

Differences in mean fibre diameter and fibre diameter variance in fine wool, strong wool, and fine × strong wool Merino sheep sampled at five body locations

J.J. Olivier*

Grootfontein Agricultural Development Institute, Private Bag X529, Middelburg, 5900 Republic of South Africa

S.W.P. Cloete

Elsenburg Agricultural Centre, Private Bag, Elsenburg, 7607 Republic of South Africa

A.G. Bezuidenhout

Cradock Experimental Station, Cradock, 5880 Republic of South Africa

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Values for mean fibre diameter (FD) and FD variance were determined on wool samples obtained from five different locations on the bodies of progeny in fine wool, strong wool and fine × strong wool Merino sheep. The respective genetic groups numbered 48, 23 and 37 and were maintained as one flock on irrigated lucerne, rye grass and small grain pastures. Mean FD and FD variance values were lower ($P \leq 0.05$) in fine wool progeny than in fine × strong wool contemporaries, which in turn had lower ($P \leq 0.05$) means for both traits than strong wool progeny. Values for mean FD and FD variance of fine × strong wool progeny were roughly on midparent values. Both traits increased from the anterior to the posterior position of the fleece, with the means for samples obtained from the shoulder being lower ($P \leq 0.05$) than those of breech samples. The mean FD values of belly and midrib samples were generally lower ($P \leq 0.05$) than those of back samples, except in the fine wool progeny. The variance of FD decreased ($P \leq 0.05$) dorsoventrally in strong and fine × strong progeny. In fine wool progeny, a similar tendency was small and insignificant. Concern for excessive FD variation in progeny of fine wool rams mated to strong wool ewes is unwarranted. The processing performance of wool so produced is unlikely to be negatively affected.

Waardes vir gemiddelde veseldikte (VD) en VD-variansie is bepaal op wolmonsters wat vanaf vyf verskillende lokaliteite oor die liggamme van nageslag van fynwol-, sterkwol- en fynwol × sterkwol-Merino's verkry is. Die proefdiere in die onderskeie genetiese groepe was 48, 23 en 37 en is as een groep op besproeide lusern-, raaigras- en kleingraanweidings aangehou. Die gemiddelde waardes vir VD en VD-variansie van fynwolnageslag was laer ($P \leq 0.05$) as by fyn- × sterkwoltydgenote, wat weer laer ($P \leq 0.05$) gemiddeldes as sterkwolnageslag gehad het vir beide eienskappe. Waardes vir fyn- × sterkwolnageslag was ongeveer op die midouerwaarde vir gemiddelde VD en VD-variansie. Beide kenmerke het toegeneem ($P \leq 0.05$) van die voor- na die agterkant van die vag. Gemiddeldes vir monsters verkry vanaf die skouer was laer ($P \leq 0.05$) as dié van broekmonsters. Die gemiddelde VD waardes van pens- en midribmonsters was in die algemeen laer ($P \leq 0.05$) as dié van rugmonsters, maar hierdie effek was afwesig by fynwolnageslag. Die variansie van VD het dorsoentraal afgeneem ($P \leq 0.05$) in sterkwol-, en fyn- × sterkwolnageslag. Verskille in fynwolnageslag was klein en nie-betekenisvol. Vrese vir oormatige variansie in VD by nageslag van fynwolramme wat met sterkwoloë gepaar is, blyk ongegrond te wees. Die verwerkingsprestasie van wol wat so geproduseer is, sal waarskynlik nie nadelig beïnvloed word nie.

Keywords: Body locations, fibre diameter variance, fine × strong wool progeny, mean fibre diameter.

* Author to whom correspondence should be addressed.

The fibre diameter of wool varies over the whole fleece, within a staple and between fibres within the same staple (Dunlop & McMahon, 1974; Denney, 1990). The markedly higher realization value of finer wools in the late 1980s resulted in a higher demand for fine wool rams. Insufficient numbers of genetically fine wool ewes were available, and the mating of strong wool ewes with fine wool rams became a common practice. This led to doubts about the accuracy of mean fibre diameter of the progeny of such matings. Conventional wisdom warns against the mating of extremes, since it is alleged to cause increased fibre diameter variance in offspring. Since fibre diameter variability probably plays a role in the processing performance of wool (Whiteley & Jackson, 1982), it needs to be investigated so that sound recommendations may be made to the industry.

Progeny born from three genetically different Merino groups, maintained on the Cradock experimental farm, were

used in this investigation. These groups consisted of progeny from a fine group (ca. 20 μm), a genetically strong group (ca. 26 μm) and a cross between strong ewes and fine rams. All animals were reared as a single group on irrigated pastures which consisted of lucerne, rye grass and small grains. In total, 48 fine, 23 strong and 37 fine × strong animals were sampled at five different body locations (Figure 1) at an age of 15 months. Samples were analysed by the Wool Testing Bureau, using an Optical Fibre Diameter Analyser which measured 4000 individual fibres in each sample. Apart from the mean, the variance of fibre diameter within samples was available.

The statistical assessment of effects owing to genetic group or body location was complicated by the association between samples obtained from different body locations on the same animal. The repeatability of mean fibre diameter (FD) and of the variance of FD was estimated by nesting random, between-

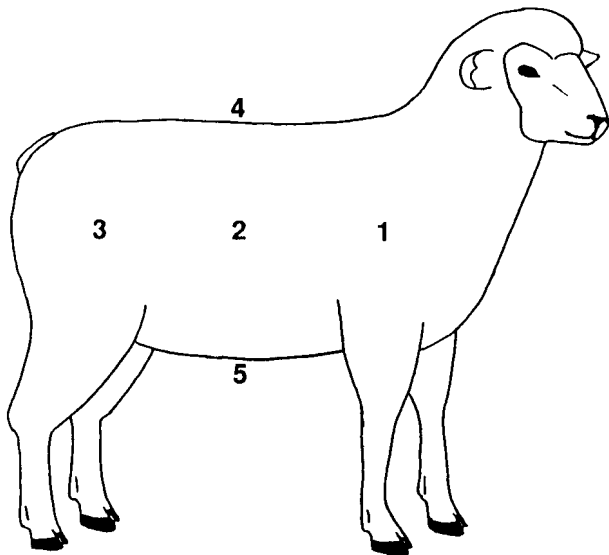


Figure 1 Body locations where individual sheep were sampled; 1 – shoulder; 2 – midrib; 3 – britch; 4 – back; 5 – belly.

animal effects within fixed contemporary group equations (consisting of genetic group, sex and weaning status; Harvey, 1987). Repeatability (t) was calculated as the following intra-class correlation (Turner & Young, 1969):

$$t = \frac{\sigma_a^2}{\sigma_a^2 + \sigma_e^2}$$

with: σ_a^2 = between-animal variance component,
 σ_e^2 = error variance component.

Animal effects were absorbed by maximum likelihood (using absorption option 3) in the analyses on mean FD and FD variance (Harvey, 1987). This procedure allowed the effects of genetic group and body location to be assessed despite the fact that samples were obtained from different body locations on the same animal. Other effects in the model included sex and weaning status as well as all two-factor interactions. The hypothesis that midrib samples provide a fair reflection of the overall mean FD over the fleece within the three genetic groups was also tested. For this purpose, linear contrasts were computed between midrib samples and samples obtained from other body locations in the group \times body location interaction (Harvey, 1987).

Both mean FD and FD variance were highly repeatable ($t \geq 0.61$; Table 1). One sample per animal (i.e. a midrib sample) should give a fair reflection of both traits measured at different locations across the fleece.

Table 1 Variance components and obtained repeatability estimates calculated for use in the absorption process

Trait	Variance component		Repeatability ¹ t
	Between animals	Error	
Mean fibre diameter	1.67217	0.55595	0.7505
Fibre diameter variance	10.79110	6.89262	0.6102

¹ Based on 96 degrees of freedom (df) for animals within contemporary groups, 384 df for error and a k value of 5.0.

Genetic group interacted ($P \leq 0.01$) with body location for both mean FD and FD variance. Mean FD of fine progeny was finer ($P \leq 0.05$) than in fine \times strong contemporaries, which in turn were finer ($P \leq 0.05$) than strong progeny (Table 2). Values for the mean FD of progeny of strong wool ewes mated to fine wool rams was roughly on midparent values for all body locations.

Table 2 Least-squares means for mean fibre diameter (μm) of samples taken from five body locations on sheep belonging to three genetic groups

	Genetic group		
	Fine	Strong	Fine \times Strong
Number of observations	240	115	185
Body location			
Shoulder	19.60 ^{1a}	22.87 ^{3a}	20.82 ^{2a}
Midrib	19.96 ^{1a}	23.21 ^{3ab}	21.07 ^{2a}
Britch	21.55 ^{1b}	25.53 ^{3c}	23.09 ^{2c}
Back	20.07 ^{1a}	25.1 ^{3c}	22.16 ^{2b}
Belly	19.99 ^{1a}	23.72 ^{3b}	21.07 ^{2a}
Standard error	0.22	0.32	0.26

^{a-c} Denote significance ($P \leq 0.05$) between body locations in columns.

¹⁻³ Denote significance ($P \leq 0.05$) between genetic groups in rows.

Mean FD increased ($P \leq 0.05$) from the anterior to the posterior position of the fleece (Table 2). Samples obtained from the shoulder were finer ($P \leq 0.05$) than britch samples in all three groups as was concluded by Stobart *et al.* (1986) and Denney (1990). No differences were found between samples obtained from the back, midrib and belly in fine progeny. The mean FD of midrib and belly samples of fine \times strong progeny was similar, with a stronger ($P \leq 0.05$) mean FD on the back. The same basic pattern was observed in the strong progeny, but there was also a tendency for belly samples to be stronger than midrib samples. Although mean FD is expected to decrease dorsoventrally, this effect is not always consistent (Denney, 1990). The mean FD of the midrib sample gave a fair reflection of the average sample from the other locations in fine progeny (20.0 vs. 20.3 μm). In strong progeny, the mean FD of the midrib sample appeared to underestimate the average of samples from other locations by roughly 1 μm (23.2 vs. 24.3 μm). Linear contrasts between the midrib sample and samples obtained from other body locations were significant ($P \leq 0.05$) in strong and fine \times strong progeny, but not so in fine progeny ($P = 0.83$).

The variance in FD of fine progeny was found to be smaller ($P \leq 0.05$) than that of fine \times strong contemporaries, which in turn had smaller ($P \leq 0.05$) variances when compared to strong progeny (Table 3). Similarly, Dunlop & McMahon (1974) found that a fine strain had the smallest FD variance (9.74 μm^2), and a strong strain the largest (29.26 μm^2). The large genetic group differences are indicative of genetic variability in FD variance, and consistent with relatively high heritability estimates recently reported for FD standard deviation (James *et al.*, 1990) and FD coefficient of variation (Iman *et al.*, 1992).

Table 3 Least-squares means for the variance of fibre diameter (μm^2) of samples taken from five body locations on sheep belonging to three genetic groups

	Genetic group		
	Fine	Strong	Fine \times Strong
Number of observations	240	115	185
Body location			
Shoulder	12.33 ^{1a}	20.74 ^{3ab}	17.19 ^{2ab}
Midrib	13.25 ^{1a}	22.85 ^{3b}	18.54 ^{2bc}
Britch	16.91 ^{1b}	30.24 ^{3d}	25.20 ^{2d}
Back	13.46 ^{1a}	26.44 ^{3c}	20.60 ^{2c}
Belly	12.75 ^{1a}	19.08 ^{3a}	15.82 ^{2a}
Standard error	0.65	0.95	0.76

^{a-d} Denote significance ($P \leq 0.05$) between body locations in columns.

¹⁻³ Denote significance ($P \leq 0.05$) between genetic groups in rows.

Variance in FD increased ($P \leq 0.05$) from the anterior to the posterior position of the fleece, although differences between midrib and shoulder samples were not significant (Table 3). Similar results were reported by Stobart *et al.* (1986). The variance of FD decreased ($P \leq 0.05$) dorso-ventrally in strong progeny. A similar tendency was observed in the fine \times strong genetic group, with a significant ($P \leq 0.05$) difference between midrib and belly samples. The general pattern was similar in fine progeny, but differences were small and insignificant. The values for FD variance of belly samples were, with the exception of the fine group progeny, the lowest in absolute terms. The FD variance of the fine \times strong progeny was roughly on midparent values.

A change of two per cent per year is regarded as the maximum attainable by within-flock selection (Davis & McGuirk, 1987), which implies that it may take up to 10 years to reduce the FD of a breeding flock by 1 μm . Obviously, this process can be accelerated if genetically fine wool rams are mated to

strong wool ewes. The licensing of rams for artificial insemination may assist in the rapid dissemination of fine wool genes in the industry (De Lange & Olivier, 1991), if required. Since the FD variance of fine \times strong progeny was in accordance with expectations based on mean FD, concern for excessive variation in fibre diameter as a result of crossing fine and strong genotypes appears to be unwarranted. Seen in relation to results reviewed by Whiteley & Jackson (1982), it is unlikely that the processing performance of wool so produced will be affected adversely.

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