

## **FIBRE DIAMETER CORRECTED WOOL CLEAN COLOUR - THE IMPACT ON GENETIC PARAMETERS**

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### **SUMMARY**

The brightness (Y) and yellowness (Y-Z) of wool is highly correlated with mean fibre diameter (MFD). The Cooperative Research Centre for Sheep Industry Innovation (Sheep CRC) and the Australian Wool testing Authority Limited (AWTA Limited) have recently developed an algorithm to correct Y and Y-Z for MFD which significantly reduces the fibre diameter covariance with colour. This paper demonstrates that correcting Y, Z and Y-Z for fibre diameter had little to no impact on the phenotypic or genetic relationships between the various wool colour traits. Therefore removing the diameter covariance in Y, Z or Y-Z using fibre diameter correction algorithm will not dramatically change the phenotypic and genotypic correlations between colour and other key wool production and quality traits. This analysis indicates it is not necessary to correct wool colour for fibre diameter when colour is included in Merino breeding programs.

### **INTRODUCTION**

A key objective of the Sheep CRC's Wool Program is to provide Australian sheep breeders with the genetic information required to improve the clean wool whiteness and brightness of the Australian wool clip. The yellowness (i.e. Y-Z) of clean wool is highly correlated with the mean fibre diameter (MFD) of wool fibres (Fleet *et al.* 2009; Hebart and Brien 2009; Smith and Purvis 2009). This has the potential to confound genetic parameter estimates for colour traits; significantly impairing the ability of the Australian wool industry to improve wool colour using genetic selection (Wang *et al.* 2011). The Sheep CRC and AWTA Limited developed a mathematical diameter-scatter correction algorithm for clean colour measurement using selected midside samples from the Information Nucleus Flock (INF). The algorithm was subsequently validated on all INF samples measured during 2008-2009 which proved it was possible to remove the fibre diameter artefact from the phenotypic relationship between clean colour and fibre diameter (Wang *et al.* 2011). The objective of this paper was to investigate the impact of the diameter-scatter correction on the genetic parameter estimates for brightness (Y) and Y-Z and their phenotypic and genetic correlations with wool production and other wool quality traits. The likely consequences for Merino breeding objectives aimed at producing whiter wool are discussed.

### **MATERIALS AND METHODS**

Data from the Sheep CRC's INF (van der Werf *et al.* 2010) Merino progeny run at each of the 8 IN sites measured as yearlings (approx. 11 months, n = 4,019) and adults (approx. 23 months, n = 2,012) were used for this analysis. The sheep were born between 2007 and 2009 and a comprehensive suite of wool production and quality traits (Hatcher *et al.* 2010) were assessed or measured at each shearing (2008-2010 for yearlings and 2009-2010 for adults). Midside samples (75-85 g) taken from the right side of each animal prior to shearing and measured at AWTA Limited using standard IWTO test methods as described in Hatcher *et al.* (2010). Briefly 10 staples from each midside sample were sub sampled for measurement of staple length (SL) and staple strength (SS). The remainder of each sample was weighed, washed, oven dried (105°C),

carded and conditioned for 24 hours prior to weighing to determine the washing yield (using 16% regain). A mini-corer was then used to sample 2mm fibre snippets which were measured for mean fibre diameter (FD), FD standard deviation (FDSD), FD coefficient of variation (FDCV) and mean fibre curvature (CURVE) using Sirolan™ Laserscan. The carded sample was further sub-sampled and measured for clean colour (Y-Z, yellowness) and the X, Y and Z tristimulus values (X, red; Y, green brightness and; Z, blue). Clean colour (Y-Z) and the Y and Z tristimulus values were then adjusted for fibre diameter using the correction algorithm described by Wang *et al.* (2011); yielding the additional traits CYY, CYZ and CYY-Z and CAY, CAZ and CAY-Z for the yearling (Y) and adult (A) stages respectively where 'C' denotes corrected for fibre diameter. The greasy fleece weight (GFW) of each unskirted fleece (belly wool included) was recorded at shearing with clean fleece weight (CFW) calculated as the product of GFW and the washing yield. GFW and CFW were corrected to 365-day growth equivalents (Hatcher *et al.* 2010).

ASReml 3.0 (Gilmour *et al.* 2009) was used to estimate fixed effects, variance components and genetic parameters using general linear mixed models and the residual maximum likelihood method as described by Hatcher *et al.* (2010). Phenotypic and genetic covariances were estimated from a series of bivariate analyses using fixed effects and their interactions, as appropriate from the univariate analyses. Genetic and phenotypic correlations, and their standard errors, were estimated from the appropriate variances and covariances using ASReml.

## RESULTS AND DISCUSSION

There was no significant difference in heritability between any of the yearling and adult corrected and uncorrected colour traits (Table 1). Similarly the phenotypic variance, coefficient of variation, residual, additive variance and sire.flock variance were similar for the corrected and uncorrected yearling and adult colour traits. A maternal variance term was fitted in all models but was not significant for either the corrected or uncorrected colour traits.

**Table 1: Mean, variance components, coefficient of variation and heritability for yearling and adult uncorrected and fibre diameter corrected colour traits**

Trait	Mean ( <i>tristimulus</i> values)	Phenotypic variance	Coefficient of variation (%)	Residual variance	Additive variance	Sire.flock variance	Heritability
<b>Yearling</b>							
YY	67.63	2.70	2.22	2.07	0.59	0.05	0.22 ± 0.04
YZ	62.68	4.19	3.11	2.31	1.72	0.16	0.41 ± 0.05
YY-Z	4.95	0.74	10.48	0.22	0.47	0.05	0.63 ± 0.05
CYY	73.90	2.71	2.22	2.08	0.59	0.04	0.22 ± 0.04
CYZ	65.62	4.13	3.08	2.34	1.66	0.13	0.40 ± 0.05
CYY-Z	8.28	0.69	10.18	0.24	0.41	0.05	0.59 ± 0.05
<b>Adult</b>							
AY	74.14	2.46	2.11	1.62	0.74	0.10	0.30 ± 0.07
AZ	65.81	3.39	2.79	2.11	1.13	0.15	0.33 ± 0.07
AY-Z	8.32	0.40	7.64	0.25	0.14	0.01	0.35 ± 0.07
CAY	74.15	2.46	2.11	1.62	0.74	0.10	0.30 ± 0.07
CAZ	66.01	3.37	2.78	2.12	1.10	0.15	0.33 ± 0.07
CAY-Z	8.14	0.35	7.31	0.25	0.09	0.01	0.27 ± 0.07

The means for the yearling corrected colour traits were higher than the uncorrected traits (+6.3, +2.9 and +3.3 for YY, YZ and YY-Z respectively), but smaller differences were evident for the adult colour traits (+0.01, +0.20 and -0.18 for AY, AZ and AY-Z respectively). These differences

could be due to a 1.2 $\mu$ m difference between the yearling and adult FD (YFD = 16.9  $\mu$ m AFD = 18.1 $\mu$ m) in this study as higher diameter wool tends to be more yellow (Wang *et al.* 2011). The heritability estimate for YY-Z was significantly higher than previous reports (Fleet *et al.* 2009; Hebart and Brien 2009; Smith and Purvis 2009) which may be due to the differing average FD and low FD spread of the flocks in those studies compared to the 14  $\mu$ m FD range in the INF. The heritability of AY-Z in the INF agrees with the adult estimate of Smith and Purvis (2009).

Correcting Y, Z and Y-Z for fibre diameter had little to no impact on the phenotypic ( $r_p$ ) or genetic ( $r_g$ ) relationships between the various colour traits (Table 2). Each of the correlations, both  $r_p$  and  $r_g$ , between the uncorrected and corrected colour traits were all high (i.e. >0.6), except for the  $r_p$  between CY and Y-Z and between CY-Z and Y which were low (both -0.26). These low  $r_p$  are the result of the relatively lower heritability of Y compared to Z (Table 1), which indicates that reflectance of green light from wool fibres (i.e. Y) is more affected by the environment than the animals genes compared to the reflectance of blue (i.e. Z) leading to the lower  $r_p$ . The same trends occurred between the corrected and uncorrected adult measurements of these colour traits. The generally high  $r_p$  and  $r_g$  between the corrected and uncorrected colour traits indicates that removing the diameter co-variance does not change the phenotypic or genetic relationships between the colour traits whether measured either as yearlings or adults.

**Table 2- Phenotypic ( $r_p$ ) and genetic ( $r_g$ ) correlations between uncorrected and fibre diameter corrected colour traits**

FD corrected colour traits	Uncorrected colour traits					
	YY		YZ		YY-Z	
	$r_p$	$r_g$	$r_p$	$r_g$	$r_p$	$r_g$
CYY	0.99 $\pm$ 0.00	0.99 $\pm$ 0.00	0.92 $\pm$ 0.00	0.92 $\pm$ 0.02	-0.26 $\pm$ 0.02	-0.65 $\pm$ 0.07
CYZ	0.91 $\pm$ 0.00	0.91 $\pm$ 0.02	0.99 $\pm$ 0.00	0.99 $\pm$ 0.00	-0.63 $\pm$ 0.01	-0.89 $\pm$ 0.02
CYY-Z	-0.26 $\pm$ 0.02	-0.64 $\pm$ 0.07	-0.62 $\pm$ 0.01	-0.86 $\pm$ 0.03	0.98 $\pm$ 0.00	0.98 $\pm$ 0.00

Correcting Y, Z or Y-Z for fibre diameter had very little impact on the  $r_p$  or  $r_g$  between the various colour and key wool production and quality traits (Table 3). The  $r_p$  between the uncorrected colour traits and key wool production and quality traits were all negligible in magnitude (i.e. <0.2) except for between YFD and corrected Y-Z (0.28) was lowly correlated. The  $r_p$  between the corrected colour traits and key wool production and quality traits were all negligible. Similarly the majority of the  $r_g$  were also negligible except for those between Y and CY with YSS (0.34 and 0.33 respectively), Z and YFD (0.29), Y-Z and CY-Z with YCFW (0.41 and 0.37), Y-Z and YFD (0.39) and Y-Z and YSL (0.22). The  $r_p$  and  $r_g$  between YFD and YY-Z are similar to those of Smith and Purvis (2009) but lower than those of Hebart and Brien (2009).

There was no major difference in either the  $r_p$  or  $r_g$  between YY and CYY and any of the key wool production and quality traits (Table 3). Similarly there was no difference between the correlations with YZ or CYZ, except for the  $r_p$  and  $r_g$  with YFD, which were both lower with CYZ (-0.17 vs -0.08 and -0.29 vs -0.18 respectively). The same trend was evident for the  $r_p$  and  $r_g$  between YY-Z and YFD (0.28 vs -0.08 and 0.39 vs -0.18 respectively). The same trends were evident for the adult measurements of these traits. A possible reason for the change observed in the  $r_p$  and  $r_g$  with YFD could be due to using fibre diameter as the basis for correcting the colour traits. The FD covariances are therefore likely to be most impacted by the correction thus producing the greatest difference observed in the estimated correlations. Small differences in the  $r_p$  and  $r_g$  with YSL and YSS were also identified; however given the relative size of the standard error for each estimate these differences are unlikely to be important. The observed differences in the YSL and YSS covariance with colour when correcting for FD maybe related to the antagonistic phenotypic

and genetic relationships between FD, SL and SS (i.e. finer fleeces are associated with shorter weaker staples) (Safari *et al.* 2005).

**Table 3. Phenotypic and genetic correlations between uncorrected and FD corrected colour traits and key wool production and quality traits measured as yearlings**

	YY		YZ		YY – Z	
	Uncorrected	Corrected	Uncorrected	Corrected	Uncorrected	Corrected
<i>Phenotypic correlations</i>						
YCFW	0.10 ± 0.02	0.10 ± 0.02	0.01 ± 0.02	0.03 ± 0.02	0.16 ± 0.02	0.12 ± 0.02
YFD	-0.06 ± 0.02	-0.05 ± 0.02	-0.17 ± 0.02	-0.08 ± 0.02	0.28 ± 0.02	0.08 ± 0.02
YFDCV	-0.07 ± 0.02	-0.07 ± 0.02	-0.05 ± 0.02	-0.06 ± 0.02	-0.02 ± 0.02	0.01 ± 0.02
YSL	-0.01 ± 0.02	0.00 ± 0.02	-0.04 ± 0.02	-0.01 ± 0.02	0.08 ± 0.02	0.02 ± 0.02
YSS	0.12 ± 0.02	0.13 ± 0.02	0.08 ± 0.02	0.11 ± 0.02	0.05 ± 0.02	0.00 ± 0.02
<i>Genetic correlations</i>						
YCFW	0.09 ± 0.11	0.09 ± 0.11	-0.18 ± 0.09	-0.13 ± 0.09	0.41 ± 0.07	0.37 ± 0.07
YFD	-0.12 ± 0.09	-0.10 ± 0.09	-0.29 ± 0.07	-0.18 ± 0.07	0.39 ± 0.06	0.18 ± 0.06
YFDCV	-0.17 ± 0.10	-0.18 ± 0.10	-0.11 ± 0.08	-0.12 ± 0.09	-0.03 ± 0.07	0.00 ± 0.08
YSL	-0.15 ± 0.10	-0.15 ± 0.10	-0.19 ± 0.08	-0.16 ± 0.08	0.22 ± 0.07	0.16 ± 0.07
YSS	0.34 ± 0.10	0.33 ± 0.11	0.16 ± 0.09	0.20 ± 0.09	0.11 ± 0.08	0.04 ± 0.09

These differences between the corrected and uncorrected colour traits in either the phenotypic or genetic correlations are likely be of low practical relevance to Merino breeding programs as all the correlations are classified as low to negligible. Therefore removing the diameter covariance in Y, Z or Y-Z by using the correction algorithm will not dramatically change the phenotypic and genotypic correlations between colour and other key wool production and quality traits. This analysis indicates that it is not necessary to correct wool colour for FD when colour is included in Merino breeding programs.

Light reflectance in lower wavelength zone of the spectrum (i.e. < 470nm or the ‘blue’ light range represented by the Z tristimulus value) is more affected by light scattering behaviour due to the morphological structure of the scales on the surface of the fibre (Wang *et al.* 2011). This may explain the differences observed in the variance components as well as the heritability, phenotypic and genetic correlation estimates between the colour traits and warrants further investigation.

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#### REFERENCES

- Fleet M.R., Millington K.R., Smith D.H. and Grimson R.J. (2009) *Assoc. Advmt. Anim. Breed. Genet.* **18**: 556
- Gilmour A.R., Gogel B.J., Cullis B.R. and Thompson R. (2009) ‘ASReml User Guide Release 3.0’. (VSN International Ltd: Hemel Hempstead, HP1 1ES, UK)
- Hatcher S., Hynd P.I., Thornberry K.J. and Gabb S. (2010) *Anim. Prod. Sci.* **50**: 1089
- Hebart M.L. and Brien F.D. (2009) *Assoc. Advmt. Anim. Breed. Genet.* **18**: 500
- Safari E., Fogarty N.M. and Gilmour A.R. (2005) *Livest. Prod. Sci.* **92**: 271.
- Smith J.L. and Purvis I.W. (2000) *Assoc. Advmt. Anim. Breed. Genet.* **18**: 390
- van der Werf J.H.J., Kinghorn B.P., and Banks R.G. (2010) *Anim. Prod. Sci.* **50**: 998.
- Wang H., Mahar T., Liu X., Swan P. and Wang X. (2011) *J. Text. Inst.* **102**: 1031.