-0.03**	**-0.26**	**-2.90**	**-2.49**	**3.35**	**5.61**
+ SS_M	CV	17.97		0.09		-2.12		8.19	
BASE +CV	BASE +	**15.50**	**12.75**	**1.30**	**1.15**	**-4.28**	**-3.79**	**7.43**	**9.82**
+ SS_H	CV	13.19		0.45		-3.39		10.61	
BASE +CV	BASE	**21.00**	**19.70**	**-1.04**	**-1.25**	**-1.62**	**-1.30**	**0.75**	**2.74**
+ SS_L	+CV +SS	21.46		-0.05		-1.22		9.36	
BASE +CV	BASE	**19.06**	**17.36**	**-0.11**	**-0.25**	**-2.94**	**-2.52**	**4.66**	**7.03**
+ SS_M	+CV +SS	18.64		0.26		-2.32		12.24	
BASE +CV	BASE	**13.53**	**11.59**	**1.08**	**1.06**	**-4.15**	**-3.66**	**8.88**	**11.35**
+ SS_H	+CV +SS	14.48		0.56		-3.30		14.38	
12 % micron premium									
BASE	BASE	**9.80**	**8.34**	**-3.60**	**-4.02**	**1.07**	**1.39**	**-8.49**	**-7.40**
		5.64		-3.01		0.57		-2.25	
BASE + CV	BASE	**10.23**	**7.06**	**-3.44**	**-3.98**	**-0.70**	**-0.07**	**-5.38**	**-4.33**
	+CV	3.40		-3.02		-0.80		0.62	
BASE + CV	BASE +	**11.09**	**7.33**	**-3.19**	**-3.76**	**-1.48**	**-0.75**	**-5.06**	**-2.63**
+ SS_L	CV	3.75		-2.74		-1.71		3.00	
BASE + CV	BASE +	**11.77**	**7.45**	**-2.85**	**-3.44**	**-2.30**	**-1.47**	**-3.51**	**-0.72**
+ SS_M	CV	3.94		-2.41		-2.48		5.05	
BASE + CV	BASE +	**12.29**	**7.14**	**-1.91**	**-2.49**	**-3.86**	**-2.89**	**0.06**	**3.38**
+ SS_H	CV	3.99		-1.72		-3.53		8.00	
BASE + CV	BASE +	**10.82**	**7.25**	**-3.21**	**-3.74**	**-1.53**	**-0.79**	**-4.46**	**-1.97**
+ SS_L	CV + SS	5.29		-2.58		-1.91		5.34	
BASE + CV	BASE +	**11.21**	**7.26**	**-2.86**	**-3.38**	**-2.36**	**-1.53**	**-2.46**	**0.40**
+ SS_M	CV + SS	6.07		-2.13		-2.67		8.23	
BASE + CV	BASE +	**10.99**	**6.63**	**-1.90**	**-2.35**	**-3.82**	**-2.88**	**1.78**	**5.14**
+ SS_H	CV + SS	6.74		-1.33		-3.57		11.77	

[A] The genetic changes derived from the WAp&g are placed in the hogget sections of this Table.

Overall the results show a striking contrast between the predicted genetic changes in SS using the SAp&g and the WAp&g. This may be attributed to the differences in the genetic models assumed, as well as to the actual phenotypic and genetic parameter values used. Both differences (i.e. the genetic model and the parameter values) contribute towards reduced expectations about the prospects of improving SS by genetic means using the South Australian approach.

Note that using the SAp&g approach genetic gains were greater (or losses smaller) for aSSf than for hSSf. This was due to a combination of factors, namely, greater economic value for aSSf than for hSSf, and stronger correlations of hFDCVm and hSSm with aSSf than with hSSf. When these values were 'smoothed' (i.e. hFDCVm with hSSf and aSSf set equal to –0.45, and hSSm with hSSf and aSSf set equal to 0.6) the differences in genetic change between hSSf and aSSf were smaller, but still in favour of the latter trait. However, the overall conclusions drawn from the study remained unchanged.

The results based on the SAp&g suggest that although there is scope for genetic improvement of SS in Australian Merino sheep, gains are likely to be smaller and harder to achieve than earlier suggested by Western Australian studies based on WAp&g and on an over-simplified breeding objective. We conclude that the elucidation of an appropriate genetic model and the choice of the most appropriate phenotypic and genetic parameters are critical if realistic predictions of genetic change in SS are to be made.

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