GENETICS OF WOOL COLOUR IN THE SOUTH AUSTRALIAN SELECTION DEMONSTRATION FLOCKS

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SUMMARY

A wide range of objectively measured and subjectively assessed characters were recorded in the South Australian Selection Demonstration Flocks between 1997 and 2005. These data provided an opportunity to study the genetics of wool colour and relationships with other traits, as part of a wider study by the Sheep CRC. In 2000, 2001 and 2002 clean wool colour was objectively measured by the Australian Wool Testing Authority on wool samples from 1,116 hogget rams. Clean colour was highly heritable (0.45). For assessed greasy colour the heritability was even higher (0.53), with a favourable negative genetic correlation (-0.38) between the two traits. There was a strong (0.57) positive genetic correlation between mean fibre diameter and clean wool colour and similarly a moderate negative genetic correlation with greasy wool colour. There was also a positive genetic correlation between clean colour and greasy fleece weight (0.34), dust penetration (0.35), and the standard deviation of fibre diameter (0.33). This indicates that selecting animals with heavier fleece weights tends to lead to progeny with wool that is more yellow in clean colour and that selecting animals with lower fibre diameter tends to lead to progeny that have whiter, more lustrous wool. The implications of these findings are discussed.

INTRODUCTION

A current challenge for the Australian wool industry is to produce a product that can compete in the light weight, trans-seasonal, next-to-skin capable market. This requires whiter, more photostable wool. Currently wool requires the application of oxidative bleaches and fluorescent whiteners to bring it to an acceptable white colour that is comparable with its competitor, cotton, but unfortunately these treatments have a detrimental effect on photostability, placing wool at a distinct disadvantage (Millington *et al.* 2008). Unbleached cotton measures approximately 7 tristimulus units (Y-Z), where lower tristimulus units equal whiter colour. It has been estimated that between 1 – 3% of the Australian wool clip currently measures 7 tristimulus units (Y-Z) or lower, with 70 – 80% greater than 8.5. Consequently, there is economic merit in improving clean wool colour (Millington, unpublished; Millington *et al.* 2008).

Genetic improvement through direct or indirect selection is one method of improving clean wool colour. Currently greasy wool colour, a component of style is estimated as a subjective measure of wool colour rather than objectively measured wool colour. There are many genetic parameter estimates of greasy wool colour (most recently reviewed by Mortimer 2007). However the relationship between greasy and clean wool colour is not clear, with the most recent estimates indicating a poor genetic correlation between the two traits. The aim of this study, as part of a wider Sheep CRC project (see also Smith and Purvis 2009) was to estimate the relationship between clean and greasy wool colour and their relationship with other important wool traits.

MATERIALS AND METHODS

SA Selection Demonstration Flocks Project (SDFs). In 1996, SA Merino ewes were sourced from a previous trial conducted at Turretfield Research Centre (the SA Merino Resource Flock, Gifford *et al.* 1990) to establish four flocks of 200 ewes each, representing three major selection approaches and a randomly selected control. In 1999, a Meat Merino line was added. All SDF lambs were born in June-July of each year. For more details, see Kemper *et al.* (2006).

A wide range of objectively measured and subjectively assessed characters were recorded on the SDFs between 1997 and 2005. For this paper the objectively measured traits analysed included greasy fleece weight (GFW), clean scoured yield (CSY), clean fleece weight (CFW), mean fibre diameter (MFD), standard deviation of fibre diameter (SDFD), coefficient of variation of fibre diameter (CVFD), staple length (SL), staple strength (SS), mean fibre curvature (MFC), body weight (BWT) and dust penetration (DUST) recorded at 16 months of age on both sexes.

In 2000, 2001 and 2002 clean wool colour (CCOL) was objectively measured on 1,116 hogget rams in tristimulus units (Y-Z), where lower values equal whiter colour (Table 1). The subjectively measured traits reported were also measured at 16 months and include handle (HAND, 1 harsh – 5 very soft) and greasy colour (GCOL, 1 yellow – 4 lustrous white). Table 2 indicates the numbers of animals with each of these traits recorded.

Table 1. Sire representation among clean wool colour (CCOL) records

	Total records[#]	CCOL records	Total sires represented	Progeny group size	No. sires with >9 progeny & Ccol
Hoggets	9436	1116	124	1-168	81

[#] fully pedigreed

The initial data analyses fitted a univariate animal model to determine the main effects for the subsequent multivariate analyses using ASReml (Gilmour *et al.* 2006). The model included the fixed effects of flock (SDF, 1-5), drop (1997-2005), age of dam (2 – 6 years of age), type of birth and rearing (born as a single and raised as a single, born as a multiple and raised as a single, born as a multiple and raised as a multiple) and age to first shearing fitted as a covariate. For the subjectively measured traits that were measured by more than one classer, classer was added as a fixed effect to the model. The final models used for the multivariate analyses were determined by iteratively removing any non-significant terms from the univariate model. Variance and covariance components were used to estimate heritability and phenotypic and genetic correlations. While CCOL was normally distributed, GCOL was slightly right-skewed. However, no data transformation was undertaken.

Table 2. Summary statistics for (16mth) hogget traits in the Selection Demonstration Flocks

Trait	Mean	SD	Min.	Max.	Count
GFW (kg)	6.6	1.2	2.1	11.5	7,066
CSY (%)	71.9	5.5	50.8	85.0	7,103
CFW (kg)	4.8	1.0	1.6	8.8	7,055
MFD (µm)	20.1	2.0	14.1	29.2	7,103
SDFD (µm)	4.5	0.7	2.7	8.3	7,103
CVD (%)	22.1	2.9	13.5	34.8	7,103
SL (mm)	100.0	15.6	56.7	157.1	7,095
SS (N/kTex)	30.7	11.9	3.9	98.1	7,092
MFC (°/mm)	83.7	10.7	52.6	126.1	7,103
CCOL (Y-Z)	9.6	0.7	7.5	14.4	1,116
BWT (kg)	59.2	11.4	19.5	96.4	7,068
HAND (1-5)	3.0	0.9	1.0	5.0	4,162
DUST (1-5)	5.1	1.1	0.5	9.5	5,601
GCOL (1-5)	2.5	0.8	1.0	5.0	4,162

RESULTS AND DISCUSSION

Fixed Effects. The SDFs were significantly different for both greasy and clean wool colour (Table 3), with wool from the control flock being significantly more yellow than the other flocks for both traits. There was a significant effect of drop on both traits with those animals born in the year 2000 producing more lustrous, white wool than those born in 2001 and 2002. Interestingly animals born and reared as multiples tended to have more yellow greasy wool than those reared as singles (and born as either singles or multiples). This result was not reflected in the objectively measured wool colour (CCOL) with no significant difference between birth and rearing types.

Table 3. Significance of fixed effects on yearling and adult clean and greasy wool colour

Trait	Dam age	Birth-Rear type	Sex	Flock	Age	Classer	Drop
CCOL (Y-Z)	n.s.	n.s.	-	***	*	-	***
GCOL (1-5)	n.s.	***	**	***	***	**	***

*** P<0.001, ** P<0.01, * P<0.05, ns not significant

Table 4. Hogget (16mth) heritability (h^2) and phenotypic (r_p) and genetic (r_g) correlations among clean scoured wool colour (CCOL) and assessed greasy wool colour (GCOL) and other production traits with s.e's in parentheses

Trait	h^2	CCOL		GCOL	
		r_p	r_g	r_p	r_g
GFW (kg)	0.46 (0.03)	0.21 (0.03)	0.34 (0.09)	-0.15 (0.02)	-0.36 (0.04)
CSY (%)	0.52 (0.03)	-0.07 (0.03)	-0.13 (0.10)	0.29 (0.01)	0.56 (0.03)
CFW (kg)	0.38 (0.03)	0.10 (0.03)	0.20 (0.10)	0.01 (0.02)	-0.03 (0.04)
MFD (μm)	0.63 (0.03)	0.32 (0.03)	0.57 (0.08)	-0.17 (0.02)	-0.36 (0.03)
SDFD (μm)	0.56 (0.02)	0.20 (0.03)	0.33 (0.09)	-0.26 (0.02)	-0.47 (0.03)
CVD (%)	0.50 (0.03)	0.02 (0.03)	-0.03 (0.10)	-0.17 (0.02)	-0.30 (0.03)
SL (mm)	0.49 (0.03)	-0.04 (0.03)	0.05 (0.10)	0.07 (0.02)	0.05 (0.04)
SS (N/kTex)	0.27 (0.02)	0.14 (0.03)	0.21 (0.11)	0.03 (0.02)	0.07 (0.05)
MFC (°/mm)	0.62 (0.02)	-0.23 (0.03)	-0.35 (0.09)	-0.01 (0.02)	0.01 (0.03)
CCOL (Y-Z)	0.45 (0.08)			-0.15 (0.03)	-0.38 (0.07)
BWT (kg)	0.48 (0.03)	0.01 (0.03)	0.02 (0.10)	-0.01 (0.02)	-0.06 (0.04)
HAND (1-5)	0.46 (0.01)	-0.12 (0.03)	-0.31 (0.08)	0.48 (0.01)	0.79 (0.02)
DUST (1-5)	0.25 (0.03)	0.12 (0.03)	0.35 (0.12)	0.02 (0.02)	-0.10 (0.06)
GCOL (1-5)	0.53 (0.01)	-0.15 (0.03)	-0.38 (0.07)		

Genetic parameters. The estimates of phenotypic variance and heritability and genetic correlations for most of the hogget production traits in table 4 are in agreement with those already published on this dataset (Safari *et al.* 2007, 2008). Clean colour was highly heritable (0.45) indicating that genetic improvement for clean colour can be made through selection. For assessed greasy colour the heritability was even higher (0.53), with a favourable negative genetic correlation (-0.38) between the two traits. These estimates are similar to those of James *et al.* (1990) who reported heritability estimates of 0.42 for both CCOL and GCOL and a high favourable genetic correlation of 0.87 (GCOL was scored in the opposite direction to our study) between the two traits in Collinsville Merino sheep. However in fine wool Merinos, Smith and Purvis (2009) estimated low genetic correlations between the two colour measures of 0.13 and 0.18 in yearling and adult sheep respectively, where GCOL was also scored in reverse to our study.

Interestingly, there was a strong (0.57) positive genetic correlation between mean fibre diameter and clean wool colour and similarly a moderate negative genetic correlation with greasy wool colour. There was also a positive genetic correlation between clean colour and GFW (0.34), DUST (0.35), and SDFD (0.33). This indicates that animals with heavier fleece weights would also have hogget progeny with wool that has a yellower clean colour. Two other genetic correlations of note between clean colour and key productions traits, although only slight, are those with CFW (0.20) and SS (0.21). These values are slightly higher than those estimated by Smith and Purvis (2009) in fine wool Merinos at both yearling and adult time points.

In conclusion, our results suggest that either direct selection of hogget animals for improved clean wool colour or indirect selection based on greasy wool colour will lead to genetic improvement in clean wool colour in hogget animals. The consequences of such selection for hogget production traits likely include a slight reduction in hogget fleece weight, a lower fibre diameter and a slight reduction in staple strength. Whilst these genetic parameters for hogget performance are an important step to the implementation of selection for improved wool colour in commercial breeding programs, so too are genetic parameters linking hogget and adult production and the development of economic values (Smith and Purvis 2009). Finally, current breeding programs placing strong emphasis on improving fleece weight (but not fibre diameter), unless counter-balanced by other selection efforts, may unintentionally lead to increases in wool colour. This may not be an issue for traditional end uses for wool, but would limit the availability of suitable wools for supplying a developing market in light weight, trans-seasonal, next-to-skin wear.

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