

**GENETIC ESTIMATES FOR ALONG AND ACROSS FIBRE DIAMETER VARIATION
AND ITS USE TO IMPROVE STAPLE STRENGTH IN MERINO SHEEP**

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SUMMARY

Genetic parameters for a range of along and across fibre diameter traits measured from the Optical Fibre Diameter Analyser 2000 (OFDA2000) were estimated and correlated to staple strength and percentage of midbreaks. Fibre diameter, overall fibre diameter standard deviation, overall fibre diameter coefficient of variation, across fibre coefficient of variation, minimum fibre diameter along the fibre and maximum fibre diameter along the fibre were all highly heritable ($h^2 > 0.30$); however along fibre coefficient of variation was lowly heritable ($h^2 = 0.07$). Fibre diameter had a strong positive genetic correlation with maximum fibre diameter along the fibre and minimum fibre diameter along the fibre (≥ 0.86). Along fibre coefficient of variation had a low genetic correlation with across fibre coefficient of variation (0.22), which suggests that selecting for along fibre diameter distribution components will result in small changes in across fibre diameter distribution overtime. Staple strength had moderate negative genetic correlations with overall fibre diameter coefficient of variation (-0.59) and across fibre coefficient of variation (-0.51), while all other genetic correlations were low to negligible (< 0.4). However genetic correlations between the percentage of midbreaks and across fibre coefficient of variation (0.45) and along fibre coefficient of variation (-0.40) had opposing direction of effect.

Therefore overall fibre diameter coefficient of variation had a greater heritability albeit lower observed variation and stronger correlation with staple strength than either the along or across fibre components. This would result in greater genetic gain when used in a breeding program to improve staple strength. However across fibre coefficient of variation proved to be useful in indirectly reducing the percentage of midbreaks and maybe valuable as a secondary trait to improve staple strength properties.

INTRODUCTION

OFDA2000 measures fibre diameter and splits the profile into along and across fibre diameter attributes. OFDA2000 has been utilised to monitor fibre diameter changes in response to environment (Gloag *et al.* 2004), aid clip preparation (Brien *et al.* 2001; Ferguson *et al.* 2002; Hansford *et al.* 2002) and to indirectly select for staple strength (Greeff 2002; Yamin *et al.* 1999). The importance of fibre diameter distribution to wool processing is considered significant as it affects the average fibre length in top (Lamb 2000), yarn evenness (Lamb 1992), fabric bending/rigidity (Degroot 1992) and yarn tenacity (Lamb 1992). Overall fibre diameter coefficient of variation has been used as a indirect selection criteria for staple strength and correlates to processing performance (Rottenbury *et al.* 1983). The position of break in tender wool is important as fibre breakage in the middle of the staple has greater implications on wool processing. Therefore, overall fibre diameter coefficient of variation is included in breeding objectives (Piper and Lax 1992) and is used in current MERINOSELECT™ breeding indexes. However there are few genetic estimates for the along and across fibre components of fibre diameter coefficient of variation measured by the OFDA2000. Providing an accurate estimation of the genetic parameters will allow the likely response to selection on staple strength and the percentage of midbreaks to be predicted. Other studies have reported high heritability estimates for along and across fibre components but with relatively high standard errors (Greeff 2002; Yamin *et al.* 1999). This paper

reports genetic parameters for along and across fibre traits and provides comment on the use of these traits to influence staple strength properties.

MATERIALS AND METHODS

Data was obtained from the Sheep CRC Information Nucleus Flock (INF) (Fogarty *et al.* 2007; van der Werf *et al.* 2010). The INF is comprised of eight diverse flocks located around Australia in geographically different locations. All sites were linked by common sires via the use of an extensive artificial insemination program. This paper presents results from 4,958 Merino progeny that were born between 2007-2010, drawn from 143 sires from a range of Merino wool types. Midside samples were collected at yearling age (10-13 months) and measured at a commercial fleece measurement laboratory (AWTA Limited Melbourne). OFDA2000 traits were measured by choosing one staple at random from the midside sample and cleaving it into a number of smaller micro staples. The micro staples were then placed on the OFDA2000 fibreglass xy slide; measured for fibre diameter and divided into its along and across fibre components. The traits measured included minimum fibre diameter along the fibre (AMIN), maximum diameter along the fibre (AMAX), fibre diameter (FD), overall fibre diameter standard deviation (FSDS), overall fibre diameter coefficient of variation (FDCV), across fibre diameter coefficient of variation (ACCV) and along fibre diameter coefficient of variation (ALCV). For staple strength (SS) and percentage of mid breaks (MID), ten staples were chosen from the midside sample and measured using the automatic tester for length and strength (ATLAS) in accordance to IWTO 30 (2009).

ASReml 3.0 (Gilmour *et al.* 2009) was used to estimate the genetic parameters using general linear mixed and residual maximum likelihood methods. Initially, a univariate analysis of all traits included the following fixed effects: flock (8 sites), year of birth (2007, 2008, 2009, 2010), sex (male, female), dam age (2, 3, 4, 5, 6), birth type rearing type (born single raised single, born twin raised single, born and raised as a multiple) and siregroup (ultra/superfine, fine/fine-medium & medium/strong), with significant two way interactions. A sequence of models was fitted to each trait including varying combinations of random effects (i.e. effect of animal, sire.flock and overall maternal effect) and an effect to account for genetic groups (fitted as random or fixed). Genetic groups were allocated according to the back pedigree obtained from the data set. Ancestors with only 1 progeny were removed and groups with insufficient data merged. The genetic grouping accounted for the differing ewe foundation flocks at each of the sites and strain differences within the INF. The most appropriate model for each trait was determined by log likelihood ratio tests. Phenotypic and genetic correlations for each combination of traits with standard errors were estimated from bivariate analyses.

RESULTS AND DISCUSSION

Based on the log likelihood ratio test; fitting genetic groups as fixed was the most appropriate method for FD, FSDS, AMAX, AMIN, ALCV, ACCV and MID. FDCV and SS were best modelled with genetic groups as random. There was a significant sire.flock interaction (Table 1) for all traits. ALCV and SS were influenced by a maternal effect. Heritability estimates for FD, FSDS, FDCV, AMAX, AMIN, ACCV and SS were all high (>0.30), while ALCV and MID were lowly heritable (≤ 0.13). FD, FDCV and AMIN heritability estimates were consistent with previous reports; while AMAX was considerably higher (Greeff 2002; Yamin *et al.* 1999). ACCV and ALCV were lower (Greeff 2002; Yamin *et al.* 1999). The data recorded (amount and structure) and genetic diversity of the INF compared to the flocks studied by Greeff (2002) and Yamin *et al.* (1999) may have contributed to the differences in the estimates. Greeff (2002) recorded progeny bred from sires of Collinsville, Peppin, and Bungaree Merino families (12 studs, 100 sires); while Yamin *et al.* (1999) recorded progeny bred from Collinsville and Bungaree Merino families (4 studs, 47 sires). The phenotypic variation of fibre diameter distribution traits estimated in our

study was similar to that of Yamin *et al.* (1999); though lower than estimated by Greeff (2002).

Table 1. Variance components, coefficient of variation (CV %) and heritability (h^2) for yearling OFDA2000 and staple strength properties

Trait	Mean	Variance components					CV (%)	Heritability h^2
		Phenotypic	Residual	Additive	Sire.flock	Maternal		
FD	17.15	1.54	0.39	1.12	0.03	-	8.98	0.73±0.05
FSD	3.16	0.14	0.06	0.07	0.00	-	4.43	0.52±0.05
FDCV	18.46	3.09	1.46	1.53	0.10	-	16.73	0.49±0.05
AMAX	18.78	2.11	0.62	1.43	0.06	-	11.24	0.68±0.05
AMIN	15.80	1.38	0.51	0.85	0.02	-	8.73	0.62±0.05
ACCV	20.42	5.85	3.80	1.85	0.20	-	28.65	0.32±0.04
ALCV	5.69	2.58	2.14	0.19	0.11	0.13	45.34	0.07±0.03
SS	31.84	85.93	50.72	28.72	2.43	4.32	269.59	0.33±0.06
MID	62.59	771.24	641.54	103.64	26.06	-	1232.21	0.13±0.03

There were strong positive genetic correlations between FD and FSD, AMIN and AMAX (≥ 0.64) (Table 2) which suggests that as fibre diameter becomes finer, the maximum and minimum diameter along the fibre will also become finer and result in less fibre diameter variation. This is in agreement with Greeff (2002) and Yamin *et al.* (1999). ACCV and ALCV both had moderate to strong positive genetic correlations with FSD and FDCV (≥ 0.42). ALCV and ACCV had low positive genetic correlation between each other and indicates that they are controlled by different genes. The unfavourable negative genetic correlation between ACCV with both AMIN (-0.37) and AMAX (-0.25) indicates that as fibre diameter distribution across the fibre is less variable; the maximum and minimum diameter along the fibre will be broader.

Table 2. Phenotypic correlations (below diagonal) and genetic correlations (above diagonal)

	FD	FSD	FDCV	AMAX	AMIN	ACCV	ALCV
FD		0.64±0.04	-0.09±0.06	0.99±0.00	0.86±0.02	-0.33±0.07	0.30±0.09
FSD	0.58±0.01		0.70±0.03	0.70±0.03	0.56±0.05	0.42±0.06	0.57±0.08
FDCV	-0.05±0.02	0.77±0.01		0.00±0.06	-0.18±0.07	0.42±0.06	0.40±0.09
AMAX	0.93±0.00	0.65±0.01	0.09±0.02		0.95±0.01	-0.25±0.07	0.41±0.09
AMIN	0.88±0.00	0.43±0.01	-0.17±0.02	0.78±0.01		-0.37±0.07	0.15±0.10
ACCV	-0.21±0.02	0.41±0.01	0.67±0.01	-0.09±0.02	-0.18±0.02		0.22±0.12
ALCV	0.03±0.02	0.35±0.01	0.41±0.01	0.32±0.01	-0.30±0.01	0.13±0.02	

Phenotypic correlations for SS and MID with along and across fibre components were shown to have a similar direction of effect as genetic correlations but in smaller magnitude (Table 3). Negative genetic correlations were estimated between both SS and FDCV (-0.59) and SS and ACCV (-0.51). All other correlations were low to negligible (< 0.40). MID had a moderate positive genetic correlation with ACCV (0.45) and an antagonistic moderate negative correlation with ALCV (-0.40). Therefore selecting for low ACCV or low FDCV would result in improvements in both SS and the percentage of midbreaks, while selection for low ALCV would result in a decrease in SS and a higher percentage of midbreaks.

Table 3. Phenotypic (r_p) and genetic (r_g) correlations between staple strength (SS), percentage of midbreaks (MID) and along and across fibre diameter distribution traits

Trait	SS		MID	
	$r_p \pm SE$	$r_g \pm SE$	$r_p \pm SE$	$r_g \pm SE$
FD	0.16±0.02	0.19±0.07	-0.14±0.02	-0.23±0.10
FSDSD	-0.25±0.02	-0.32±0.07	-0.04±0.02	0.04±0.11
FDCV	-0.43±0.01	-0.59±0.06	0.06±0.02	0.33±0.11
AMAX	0.08±0.02	0.14±0.07	-0.17±0.02	-0.25±0.10
AMIN	0.23±0.02	0.26±0.07	-0.07±0.02	-0.16±0.10
ACCV	-0.29±0.02	-0.51±0.07	0.11±0.02	0.45±0.11
ALCV	-0.20±0.02	-0.21±0.12	-0.16±0.02	-0.40±0.13

The high heritability of FDCV (0.49) and moderate favourable correlations with SS confirms Greeff's (2002) conclusion that it is unnecessary to further divide this trait into its along and across fibre components when using FDCV as an alternative selection criteria for staple strength. However selection using ACCV reduces the percentage of midbreaks and therefore it would be beneficial to include ACCV in a breeding program perhaps as a secondary trait. Further work is required to evaluate the usefulness of the current staple strength measurement in a breeding program. Measurement of SS via the ATLAS was designed to provide a prediction of fibre breakage during processing and was not intended for use to compare the of rank animals to achieve on-farm genetic improvement (Semmel 2003). Other measurements that describe the shape of strength vs extension curve such as "staple specific work to rupture" produced by the ATLAS may provide a more efficient method for selection for SS.

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