GENETIC VARIATION IN CLEAN WOOL COLOUR IN FINE WOOL MERINOS

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SUMMARY

Greasy wool colour is a component of wool style and a determinant of price received, but it is clean wool colour that determines potential colour range and dye-ability of wool garments. Selective breeding is a means of improving raw wool clean colour, but its effectiveness is currently unclear due to limited existing information on clean colour variability, heritability and correlations with other fleece traits. Clean colour was measured on yearling (10mths, n=7106) and adult (21mths, n=8078) animals. Other fleece traits, including assessed greasy wool colour, were also recorded and genetic parameters for clean and greasy wool colour estimated. Clean wool colour was moderately to highly heritable at both yearling and adult ages (0.25 and 0.29 respectively), as was greasy colour (0.33 and 0.40). Clean wool colour at yearling and adult age was moderately genetically correlated (0.52), suggesting that selection using yearling measurements would be effective for improving lifetime clean wool colour. Greasy and clean wool colour were poorly correlated phenotypically and genetically at both yearling and adult age. Of the measured fleece traits, fibre diameter and curvature were those with highest genetic correlations with clean wool colour (yearling, 0.52, -0.34). These correlations indicate that superfine wool animals with a classical crimp frequency to fibre diameter ratio (true-to-type) tend to have superior clean wool colour compared to other wool types included here.

INTRODUCTION

Greasy wool colour impacts on price received for wool at auction. With potential development of new markets in trans-seasonal apparel, selective breeding for clean colour is a means of increasing the quantity of white wool supplied to the market. There are many estimates of greasy wool colour genetic parameters for Australian Merinos in the literature (Mortimer 2007) and stud breeders routinely rely on subjective assessment of greasy colour rather than objective measurement of clean colour (Brown 2006). However phenotypically, the relationship between greasy and clean wool colour is poor. There is some evidence though from genetic analysis of other Merino resource flocks (Dowling *et al.* 2007; Hebart and Brien 2009) indicating moderate genetic correlation between greasy and clean wool colour which suggests that selection for clean wool colour based on greasy colour could be effective.

Using data from CSIRO fine wool resource flocks, the aims of this study were to estimate: the variability and heritability of greasy and clean wool colour; phenotypic and genetic correlations between greasy and clean colour and a suite of fleece and production traits; and phenotypic and genetic correlations between clean colour at yearling and adult age. These parameters are necessary for inclusion of clean wool colour in Merino breeding programs.

METHOD

Animals. Measured clean wool colour (cCOL, yellowness Y-Z) and assessed greasy wool colour (gCOL) were recorded on fully pedigreed yearling (10mth) and adult (2yo) sheep in the CSIRO Fine Wool Project (FWP) (Swan *et al.* 2008) and the CSIRO Toward 13 Micron Flock (T13) (Swan and Purvis 2005) (Table 1). Of the 12 bloodlines represented, there were 9 fine/superfine lines and 2 medium lines, plus the T13 ultrafine wool line which was founded on ewes from the fine/superfine lines in the FWP.

Table 1. Sire representation among yearling and adult clean wool colour (cCOL) records

	Animals	Sires	cCOL	Mean progeny group size (range)
Yearling	11856	473	7106	25.1 (1-173)
Adult	8226	416	8078	19.5 (1-106)
Yearling & Adult	8826	296	5598	18.9 (3-87)

Wool colour measurements. cCOL measurements were made by the Australian Wool Testing Authority in CIE tristimulus values as Y-Z (yellowness). gCOL was assessed on a 1-5 scale where 1=whitest. Swan *et al.* (1997) reported a strong association between assessed and measured greasy wool colour, indicating subjective assessment is an accurate method to determine greasy wool colour.

Other measurements. In addition to cCOL and gCOL, traits included in this analysis were greasy and clean fleece weight (GFW and CFW); clean scoured yield (CSY); mean fibre diameter (MFD); standard deviation and coefficient of variation of fibre diameter (SDFD and CVD); staple length and strength (SL and SS); mean fibre curvature (CURV); and bodyweight (BWT). Fleece and bodyweight trait abbreviations are henceforth prefixed with y (yearling) or a (adult) as appropriate.

Statistical analysis. Initially, fixed effects models were fitted using ASReml (Gilmour *et al.* (2002) to determine significance of main effects which included bloodline (12 levels, described above), dam age (maiden and adult), birth-rearing type (born and reared single; born multiple and reared single; born and reared multiple), sex (male and female), flock (combined birth year-management group effect) and age (to first shearing for yearlings and between first and second shearing for adults) which was fitted as a covariate. Scorer of gCOL was also included. Non-significant fixed effects were iteratively removed from the model and no interactions were included in the final models. In analysis of adult records, location (Armidale, Condobolin and Camden) was an additional main effect. For the drops 1991 and 1993-1996 inclusive, approximately ¾ (n=2314, balanced for bloodline and sire) of male progeny from the FWP flock were relocated to the NSW DPI site at Condobolin following hogget shearing for the purpose of determining genotype by environment interactions. In 1992, approximately ¾ (n=396) of the male progeny were re-located to The University of Sydney, Camden, NSW for footrot-related studies. Heritability and correlations among cCOL, gCOL and the suite of fleece and production traits were estimated from bivariate mixed animal models.

RESULTS

Main effects. Bloodlines were significantly different in both gCOL and cCOL and at both ages (Table 2). For ycCOL, the ultrafine bloodline and medium wool bloodlines were significantly different to each other and all the fine/superfine wool bloodlines (P<0.001). As adults, the ultrafine line was not significantly different in cCOL to any of the fine wool lines, but the wool from the medium lines remained significantly more yellow than that from the other bloodlines (P<0.001).

For ycCOL (P<0.01), acCOL (P<0.001) and agCOL (P<0.001), animals reared as multiples tended to have more yellow wool than those born and reared as singletons. Among adults, males had more yellow wool than females (P<0.05). Location was a significant effect on acCOL and agCOL where animals at Camden had more yellow gCOL and less yellow cCOL (P<0.001). acCOL and agCOL tended to be more yellow at Condobolin than Armidale (P<0.001).

Table 2. Predicted bloodline means for clean (cCOL) and greasy (gCOL) wool colour among yearlings (10mth) and adults (21mth)

Age	Trait	Bloodline											
		1	2	3	4	5	6	7	8	9	10	11	12
Yearling	cCOL	8.2	8.4	8.3	8.3	8.2	8.7	8.1	8.8	8.3	8.1	8.1	7.8
	gCOL	2.3	2.9	2.7	2.4	2.8	3.2	2.1	3.5	2.7	2.2	2.6	2.6
Adult	cCOL	8.3	8.4	8.5	8.4	8.3	9.2	8.4	9.2	8.4	8.3	8.3	8.5
	gCOL	2.1	3.2	2.4	2.3	3.1	3.6	1.8	3.6	2.8	2.1	2.4	2.7

Bloodline 12 = ultrafine wool, 6 and 8 = medium wool, rest = superfine/fine wool
cCOL s.e.'s 0.02 – 0.05; gCOL s.e.'s 0.02 – 0.04

Genetic parameters. The heritability of cCOL was similar, but slightly higher in adults than yearlings (0.29 and 0.25 respectively). For gCOL, the heritability was also higher at adult than yearling age (0.40 and 0.33 respectively), but cCOL and gCOL were poorly correlated both phenotypically and genetically at both ages (Table 3). MFD and CURV were the fleece traits most closely associated with cCOL and those phenotypic and genetic relationships appeared stronger in yearlings than adults (Table 3). Whiter wools tended to have lower MFD and higher CURV.

Table 3. Phenotypic (r_p) and genetic (r_g) correlations among clean wool colour (cCOL, Y-Z) and assessed greasy wool colour (gCOL) and other production traits (s.e. in parentheses) in Yearlings (10mth) and adults (21mth)

	Yearling (10mths)						Adult (21mths)					
			cCOL x		gCOL x				cCOL x		gCOL x	
Trait	V_p	h^2	r_p	r_g	r_p	r_g	V_p	h^2	r_p	r_g	r_p	r_g
GFW (kg)	0.11	0.35	0.04	0.12	0.10	0.26	0.20	0.40	-0.01	0.09	0.08	0.25
CFW (kg)	0.07	0.34	0.05	0.14	0.00	0.15	0.13	0.38	0.00	0.15	-0.02	0.07
CSY (%)	15.6	0.55	0.03	0.07	-0.32	-0.45	17.6	0.55	0.00	0.15	-0.26	-0.37
MFD (μm)	1.07	0.68	0.24	0.52	0.10	0.14	1.30	0.69	0.19	0.35	0.06	0.10
SDFD (μm)	0.14	0.50	0.10	0.28	0.14	0.27	0.15	0.52	0.11	0.21	0.10	0.21
CVD (%)	4.7	0.45	-0.03	-0.05	0.10	0.20	3.6	0.44	0.00	0.00	0.08	0.18
SL (mm)	72	0.54	0.04	0.04	-0.04	-0.05	64	0.51	-0.04	-0.03	-0.02	0.05
SS (N/kTex)	89	0.35	0.07	0.04	-0.08	-0.23	83	0.33	0.04	0.12	-0.11	-0.22
CURV (°/mm)	110	0.59	-0.21	-0.34	-0.06	-0.16	109	0.49	-0.13	-0.30	-0.09	-0.24
YBWT (kg)	11.6	0.49	0.02	0.07	-0.02	0.02	20.0	0.50	-0.03	-0.10	-0.03	0.03
cCOL (Y-Z)	0.31	0.25	-	-	0.06	0.13	0.37	0.29	-	-	0.08	0.18
gCOL (1-5)	0.40	0.33	0.06	0.13	-	-	0.52	0.40	0.08	0.18	-	-

s.e on h^2 estimates 0.02-0.04; s.e. on r_p estimates 0.01-0.02; s.e. on r_g estimates 0.04-0.07

The genetic correlation between cCOL at yearling and adult age was moderate (0.52), suggesting that selection using yearling measurements would be reasonably effective for improving clean wool colour of adult animals. gCOL at yearling and adult age was moderately correlated phenotypically (0.40) and highly correlated genetically (0.84). This is of limited practical use for improving clean wool colour due to the poor relationship between the two, but could be a useful selection aid for those wool producers with a focus on wool style, of which greasy colour is a component.

DISCUSSION

The genetic correlation between cCOL at yearling and adult age is moderate, and between gCOL of yearlings and adults is high. That, accompanied by moderate heritabilities and adequate phenotypic variance, bodes well for selection for lifetime greasy or clean colour based on yearling

measurements. However, the genetic correlation between greasy and clean colour at both ages is low at best, which is limiting to the potential for improvement in clean wool colour through indirect selection on greasy wool colour. Clean colour heritability and correlations with key economically important fleece traits are lower here than reported for mainly medium wool types by Hebart and Brien (2009) which may suggest differences among Merino genotypes in clean colour.

At approximately $10 per animal, clean wool colour is an expensive trait to measure and with no clear economic signals to wool producers in improving clean wool colour it is difficult for stud breeders to justify the measurement and inclusion of clean wool colour in breeding programs. Given the genetic correlations between cCOL and MFD and CURV, and the fact that those two traits are more highly heritable than cCOL, a higher rate of response in cCOL may be achievable through indirect selection on MFD and CURV than gCOL.

Benavides *et al.* (1998) argue that the poor association between greasy and clean colour is not surprising as scoured wool colour is dependent upon environmental challenge (Wilkinson 1981). Therefore, selection on cCOL is likely to be ineffective because yellowness is only expressed when environmental conditions are conducive. In effect, this is a genotype by environment interaction. Wilkinson's observation of wool colour deterioration with exposure to heat and humidity led to development of a greasy wool incubation test for prediction of cCOL. Raadsma and Wilkinson (1990) applied that predictive test in genetic studies of wool yellowing. Heritability of the predictive test in Merinos was estimated at 0.31. Further investigation of the relationship between 'incubated' greasy colour and clean colour might be warranted as a means of including a measure of wool colour in Merino breeding programs. To further facilitate inclusion of clean wool colour in breeding programs analysis of auction data to calculate the relative economic value of that trait is needed.

ACKNOWLEDGEMENTS

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