IS FIBRE COMFORT FACTOR REQUIRED IN MERINO BREEDING PROGRAMS?

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SUMMARY

Genetic parameters for fibre comfort factor (FCF) and correlations with key production traits were estimated from research (Cooperative Research Centre for Sheep Industry Innovation Information Nucleus) and industry data (Sheep Genetics MERINOSELECT). FCF is moderately to highly heritable and genetically consistent through life, with the yearling, hogget and adult expressions phenotypically (0.54 to 0.73) and genetically (0.97 to 0.98) correlated. The strong genetic correlations (r_g) between FCF and both fibre diameter (FD) and FD standard deviation (FDSD) (range -0.58 and -0.92) indicate that selection to reduce FD or FDSD will generate favourable correlated increases in FCF. There would be little to be gained from including FCF in Merino breeding programs with an existing emphasis on reducing FD and it would be difficult for medium to strong wool breeders to add FCF to their breeding programs and maintain FD.

INTRODUCTION

Coarser fibres in a fibre diameter distribution are responsible for the fabric-evoked prickle sensation felt by wearers of next-to-skin garments. Coarser fibre ends buckle less readily when fabric pushes against the skin during wear and mechanically stimulate particular nerve cells lying close to the skin surface (Naylor 1992). The threshold value of buckling force required to trigger the nerve cell response corresponds to a FD of approximately 30 µm (Naylor 1992) and this finding led to the use of FCF, the percentage of fibres in the FD distribution < 30 µm, as a means of categorising apparel fibres in terms of their propensity to cause prickle when worn next-to-skin. The prickle sensation is not exclusive to wool and depends on a large number of other parameters including fabric construction and physiological state of the wearer (Naylor 1992). Despite this, consumers in key markets for Australian wool consistently associate prickle with wool and many Merino breeders are seeking to genetically increase FCF to a level, >95%, beyond which prickle cannot be perceived by most people under normal conditions (Garnsworthy *et al.* 1988). While fine wool sheep will typically have high FCF levels due to their low average FD (Baxter and Cottle 1998), some breeders of medium and strong wool sheep have expressed interest in breeding sheep with a higher FCF without changing average FD. This paper reports the genetic parameters for FCF and the phenotypic and genetic correlations with liveweight, wool production and a suite of measured and visual wool quality traits in Merino sheep using a combination of industry and research data.

MATERIALS AND METHODS

Research data. Data from Merino progeny (n = 4,958) born into the Sheep CRC Information Nucleus (IN) Flock (van der Werf *et al.* 2010) between 2007 and 2010 were used. Yearling (Y, 10 – 13 months) and adult (A, 22 – 25 months) performance for a suite of wool production and quality traits were assessed or measured prior to the yearling and adult shearings. Fleece rot (FLROT), colour (COL), character (CHAR), dust penetration (DUST), staple weathering

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(WEATH) and staple structure (SSTRC) were scored using the Visual Sheep Scores guide (AWI Ltd and MLA Ltd 2013), with handle (HAND) scored according to Casey and Cousins (2010) and coverage (COV), fleece density (DENS) and nourishment (NOUR) assessed according to AMSEA guidelines (Casey *et al.* 2009). Right midside samples (approx. 80g) from each animal were measured at AWTA Limited (Melbourne) using standard IWTO test methods for yield (YIELD), staple length (SL), staple strength (SS), FD, FDSD, FD coefficient of variation (FDCV), FCF, mean fibre curvature (CURVE), brightness (Y), clean colour (Y–Z) and resistance to compression (RTOC). The unskirted greasy fleece weight (GFW) (belly wool included) was recorded at shearing with clean fleece weight (CFW) calculated as the product of GFW and YIELD. Both GFW and CFW were corrected to 365-day growth equivalents. Following shearing, the liveweight (LWT) of every sheep was recorded after being held off feed for approximately 2 hours.

Industry data. Pedigree and performance data were extracted from the Sheep Genetics (SG) MERINOSELECT database (Brown *et al.* 2007). A subset of flocks was selected based on their recording of FCF and were a mix of industry ram breeding, research and sire evaluation flocks. Only those animals with both sire and dam pedigree, and born from 2005 onwards were included. The traits analysed were LWT, GFW, CFW, FD, FDCV, FCF, CURVE, SL, SS and COL recorded at yearling and hogget (H, 13 – 18 months) ages. The pedigree was built using all ancestral information available.

ASReml 3.0 (Gilmour *et al.* 2009) was used to estimate variance components and genetic parameters. For both data sets, birth type, rearing type, and age of dam were fitted as fixed effects. Age of shearing was fitted as a covariate to the yearling IN data but fitted as fixed to the SG data. Flock and drop were also fitted as fixed to the IN data with genetic group, sire by flock and a maternal genetic effect fitted as random effects. For the SG data, a fixed effect of contemporary group (defined as flock, year of birth, sex, date of measurement, management group subclass), was also fitted for all traits along with random terms for the direct genetic effects and sire by flock year interaction. Maternal permanent environment effects were included for the SG LWT, GFW and CFW data with genetic groups, allocated on a flock basis for link flocks with sufficient data, fitted for all traits. Phenotypic and genetic correlations, with standard errors, were estimated from the appropriate covariances using a series of bivariate analyses.

RESULTS AND DISCUSSION

The mean FCF were similar for both data sources, as were the phenotypic variances which tended to increase with age (Table 1). Within the IN data, there was no evidence of sire by flock or maternal genetic effects for YFCF but these were both significant for AFCF representing 2.2 and 20.1% of the phenotypic variance respectively. For the SG data both the sire by flock and maternal genetic effects were also significant for YFCF (6% of the phenotypic variance) but not for HFCF.

Table 1. Mean, variance components, coefficient of variation (%) and heritability for FCF measured as yearlings, hoggets and adults from each data set

Trait	Mean	Variance components						CV	Heritability
		Phenotypic	Residual	Additive	Sire by flock	Maternal	Genetic gp	(%)	(h^2)
IN									
YFCF	99.58	0.34±0.01	0.25±0.01	0.09±0.01	-	-	0.07±0.06	0.59	0.27 ± 0.04
AFCF	99.40	1.34±0.03	0.72±0.04	0.32±0.04	0.03±0.02	0.27±0.06	0.20±0.18	1.16	0.20 ± 0.04
SG									
YFCF	99.60	0.47±0.01	0.35±0.01	0.07±0.01	0.03±0.00	0.03±0.00		0.63	0.14 ± 0.01
HFCF	99.11	1.52±0.02	0.22±0.02	1.30±0.03	0.01±0.00	0.00±0.00		1.82	0.85 ± 0.03

Genetic group was a significant source of variation in both the IN yearling and adult FCF,

representing 21 and 15% respectively of the phenotypic variance, however this is not surprising given the genetic grouping of the IN Merino progeny is largely based on a FD classification via their pedigree (i.e. ultra/superfine, fine fine/medium, medium strong) and the strong relationship between FCF and FD (Baxter and Cottle 1998). The heritability estimates for the IN yearling and adult FCF were both moderate, however the SG YFCF estimate was low (approximately half that of IN) while that for HFCF was high due to low residual and high additive variance at the hogget expression.

Table 2: Phenotypic and genetic correlations (± s.e.) between a) yearling and adult FCF and yearling LWT, wool production, wool quality and visual wool quality scores estimated from the IN and b) yearling and hogget FCF and yearling and hogget LWT, wool production, wool quality and greasy colour from SG.

a)

Trait*	Yearling FCF		Adult FCF	
	r_p	r_g	r_p	r_g
YLWT	-0.09 ± 0.02	-0.25 ± 0.09	-0.13 ± 0.03	-0.22 ± 0.07
YGFW	-0.15 ± 0.02	-0.37 ± 0.09	-0.05 ± 0.03	-0.05 ± 0.08
YCFW	-0.14 ± 0.02	-0.34 ± 0.09	-0.06 ± 0.03	-0.06 ± 0.08
YFD	-0.50 ± 0.02	-0.78 ± 0.05	-0.46 ± 0.02	-0.58 ± 0.05
YFDSD	-0.62 ± 0.01	-0.89 ± 0.04	-0.46 ± 0.02	-0.57 ± 0.06
YFDCV	-0.32 ± 0.02	-0.36 ± 0.08	-0.18 ± 0.03	-0.15 ± 0.07
YCURVE	-0.08 ± 0.02	-0.16 ± 0.09	-0.06 ± 0.02	-0.32 ± 0.16
YRTOC	-0.23 ± 0.02	-0.48 ± 0.08	-0.33 ± 0.03	-0.57 ± 0.06
Y(Y-Z)	-0.12 ± 0.02	-0.24 ± 0.09	-0.11 ± 0.03	-0.17 ± 0.08
YCOL	-0.12 ± 0.02	-0.40 ± 0.10	-0.17 ± 0.03	-0.43 ± 0.08
YCHAR	-0.20 ± 0.02	-0.71 ± 0.08	-0.27 ± 0.03	-0.73 ± 0.06
YSSTRUC	-0.27 ± 0.02	-0.86 ± 0.07	-0.29 ± 0.02	-0.77 ± 0.06
YHAND	-0.20 ± 0.02	-0.63 ± 0.11	-0.15 ± 0.03	-0.36 ± 0.11
YNOUR	-0.02 ± 0.02	-0.24 ± 0.14	-0.06 ± 0.03	-0.34 ± 0.13

*IN traits listed in the materials and methods with 4 negligible correlations (|r|<0.2) are omitted from the table.

b)

Trait	Yearling FCF		Trait	Hogget FCF	
	r_p	r_g		r_p	r_g
YLWT	-0.04 ± 0.01	-0.09 ± 0.07	HLWT	0.01 ± 0.01	-0.11 ± 0.05
YGFW	-0.09 ± 0.01	-0.21 ± 0.07	HGFW	-0.19 ± 0.01	-0.32 ± 0.04
YCFW	-0.11 ± 0.01	-0.58 ± 0.10	HCFW	-0.19 ± 0.01	-0.43 ± 0.05
YFD	-0.34 ± 0.01	-0.63 ± 0.03	HFD	-0.47 ± 0.01	-0.54 ± 0.02
YFDCV	-0.24 ± 0.01	-0.35 ± 0.05	HFDCV	-0.31 ± 0.01	-0.35 ± 0.03
YCURVE	0.08 ± 0.01	0.29 ± 0.05	HCURVE	0.21 ± 0.01	0.34 ± 0.03
YSL	-0.03 ± 0.01	-0.09 ± 0.06	HSL	-0.08 ± 0.01	-0.17 ± 0.03
YSS	0.03 ± 0.01	0.29 ± 0.12	HSS	-0.03 ± 0.02	0.06 ± 0.07
YCOL	-0.27 ± 0.10	0.73 ± 0.34			

The IN yearling and adult expressions of FCF were strongly correlated with each other, both phenotypically (0.73 ± 0.01) and genetically (0.98 ± 0.02) while the SG yearling and hogget expressions were equally highly correlated (phenotypic: 0.54 ± 0.01 and genetic: 0.97 ± 0.02). Most of the phenotypic correlations (r_p) between FCF and other key production traits in both data sets were negligible (i.e. <0.2). The exceptions were r_p with FD, FDSD, FDCV, RTOC, HAND, CHAR and SSTRC in the IN which varied in magnitude from low to high, depending on the age of expression (Table 2a) and r_p with FD, FDCV, CURVE and COL in the SG data which were all low except for HFD and HFCF which was medium (Table 2b). All of the r_p were negative indicating that animals with high FCF had finer less variable FD, lower CURVE and RTOC, increased

textural softness, well defined crimp, fine staple bundles and whiter greasy colour.

In the IN, the majority of the genetic correlations (r_g) between FCF and key production traits were significant and negative (Table 2a). The r_g between YFCF and YFD, YFDSD, AFD and AFDSD (not presented) ranged between -0.92 to -0.67 and, although those between AFCF and YFD and YFDSD were slightly lower (-0.58 and -0.57 respectively), indicate that selection to reduce FD or FDSD will generate favourable correlated increases in FCF. Interestingly the r_g between FCF and FDCV at each age, while still significant, were at least 50% lower than those involving FD or FDSD. The r_g in the SG data were reasonably consistent with the IN estimates (Table 2b) with the exception of positive r_g with YCURVE (0.29) and HCURVE (0.34), the low positive r_g between YFCF and YSS (0.29) and the high positive r_g between YFCF and YCOL (0.73). The remaining significant r_g between FCF and the various production traits in both the IN and SG data were as expected given the strong genetic correlation between FCF and FD.

The strong r_g between FCF with FD and FDCV indicate limited benefit from including FCF as an additional trait in Merino breeding programs with an existing emphasis on reducing FD, as the percentage of fibres over 30 µm is simply a reflection of FD and FDSD. This study also indicates that it would be difficult for medium to strong wool breeders to add FCF to their breeding programs without making correlated changes in FD and to a lesser extent LWT and wool production due to the underlying biology of fleece production Moore *et al*. (1996). Naebe *et al.* (2015) recently investigated the prickle response of 48 fabrics with a range of FD, yarn and fabric construction and found that including FD in the model along with other significant fibre, yarn and fabric factors rendered measures of FD distribution, including FDCV and FCF, insignificant. Therefore variation in FD together with yarn and fabric construction factors appears to have a greater impact on prickle than FCF.

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