

GENETIC TRENDS IN A MERINO LINE SELECTED FOR A REDUCED FIBRE DIAMETER RELATIVE TO AN UNSELECTED CONTROL FLOCK

S.W.P. Cloete^{1,2}, J.J. Olivier² and E. du Toit³

¹Department of Animal Sciences, University of Stellenbosch, Matieland 7602, South Africa

²Directorate Animal Sciences: Elsenburg, Elsenburg 7607, South Africa

³Directorate Animal Sciences: Tygerhoek, Riviersonderend 7250, South Africa

SUMMARY

A Merino line selected for a reduced fibre diameter (Fine wool line) was compared with a random selection control flock. Foundation sires in the Fine wool line were initially obtained from the parent stud and industry, followed by within flock selection. Selection was for a reduced fibre diameter, while maintaining live weight. Data of ~2700 records of hogget live weight (LW), clean fleece weight (CFW), staple length (SL), staple strength (SS), and fibre diameter (FD) recorded from 1998 to 2009 were used to derive genetic parameters for all traits in a five-trait animal model. Genetic parameters were consistent with literature values. Estimated breeding values (EBVs) in each year provided genetic trends in the two flocks. In the Fine wool line, EBVs for FD were reduced by 1.01% per annum ($-0.19 \pm 0.02 \mu\text{m}$) relative to the phenotypic mean for FD. There was also some evidence of favourable genetic change in LW and CFW in the Control flock. Fine wool line progeny maintained their LW, but showed declines in CFW, SL, and SS. The improvement in FD in the Fine wool line should be balanced against the deterioration of CFW and SS.

INTRODUCTION

Fibre diameter (FD) is commonly reported to be the most important determinant of the price of Merino wool (Cottle 2010). However, there are unfavourable genetic correlations of FD with other traits of economic importance (such as LW, CFW and SS) (Safari *et al.*, 2005; 2007c; Huisman and Brown 2009). In view of the importance of FD, the South African sheep industry undertook the establishment of a genetic fine wool stud in the late 1980's (Schoeman *et al.* 2010). Cloete *et al.* (2007) reported that initial selection emphasis on LW and CFW in this stud resulted in an initially nonsignificant genetic trend for FD. After amending the selection strategy in 1995, the genetic response in LW was reduced, CFW remained stable, while FD declined by 0.67% per annum on the genetic level.

Emphasis on traits other than FD obviously compromised the genetic gain that could be obtained in FD in this stud. The interest in the response of FD in the absence of emphasis on other traits resulted in the establishment of a fine wool line at the Tygerhoek research farm where the focus was primarily on reducing FD. This study reports the genetic change in this line, in comparison with an unselected Control flock already present on the farm (Cloete *et al.* 1998).

MATERIALS AND METHODS

The experimental animals that were used were introduced from the Halesowen stud, as described by Olivier *et al.* (1999) and Schoeman *et al.* (2010). This stud was initially established by sourcing the finest maiden replacement ewes from industry flocks with a below average clip FD in the national clip, on the provision that they were above average for LW in their respective contemporary groups. The ewes were purchased from their original owners and mated to 4 Australian fine-wool rams (obtained from the Glenleigh stud in NSW and the Siera Park stud in Victoria), and were subsequently bred to rams from within the flock. During 1997, surplus ewes from this stud were transferred from the Halesowen research farm near Cradock to Tygerhoek research farm near Riviersonderend, to establish a fine-wool gene pool for further selection for a reduced fibre diameter (the Fine wool line) from 1998 up to and including 2009. This line was

maintained along with an unselected control flock described by Cloete *et al.* (1998) at Tygerhoek. The latter authors also described the experimental site. Rams in the Fine wool line were initially sourced from the parent stud (n=6) and from industry (n=4) to sire the bulk of progeny from 1998 to 2000. Such rams were treated as part of the base population in the analysis. Subsequently sires were selected from within the flock, while three migrant rams were also introduced. Two of these rams originated from the Grange stud in WA and sired progeny in 2002, while another ram from the parent stud sired progeny from 2007 to 2009. The low number of subsequent migrant rams did not validate special treatment as separate genetic groups. Selection was for a reduced FD, while it was attempted to maintain LW by ensuring that the mean estimated breeding value (EBV) for LW of rams selected for breeding exceeded the mean of all replacements.

Midrib wool samples were obtained from all hogget progeny after a growth period of approximately 10 months and analysed for clean scoured yield percentage (CY), SL, SS and FD. Greasy fleece weights were recorded at shearing about two months later. After being shorn, hogget LW was recorded. Greasy fleece weight and CY were used to calculate CFW. All the recorded traits were linked to pedigree information.

Each trait was initially subjected to single-trait genetic analyses to obtain prior values for a subsequent multi-trait analysis. The single random effect of animal was fitted, using ASREML (Gilmour *et al.* 2006). The data were then subjected to a five-trait animal model analysis to derive genetic (co)variance components to estimate the heritability (h^2) of all traits, as well as genetic and phenotypic correlations (r_g and r_p respectively). Animal solutions obtained in this way were used to construct genetic trends for the respective traits in the Control flock and the Fine wool line.

RESULTS AND DISCUSSION

The coefficients of variation (CV's) for the respective traits ranged between 10.4% for FD and 36.4% for SS (Table 1). Literature values suggested CV's of 14-28 % for LW, 18-42% for CFW and 9-11% for FD (Olivier and Cloete 2007; Safari *et al.* 2007a; Huisman and Brown 2009). The present CV's are well within this range of values.

Table 1. Descriptive statistics for the traits included in the five-trait analysis, including means, standard deviations (s.d.) and coefficients of variation (CV)

Trait	Number	Mean±s.d.	CV (%)
Live weight (kg)	2510	53.9±11.2	20.8
Clean fleece weight (kg)	2556	3.24±0.79	24.4
Staple length (mm)	2399	85.3±13.2	15.5
Staple strength (N/ktex)	2102	34.3±12.5	36.4
Fibre diameter (µm)	2622	18.3±1.9	10.4

Estimates of h^2 amounted to 0.50 for LW, 0.41 for CFW, 0.39 for SL, 0.19 for SS and 0.76 for FD (Table 2). Corresponding literature values ranged from 0.33-0.52 for LW, from 0.28-0.42 for CFW and from 0.55-0.74 for FD (Swan *et al.* 1995; Rose and Pepper 1999; Cloete *et al.* 2002; Safari *et al.* 2005; 2007b; Olivier and Cloete 2007). Estimates of h^2 for SL ranged from 0.26-0.46 (Swan *et al.* 1995; Safari *et al.* 2005; Olivier and Cloete 2007), while the h^2 of SS was estimated at 0.13-0.34 (Swan *et al.* 1995; Wuliji *et al.* 2001; Safari *et al.* 2005). The present results were all within these ranges, but the h^2 of FD (0.76) was slightly higher than the upper boundary. A similarly high h^2 estimate of 0.74 was reported for FD by Rose and Pepper (1999), suggesting that such high h^2 estimates for FD are indeed feasible. Genetic correlations were also consistent with those in the literature (Swan *et al.* 1995; Safari *et al.* 2005; 2007c; Olivier and Cloete 2007; Huisman and Brown 2009). The unfavourable r_g between FD and SS of 0.44 concurs with

literature values of 0.52 (Wuliji *et al.* 2001) and 0.37 (Safari *et al.* 2005).

Table 2. Additive and residual variance components (respectively σ^2_A and σ^2_E) and (co)variance ratios (\pm s.e.) for hogget live weight (LW), clean fleece weight (CFW), staple length (SL), staple strength (SS) and fibre diameter (FD)

Trait	LW	CFW	SL	SS	FD
Variance components					
σ^2_A	26.86	0.165	32.67	27.39	1.357
σ^2_E	26.86	0.236	50.48	113.28	0.422
(Co)variance ratios (h^2 in bold on the diagonal, r_g above the diagonal and r_p below the diagonal)					
LW	0.50±0.04	0.33±0.07	0.14±0.08	0.30±0.10	-0.10±0.06
CFW	0.36±0.02	0.41±0.04	0.54±0.07	0.09±0.12	0.06±0.06
SL	0.17±0.02	0.49±0.02	0.39±0.04	0.34±0.11	0.05±0.07
SS	0.13±0.02	0.16±0.02	0.15±0.02	0.19±0.04	0.44±0.07
FD	0.06±0.02	0.16±0.02	0.14±0.02	0.28±0.02	0.76±0.03

Phenotypic means for the 1998 progeny indicated that progeny from the Fine wool line was initially heavier (57.0±0.9 vs. 45.3±0.6 kg), with heavier fleeces (4.41±0.16 vs. 3.61±0.11 kg) and longer staples (94.7±1.9 vs. 85.9±1.3 mm) than the Control flock (all $P<0.01$). FD was nearly 1 μ m lower in the Fine Wool line than in the Control flock (19.3±0.2 vs. 20.2±0.1 μ m; $P<0.01$). These initial differences between flocks were expected, as the Fine wool line originated from the fine wool stud at Halesowen, while the Control flock was resident at Tygerhoek. Subsequent genetic change in the Control flock was below 0.3% of the overall phenotypic mean for SL, SS and FD. However, Control flock progeny became appreciably heavier with heavier fleeces with time (both $P<0.01$). A lack of genetic stability for LW has previously been reported in the Control flock, while a corresponding trend was reported for CFW (Cloete *et al.* 1998). EBVs for FD in the Fine wool line declined at 1.01% of the overall mean per annum, while a slight increase was noted for LW ($P<0.05$). Correlated responses in the Fine wool line were unfavourable in the other traits, leading to appreciable reductions in CFW and SS in particular ($P<0.01$; Table 3).

Table 3. Regressions of average EBVs on year (\pm s.e.), depicting genetic trends in the Control flock and Fine wool line at Tygerhoek

Regression Parameter	Traits*				
	LW	CFW	SL	SS	FD
Control flock					
Intercept	-6.21±0.32 ^a	-0.22±0.05 ^a	-2.00±0.04 ^a	-0.46±0.42 ^a	1.35±0.16 ^a
Regression coefficient	0.41±0.05 ^a	0.04±0.01 ^a	0.13±0.04 ^a	-0.02±0.06 ^a	-0.04±0.02 ^a
Fine wool line					
Intercept	3.59±0.42 ^b	0.18±0.04 ^b	1.94±0.06 ^b	0.85±0.55 ^b	-0.40±0.12 ^b
Regression coefficient	0.16±0.07 ^b	-0.03±0.01 ^b	-0.19±0.09 ^b	-0.30±0.09 ^b	-0.19±0.02 ^b

*Live weight (LW), clean fleece weight (CFW), staple length (SL), staple strength (SS), fibre diameter (FD); ^{a,b} – Denote differences between lines for regression parameters at $P<0.05$

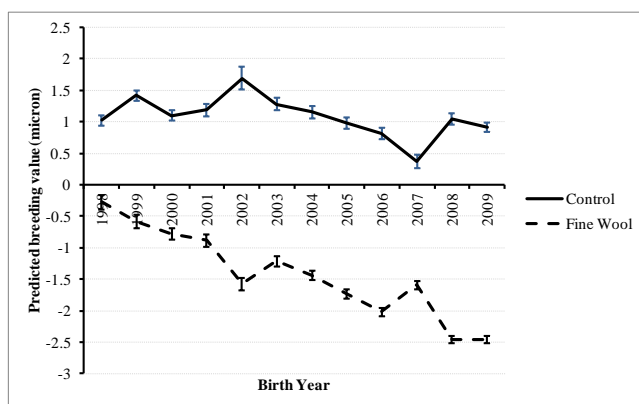


Figure 1. Genetic trends for fibre diameter in the Control and Fine Wool lines at Tygerhoek. Vertical lines about means reflect standard errors.

Averaged annual EBVs for FD in the control flock ranged from 0.5 to 1.5 μm (Figure 1). Average EBVs in the Fine wool line were reduced from -0.28 μm in 1998 to -2.46 μm in 2009.

CONCLUSIONS

Genetic trends indicated that FD was substantially reduced in the Fine wool line, while LW remained stable. However, the response in FD was associated with unfavourable correlated responses, particularly in CFW and SS. The correlated response in SS of the Fine wool line was consistent with an unfavourable within-flock genetic correlation of 0.44 between FD and SS. The premium paid for fine wool will determine whether reductions in FD will be economically viable.

REFERENCES

- Cloete S.W.P., Greeff J.C., Lewer R.P. (2002) *Aust. J. Agric. Res.* **53**, 271.
- Cloete S.W.P., Olivier J.J., Olivier W.J. (2007) *Proc. Assoc. Advmnt. Anim. Breed. Gen.* **17**: 320.
- Cloete S.W.P., Olivier J.J., Snyman M.A., Du Toit, E. (1998) *Aust. J. Exp. Agric.* **38**: 427.
- Cottle D.J. (2010) Wool Preparation, Testing and Marketing. In: Cottle D.J. (ed.) *International Sheep and Wool Handbook*, pp. 581-618. Nottingham University Press, Nottingham, UK.
- Gilmour A.R., Gogel B.J., Cullis B.R., Thompson R. (2006) *ASReml User Guide*. Release 2.0. (VSN International Ltd, Hemel Hempstead, HP1 1ES: UK).
- Huisman A.E., Brown D.J. (2009) *Anim. Prod. Sci.* **49**: 289.
- Olivier J.J., Bezuidenhout A.G., Greyling A.C., Cloete S.W.P. (1999) *Proc. Assoc. Advmnt. Anim. Breed. Gen.* **13**: 62.
- Olivier J.J., Cloete S.W.P. (2007) *Proc. Assoc. Advmnt. Anim. Breed. Gen.* **17**: 324.
- Rose M., Pepper P. (1999) *Proc. Assoc. Advmnt. Anim. Breed. Gen.* **13**: 114.
- Safari E., Fogarty N.M. and Gilmour A.R. (2005) *Livest. Prod. Sci.* **92**: 271.
- Safari E., Fogarty N.M., Gilmour A.R., Atkins K.D., Mortimer S.I., Swan A.A., Brien F.D., Greeff J.C., van der Werf J.H.J. (2007a) *Aust. J. Agric. Res.* **58**: 169.
- Safari E., Fogarty N.M., Gilmour A.R., Atkins K.D., Mortimer S.I., Swan A.A., Brien F.D., Greeff J.C., van der Werf J.H.J. (2007b) *Aust. J. Agric. Res.* **58**: 177.
- Safari E., Fogarty N.M., Gilmour A.R., Atkins K.D., Mortimer S.I., Swan A.A., Brien F.D., Greeff J.C., van der Werf J.H.J. (2007c) *J. Anim. Breed. Gen.* **124**: 65.
- Schoeman S.J., Cloete S.W.P., Olivier, J.J. (2010) *Livest. Sci.* **130**: 70-82.
- Swan A.A., Lax J., Purvis I.W. (1995) *Proc. Aust. Assoc. Anim. Breed. Gen.* **11**: 516.
- Wuliji T., Dodds K.G., Land J.T.J., Andrews R.N., Turner P.R. (2001) *Anim. Sci.* **72**: 241.