

BREEDING PLAIN-BODIED FINE WOOLS - NO PROBLEM!

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SUMMARY

The inheritance of wrinkle in fine wool sheep was investigated in a mixed bloodline flock run in western NSW. Both repeatability (0.6) and heritability (0.4) estimates agreed with published estimates from broader flocks as did the phenotypic and genetic correlations with a suite of assessed and measured traits. The correlations suggest that selection for plain-bodied easy care fine wool sheep can be achieved while maintaining wool production and quality despite medium to strong antagonistic relationships with wool production and staple strength. Furthermore the genetic relationships with liveweight were favourable, albeit small.

INTRODUCTION

The very early (to 1885) history of the Australian sheep industry was characterised by “a passionate focus on wool quality, so long as the wool produced was 80’s or 90’s nobody bothered much what the sheep cut” (Austin 1943). The early fine wools were said to carry “a beautiful, long staple of high yielding wool on a completely plain body” (Dun and Eastoe 1970). The development of the Peppin strain in the 1860s saw the focus shift to production based on the concept of “return per head” (Austin 1943). The introduction of the heavily wrinkled Vermont Merino about 20 years later was an attempt to increase the wool cut of fine wool, again to increase the return per head. Despite the subsequent downfall of the Vermont in the early 1900s, many stud breeders to this day believe that a moderate degree of skin wrinkle is required to maintain wool weight through its association with fleece density (Crook and James 1991; Sutton *et al.* 1995). The wool production focus continued for 130 years until the mid 1990s when consumer preferences for lightweight clothing and the requirement for increased processing efficiency drove a trend towards the production of finer wool (Swan *et al.* 2008). Fine wool producers are now seeking to breed ‘easy care’ plainer bodied animals with acceptable carcass traits while maintaining or improving their wool quality and production (A. Casey pers comm.). This paper reports on the genetic relationships between wrinkle score and assessed and measured traits in a mixed bloodline flock run in western New South Wales.

MATERIALS AND METHODS

The sheep used in this study were wethers born between 1991 and 1996 in the CSIRO Fine Wool Project flock at Armidale (Swan *et al.* 2000) and transferred to the Condobolin Agricultural Research and Advisory Station (ARAS) following their hogget shearing. Prior to transfer, each wether was assessed for neck and body wrinkle using a 1-6 score (1 = plainest and 6 = wrinkliest) (Turner *et al.* 1953) at 10 months of age. All wethers were mulsed when 2 months old so breech wrinkle was not scored. Total wrinkle was calculated by adding the neck and body wrinkle scores. Repeat assessments were made on the 1991 drop at 3 and 4 years of age and the 1994, 1995 and 1996 drops at 5, 4 and 3 years of age respectively. The wethers remained at Condobolin for 4 consecutive shearings. At each annual shearing a suite of measurements and assessments were taken including wool production, wool quality, liveweight (Hatcher *et al.* 2005). The wethers were assessed for disease resistance using a scoring system for the incidence of fleece rot (1-8 score), bacterial stain (1-5 score), dermatitis (1-9 score) and flystrike (1-7) where low scores indicate an absence of the disease. The occurrence of disease within the flock was low, ranging from 0.3% for bacterial stain to 6.4% for fleecerot.

Approximately 1,800 individual animals, each with an identified sire, were involved in this analysis and represented 11 bloodlines (6 superfine, 3 fine and 2 medium wool). ASReml (Gilmour *et al.* 2006) was used to estimate variance components using a general linear mixed model by residual maximum likelihood. A univariate analysis was undertaken for each wrinkle score (neck, body and total). The model included the fixed effects of drop (5 levels: 1991, 1993 to 1996), year (9 levels: 1993 to 2001) and flock (11 levels) together with significant interactions. Random effects were estimated for sire (σ^2_s), animals within sire (σ^2_b), within animals (σ^2_w) and between flocks (σ^2_f). Repeatability ($\sigma^2_s + \sigma^2_b$) / ($\sigma^2_s + \sigma^2_b + \sigma^2_w$), heritability ($4\sigma^2_s$) / ($\sigma^2_s + \sigma^2_b + \sigma^2_w$) and their standard errors were calculated from the univariate analyses. Genetic and phenotypic covariances were estimated using a series of bivariate analyses involving the wrinkle scores and each of the other traits. Fixed effects and interactions were fitted as appropriate from the univariate analyses. Genetic and phenotypic correlations with standard errors were estimated from the appropriate covariances in ASReml.

RESULTS AND DISCUSSION

The average wrinkle scores were 3.15 ± 0.21 , 2.22 ± 0.20 and 5.36 ± 0.38 for neck, body and total wrinkle respectively. Differences between flocks in wrinkle score were not large. Flock means ranged from 2.70 - 3.54 for neck wrinkle, 2.31 - 2.94 for body wrinkle and 5.00 - 6.46 for total wrinkle. Between and within animal variation in wrinkle score together accounted for 90, 91 and 88 % of the phenotypic variance for neck, body and total wrinkle respectively (Table 1). Between sire variation was the least important source for each of the 3 wrinkle scores and between flock variation was equally low. The 3 wrinkle scores were highly repeatable (0.50-0.61) with high heritability (0.35-0.44). Both the repeatability (Beattie 1961; Young *et al.* 1960a) and heritability (Beattie 1962; Brown and Turner 1968; Gregory 1982; Groenewald *et al.* 1999; Mortimer and Atkins 1993; Mortimer *et al.* 2009; Young *et al.* 1960b) estimates agree with those estimated for medium to broad wools. Wrinkle scores are therefore under a similar degree of genetic control in fine wool flocks as fibre diameter and clean fleece weight (Hatcher and Atkins 2000) and will respond to single trait selection in much the same manner as medium to broader wools (Turner *et al.* 1970).

Table 1. Variance components, heritability and repeatability (\pm se) of wrinkle scores

Wrinkle	Variance component					Repeatability t^2	Heritability h^2
	σ^2_w	σ^2_b	σ^2_s	σ^2_p	σ^2_f		
Neck	0.24 \pm 0.01	0.32 \pm 0.02	0.06 \pm 0.01	0.62 \pm 0.02	0.07 \pm 0.03	0.61 \pm 0.02	0.40 \pm 0.07
Body	0.29 \pm 0.01	0.24 \pm 0.02	0.05 \pm 0.01	0.57 \pm 0.02	0.04 \pm 0.02	0.50 \pm 0.02	0.35 \pm 0.07
Total	0.77 \pm 0.03	1.04 \pm 0.05	0.22 \pm 0.04	2.04 \pm 0.06	0.21 \pm 0.11	0.62 \pm 0.02	0.44 \pm 0.08

The phenotypic and genetic correlations (0.71 and 0.99 respectively) between neck and body wrinkle were strong, positive and close to unity indicating that either score will provide a reliable visual description of the degree and quantity of wrinkles on an individual animal. This finding agrees with previous work (Beattie 1962; Jackson and James 1970; Lewer *et al.* 1995; Mortimer and Atkins 1993; Mortimer *et al.* 2009). For the purpose of brevity total wrinkle will be used when discussing the correlations with other traits.

Phenotypic correlations between wrinkle and the other assessed traits tended to be negligible except for density (-0.3) (Table 2). So plain-bodied fine wool sheep would tend to have denser fleeces that would be marginally softer with slightly better defined crimp and enhanced style. Phenotypic correlations between wrinkle and the measured traits were generally of a higher magnitude, but still ranged from negligible to low. Most measured traits

had weak complimentary phenotypic associations with wrinkle, plain-bodied animals tended to have lower fibre diameter, lower variability in fibre diameter (both standard deviation and coefficient of variation), increased yield and lower resistance to compression. Plain-bodied individuals would also phenotypically tend to maintain liveweight. However antagonistic correlations were identified between wrinkle and wool production, with plain-bodied animals cutting lighter greasy and clean fleeces with shorter staples. There was no phenotypic relationship between wrinkle and staple strength.

Table 2. Phenotypic (r_p) and genetic correlations (r_g) (\pm se) between wrinkle scores and wool production and quality traits

Trait	Neck		Body		Total	
	r_p	r_g	r_p	r_g	r_p	r_g
<i>Assessed traits</i>						
Handle	0.12 \pm 0.02	0.30 \pm 0.13	0.11 \pm 0.02	0.28 \pm 0.14	0.12 \pm 0.02	0.30 \pm 0.13
Dust penetration	0.02 \pm 0.02	0.12 \pm 0.19	0.01 \pm 0.02	0.04 \pm 0.19	0.02 \pm 0.02	0.08 \pm 0.18
Crimp definition	0.09 \pm 0.02	0.14 \pm 0.14	0.05 \pm 0.02	0.11 \pm 0.14	0.08 \pm 0.02	0.12 \pm 0.14
Staple structure	0.02 \pm 0.02	0.08 \pm 0.17	0.04 \pm 0.02	0.07 \pm 0.18	0.03 \pm 0.02	0.07 \pm 0.17
Density	-0.28 \pm 0.02	-0.65 \pm 0.10	-0.27 \pm 0.02	-0.63 \pm 0.11	-0.30 \pm 0.02	-0.63 \pm 0.10
Colour	-0.01 \pm 0.02	-0.08 \pm 0.15	-0.03 \pm 0.02	-0.06 \pm 0.15	-0.02 \pm 0.02	-0.07 \pm 0.14
Style	0.08 \pm 0.02	0.02 \pm 0.20	0.10 \pm 0.02	0.02 \pm 0.21	0.09 \pm 0.02	0.02 \pm 0.20
Fleece rot	0.02 \pm 0.01	0.12 \pm 0.17	no estimates available			
Bacterial stain	no estimates available		-0.00 \pm 0.02	-0.21 \pm 0.14	0.00 \pm 0.02	-0.13 \pm 0.14
Flystrike	0.02 \pm 0.02	-0.06 \pm 0.21	0.01 \pm 0.02	-0.18 \pm 0.22	0.01 \pm 0.02	-0.11 \pm 0.21
Body wrinkle	0.71 \pm 0.01	0.99 \pm 0.00	no estimates available			
<i>Measured traits</i>						
GFW (kg)	0.36 \pm 0.02	0.61 \pm 0.09	0.30 \pm 0.02	0.52 \pm 0.10	0.35 \pm 0.02	0.56 \pm 0.09
CSY (%)	-0.17 \pm 0.02	-0.40 \pm 0.12	-0.15 \pm 0.02	-0.38 \pm 0.12	-0.17 \pm 0.02	-0.39 \pm 0.11
CFW (%)	0.23 \pm 0.02	0.39 \pm 0.11	0.18 \pm 0.02	0.29 \pm 0.12	0.22 \pm 0.02	0.34 \pm 0.11
LWT (kg)	-0.03 \pm 0.02	-0.05 \pm 0.15	-0.07 \pm 0.02	-0.12 \pm 0.15	-0.06 \pm 0.02	-0.07 \pm 0.15
FD (μ m)	0.19 \pm 0.02	0.34 \pm 0.12	0.16 \pm 0.02	0.31 \pm 0.13	0.19 \pm 0.02	0.31 \pm 0.12
FDSD (μ m)	0.26 \pm 0.02	0.40 \pm 0.11	0.23 \pm 0.02	0.33 \pm 0.12	0.26 \pm 0.02	0.36 \pm 0.11
FDCV (%)	0.20 \pm 0.02	0.42 \pm 0.12	0.18 \pm 0.02	0.33 \pm 0.13	0.20 \pm 0.02	0.37 \pm 0.12
FC ($^\circ$ /mm)	0.01 \pm 0.02	-0.03 \pm 0.15	0.03 \pm 0.02	-0.05 \pm 0.15	0.02 \pm 0.02	-0.04 \pm 0.14
SL (mm)	-0.23 \pm 0.02	-0.54 \pm 0.11	-0.24 \pm 0.02	-0.51 \pm 0.11	-0.26 \pm 0.02	-0.53 \pm 0.10
SS (N/ktex)	-0.00 \pm 0.02	0.06 \pm 0.14	0.03 \pm 0.02	0.09 \pm 0.14	0.02 \pm 0.02	0.08 \pm 0.13
RTOC (kpa)	0.19 \pm 0.02	0.33 \pm 0.12	0.17 \pm 0.02	0.29 \pm 0.13	0.19 \pm 0.02	0.31 \pm 0.12
Colour (Y-Z)	0.07 \pm 0.02	0.36 \pm 0.16	0.06 \pm 0.02	0.29 \pm 0.17	0.07 \pm 0.02	0.33 \pm 0.16

The genetic correlations between wrinkle and the assessed and measured traits were of the same sign, except for the incidence of flystrike, and stronger than the phenotypic correlations (Table 2). The genetic correlations between the assessed traits and wrinkle ranged from high and complimentary (density) to negligible and antagonistic (staple structure). However most were negligible. Selection for reduced wrinkle will lead to denser fleeces with a softer handle. No change would be expected in dust penetration, staple structure and assessed colour. The incidence of fleece rot would decrease and while there was evidence of an increased incidence of flystrike, the standard errors for these 2 estimates were both large. Greasy and clean fleece weights both had economically antagonistic relationships with wrinkle but the correlation with greasy fleece weight was higher (0.6 and 0.3 respectively). Staple length had a medium negative, economically favourable relationship (-0.5). Genetic correlations with the other

measured traits were low and favourable so selection for plain-bodied fine wool sheep would produce finer, higher yielding fleeces with longer staple length, lower variation in fibre diameter, improved resistance to compression and measured colour. Liveweight, fibre curvature and staple strength were only weakly correlated with wrinkle.

CONCLUSIONS

Inheritance of wrinkle in fine wool sheep is similar to broader bloodlines. The antagonistic correlation between wrinkle and clean fleece weight is of a similar magnitude to that reported between fibre diameter and clean fleece weight (Safari *et al.* 2005), and it has been demonstrated that simultaneous improvement in these two traits is achievable (Mortimer *et al.* 2006). The genetic relationships between wrinkle and liveweight were positive, albeit small indicating that selection for plain-bodied fine wools will not negatively impact carcase weight.

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