

## **WILL MERINO SHEEP WITH SMOOTH BARE BREECHES GROW SOFT, WHITE, PHOTOSTABLE WOOL?**

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### **SUMMARY**

Genetic parameters for yearling records of breech cover (BCOV), breech wrinkle (BRWR), handle (HAND), greasy colour (GCOL), clean colour (Y-Z) and photostability ( $\Delta Y-Z$ ) were estimated from the Cooperative Research Centre for Sheep Industry Innovation's (Sheep CRC) Information Nucleus Flock (INF). Heritability estimates ranged from low (BCOV,  $\Delta Y-Z$ ) to moderate (HAND, GCOL) and high (BRWR, Y-Z) so each trait will respond to selection. There were no significant phenotypic correlations between BCOV or BRWR and any of the wool quality traits, however there were significant antagonistic genetic correlations between BCOV and HAND and BRWR and HAND. Based on these estimates, Merino sheep with bare breeches and/or fewer breech wrinkles will have harsher wool. Wool colour, either GCOL or Y-Z, is unlikely to be affected but the colour fastness ( $\Delta Y-Z$ ) of the wool will be improved.

### **INTRODUCTION**

The Sheep CRC's Next Generation Wool Quality Program is seeking to improve the handle, colour and photostability of Australian Merino wool fabrics through developing metrology, processing technologies and on-farm solutions including genetic selection and flock management strategies. The wool program is aiming to position wool as a key fibre for the rapidly developing lightweight, trans-seasonal, fine-gauge, next-to-skin market segment that is currently dominated by cotton and synthetic fibres. Wool destined for this market must be soft (handle), as white as possible (clean colour) and colour fast (photostability). Currently, Australian Merino producers are under growing pressure from animal welfare advocates to develop alternatives to surgical mulesing, a practice which has been used successfully to reduce the incidence of breech strike (James 2006; Richards and Atkins 2010). Genetics is a viable alternative, as selection for bare breeches (BCOV) and/or reduced breech wrinkle (BRWR) can reduce the incidence of breech strike (Scobie *et al.* 2002; Smith *et al.* 2009; Brown *et al.* 2010). However the impact of such selection on the handle (HAND), clean colour (Y-Z) and photostability ( $\Delta Y-Z$ ) of wool is unknown. It is important to determine whether selection for smooth bare breeches is compatible with soft, white, photostable wool. This paper reports genetic parameter estimates for BCOV, BRWR, HAND, GCOL, Y-Z and  $\Delta Y-Z$  from the Sheep CRC's INF yearling Merino population and the phenotypic and genetic relationships between them.

### **MATERIALS AND METHODS**

Data describing the performance of the 2007 and 2008 drop yearling Merino progeny of the Sheep CRC's INF (Fogarty *et al.* 2007; van der Werf *et al.* 2010) were used in this analysis. Animals were visually assessed for BCOV and BRWR (AWI & MLA 2007) at marking (~8 weeks of age). Prior to their initial shearing (~11 months), GCOL was assessed along with a suite of visual wool scores using the industry standard Visual Sheep Scores (AWI & MLA 2007). HAND was assessed using the Australian Merino Sire Evaluation Association (AMSEA) protocol (Casey *et al.* 2009). Briefly, the fleece was parted at the midside and the staple chosen for assessment (one without a dusty or weathered tip) was stroked with the finger or thumb from the base to the tip with a score allocated based on the relative textural softness of the fibres. Each of the assessed

scores were made using a 1-5 system, where low scores represent desirable attributes and high scores undesirable attributes. Midside samples were then taken from the right side of each animal. These were first measured at a commercial fleece measurement laboratory (AWTA Limited, Melbourne) for Y-Z amongst a suite of other traits (Hatcher *et al.* 2010) then transported to CSIRO Material Science and Engineering's Geelong laboratory and measured for  $\Delta Y-Z$  using the method of Millington and King (2010).

ASReml 3.0 (Gilmour *et al.* 2009) was used to estimate fixed effects, variance components and genetic parameters using a general linear mixed model and the residual maximum likelihood methods. An initial univariate analysis for each trait included the fixed effects of flock (8 levels: IN01, IN02, IN03, IN04, IN05, IN06, IN07 & IN08), sex (2 levels: ewe, wether), dam age (2 levels: maiden, adult), sire group (3 levels: ultra/superfine, fine/fine medium & medium/strong), drop (2 levels: 2007 & 2008) and birth rearing rank (4 levels: SS, single born raised as a single; MS, born as a multiple raised as a single; TT, born & raised as a twin and; MM, born and raised as a multiple) with appropriate 2-way interactions. A series of models were then fitted for each trait with various combinations of random effects (i.e. sire.flock and a maternal effect) and methods of accounting for genetic groups (i.e. fitted as either random or fixed). Genetic groups were assigned by extracting the relevant back pedigree for animals included in the dataset, pruning the pedigree to remove ancestors with only 1 progeny and then merging groups with insufficient data. The genetic grouping therefore accounts for strain differences within the INF and variation in the population of base ewes used at each of the INF site as they were not from the same foundation population. All models were compared using log likelihood ratio tests.

## RESULTS AND DISCUSSION

Based on changes in log-likelihood, fitting genetic groups as fixed effects was the most appropriate strategy for BCOV, BRWR, GCOL, and Y-Z. For  $\Delta Y-Z$  fitting genetic groups as random was the best approach, however the difference in log-likelihood between the two options was just 0.27. There was no evidence of sire.flock or maternal effects for BCOV, Y-Z or  $\Delta Y-Z$ , but both were significant sources of variation in BRWR and GCOL (Table 1). Brown *et al.* (2010) identified significant effects for both direct maternal and maternal permanent environments for BRWR but only permanent environment effects for BCOV. Due to the INF structure it is not possible to partition maternal effects into the genetic and permanent environment components. Variance parameters for HAND were estimated from a simple animal model. Despite each of the models that included genetic groups achieving convergence, the sire estimated breeding values for HAND were not distributed around 0 - they were all negative. For the 2008 and 2009 drops, HAND was an optional trait and assessed at only 3 of the 8 INF sites which may be a contributing factor. Further modelling of HAND will be undertaken when the next available drop of INF data is added to the analysis as it includes HAND assessments from all 8 sites.

Not surprisingly the assessed traits (BCOV, BRWR, GCOL and HAND) were more variable than the measured traits (Y-Z and  $\Delta Y-Z$ ) (Table 1). BCOV was lowly heritable (0.10) compared to previous reports (Scobie *et al.* 2007; Edwards *et al.* 2009; Greeff and Karlsson 2009; Brown *et al.* 2010), and the high heritability estimate for BRWR (0.31) was also lower than other estimates (Brown *et al.* 2010; Richards and Atkins 2010). The moderate heritability estimates for HAND (0.26) and GCOL (0.21) were lower than those reported by Mortimer *et al.* (2009), while the high estimate for Y-Z (0.40) was similar to previous reports for medium to broad bloodlines (Hebart and Brien 2009; James *et al.* 1990) but lower than those reported for superfine and fine bloodlines (Smith and Purvis 2009; Hatcher and Atkins 2000). The present heritability estimate for  $\Delta Y-Z$  (0.10) was lower than that reported from the initial analysis of the INF data (0.18) (Hatcher *et al.* 2010). The larger dataset and different statistical modelling procedures used in the current study would likely account for the difference.

**Table 1. Variance components, cv (%) and heritability for yearling BCOV and BRWR**

Trait		Variance components					CV (%)	Heritability $h^2$
		Phenotypic	Residual	Additive	Sire.flock	Maternal		
BCOV	1-5	0.5724	0.5127	0.0597	-	-	19.44	0.10 ± 0.03
BRWR	1-5	1.0064	0.5620	0.3104	0.0391	0.0949	32.31	0.31 ± 0.07
HAND	1-5	0.5117	0.3770	0.1339	-	-	24.94	0.26 ± 0.07
GCOL	1-5	0.3855	0.2420	0.0794	0.0184	0.0457	26.13	0.21 ± 0.06
Y-Z	T units	0.4747	0.2837	0.1910	-	-	8.44	0.40 ± 0.06
$\Delta Y-Z$	T units	0.2212	0.1982	0.0230	-	-	10.68	0.10 ± 0.04

The only significant phenotypic correlation ( $r_p$ ) between the 6 traits was between Y-Z and  $\Delta Y-Z$  (-0.37) (Table 2), which indicates that within flock selection for whiteness conflicts with colour fastness as whiter wool will tend to be less photostable. The next strongest  $r_p$  were between HAND and GCOL (0.17) and Y-Z and GCOL (0.16). Both these associations were favourable such that improvements in one trait will lead to correlated improvements in the other. BCOV and BRWR were not phenotypically correlated with each other in this study ( $r_p = 0.03$ ) which is in agreement with Smith *et al.* (2009).

**Table 2. Phenotypic (above diagonal) and genetic (below diagonal) correlations between BCOV, BRWR, HAND, GCOL, Y-Z and  $\Delta Y-Z$ .**

	BCOV	BRWR	HAND	GCOL	Y-Z	$\Delta Y-Z$
BCOV		0.03 ± 0.02	0.01 ± 0.03	-0.02 ± 0.02	-0.04 ± 0.02	0.00 ± 0.02
BRWR	0.34 ± 0.16		-0.13 ± 0.03	0.01 ± 0.02	-0.04 ± 0.02	0.09 ± 0.02
HAND	-0.43 ± 0.22	-0.32 ± 0.15		0.17 ± 0.03	0.01 ± 0.03	-0.10 ± 0.03
GCOL	-0.26 ± 0.18	0.04 ± 0.12	0.33 ± 0.17		0.16 ± 0.02	-0.15 ± 0.02
Y-Z	-0.17 ± 0.16	-0.04 ± 0.11	-0.03 ± 0.16	0.52 ± 0.10		-0.37 ± 0.02
$\Delta Y-Z$	0.31 ± 0.24	0.49 ± 0.15	-0.01 ± 0.25	-0.59 ± 0.16	-0.76 ± 0.11	

The genetic correlation ( $r_g$ ) between BCOV and BRWR was positive and low (0.34). Greeff and Karlsson (2009) also reported a positive  $r_g$  between these two traits; however their estimate was 45% smaller (i.e. 0.19). Therefore genetic improvement in either trait will generate a favourable correlated improvement in the other, such that selection for increased natural bare area around the perineum and breech area of Merino sheep will lead to fewer wrinkles at the tail set and down the hind legs.

BCOV had a medium negative  $r_g$  with HAND (-0.43) and a low negative  $r_g$  with GCOL (-0.26). Both these correlations were unfavourable, as increased bare breech area was associated with a harsher textural softness and yellower greasy colour. The deterioration in HAND associated with selection for BCOV may be due to an associated decline in assessed wool quality, primarily through increased weathering and reduced fleece density (Hatcher *unpubl. data*). Deterioration in these two traits has been linked to increased dust penetration (Mortimer and Atkins 1993) which results in harsher HAND (Hatcher *et al.* 2003). The  $r_g$  between BCOV and Y-Z was also unfavourable but negligible (-0.17), however that with  $\Delta Y-Z$  (0.31) was favourable. Therefore while increased bare breech area is associated with yellower clean colour, these wools will tend to maintain that level of colour when exposed to UV light and not further yellow.

Fewer breech wrinkles was genetically correlated with harsher HAND (-0.32), and improved  $\Delta Y-Z$  (0.49) (i.e. better colour fastness). The  $r_g$  between BRWR and both GCOL (0.04) and Y-Z (-0.04) were effectively 0, so selection for fewer breech wrinkles can occur without any impact on

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either greasy or clean colour.

The  $r_g$  between HAND and GCOL (0.33), HAND and Y-Z (-0.03) and GCOL and Y-Z (0.52) were similar to those estimated from the analysis of the 2007 INF drop (Hatcher *et al.* 2010). However the various  $r_g$  with  $\Delta Y-Z$  varied in both magnitude and direction from the earlier analysis. The  $r_g$  with HAND was negligible (-0.01), with GCOL medium and negative (-0.59) and with Y-Z high and negative (-0.76). HAND and  $\Delta Y-Z$  are therefore genetically different traits, as selection for softer wool will have little to no impact on photostability. However, genetic selection for whiter wool is antagonistic with photostability as whiter wools will tend to yellow more when exposed to UV light.

In conclusion, there is sufficient genetic variation in BCOV, BRWR, HAND, GCOL, Y-Z and  $\Delta Y-Z$  for each of the traits to respond to selection. The phenotypic correlations between the 2 breech traits and the 4 wool quality traits were not significant, signifying that within flock selection for either increased bare breech area or reduced breech wrinkle could occur without any detrimental impact on softness, clean colour or colour fastness. However genetic improvement in both BCOV and BRWR is antagonistic to softness such that animals with bare breeches and fewer breech wrinkles will have harsher wool. If the genetic relationship between breech traits and HAND is mediated by staple weathering, fleece density and dust penetration, it may be possible to identify on-farm management interventions such as coating or time of shearing that will favourably modify the genetic expression of the trait.

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