WOOL CHARACTERISTICS AFFECTING DIFFERENCES AMONG SIRE PROGENY GROUPS IN STAPLE STRENGTH

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SUMMARY

This study aimed to improve the prediction of genetic differences in staple strength (SS) by defining factors that affect differences in SS among progeny groups in 2 sire test trials. The SS was related to mean fibre diameter (FD) and the standard deviation in fibre diameter (SDfd) in both trials (P<0.001), and to staple length in one trial. Sire contributed independently to SS in both trials (P<0.001). Detailed measurements on wools from Flock 2 showed that the relative importance of different components of SS differed among sires (P<0.01); for example, FD had a greater effect on SS in animals with a relatively low SDfd. An equation involving SDfd and FD accounted for only 26% of the variation in SS, but this was increased to 50% of the variation in SS by also incorporating the proportion of fibres greater than 30 m and the amount of unevenness in FD (blobs) measured on clean staples with an OFDA2000. If these findings are robust, they offer a means by which breeders who wish to avoid the expense of direct measurement of SS may improve the efficiency of their selection for this characteristic.

Keywords: coefficient of variation, fibre diameter, unevenness

INTRODUCTION

Management to reduce the variation in FD along the staple can improve SS (Adams & Kelly 2000). SS may also be improved by breeding, because the heritability of SS is moderate to high. The close negative genetic association between SS and the coefficient of variation in FD (CVfd) (Howe *et al.* 1991; Greeff *et al.* 1995), and the expense of measuring SS, has resulted in many breeders using CVfd to select for SS. However, Masters *et al.* (2000) concluded that genetic factors not captured by components of CVfd, or any of the other wool characteristics that they measured, accounted for 26% of differences in SS among progeny groups.

The failure to define the causes of differences in SS occurs because SS is a complex measurement depending on the mass of wool in the staple, the minimum diameter, and interactions among fibres (deJong *et al.* 1985). Interactions among fibres as the staple is pulled apart contribute very significantly to the final SS, but they are poorly understood so we rely on correlated measurements to estimate their impact. Furthermore, the genetic parameters of all the various components of SS might be expected to differ, resulting in genotypes being expressed differently across environments (Greeff *et al.* 1995) or management treatments (Hill & Ponzoni 1999). Clearly, our understanding of factors the contributing to genetic differences in SS is relatively limited. The present study defined wool characteristics that contributed to genetic differences in SS among groups in two progeny tests, to improve the understanding and prediction of genetic differences in staple strength.

MATERIALS AND METHODS

Data were made available from midside wool samples collected from 2 progeny tests in south-western Australia. Flock 1 consisted of 450 progeny from 9 rams, with sire groups numbering between 32 and 60. The flock had a mean SS of 28.9 N/ktex and a mean FD of 16.8 m. Flock 2 contained 682 sheep in groups between 26 and 45 offspring from 17 rams. The mean SS was 42.9 N/ktex and the mean FD was 18.5 m. Both male and female progeny were included, and sex had no independent effect on SS.

Standard wool measurements to evaluate the sires were carried out by a commercial laboratory. Further measurements were carried out on single staples washed 3 times in petroleum ether solvent from Flock 2, using an Optical Fibre Diameter Analyser (OFDA2000; BSC Electronics, Myree WA).

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Staples were measured every 3.5 mm for maximum FD, minimum FD, standard deviation in FD along the fibre (SDalong), standard deviation of FD among fibres at each position along the staple (SDacross) and the proportion of fibres greater than 30 μ m. Areas of unevenness in the FD (blobs) measured by the OFDA2000 software included total blobs (blob%), proportion of large blobs (large blobs) and proportion of small blobs. This measurement was originally developed to measure residual grease in wool, but measures variations in diameter from any cause along a 200 m length of fibre (Brims 1997).

Data were analysed by the general linear model of Systat (Wilkinson 1998). Factors were entered into the model to maximise the amount of variance accounted for by statistically significant factors. All two-way interactions were fitted and the non-significant effects deleted from the model. To explore factors that affected the interaction between sire and wool characteristics in Flock 2, mean values of wool characteristics (FD, SDalong, SDbetween, etc) for each sire were calculated and the correlation between them and SS was calculated for each of the 17 individual sires, and relationships explored by stepwise regression analysis.

RESULTS

Variation in SS among sire means

Each of the components of CVfd (ie, FD and SDfd) was related to SS (P<0.001) in each flock. Staple length affected SS in Flock 1, but the effects were not sufficient to change the ranking of the rams. Significant sire effects, not accounted for by other factors, were found in both flocks (P<0.001). The total amount of variation accounted for by these factors (adjusted multiple R^2) was 0.61 in Flock 1 and 0.37 in Flock 2.

Stepwise regression analysis of mean values from Flock 2 indicated that CVfd alone accounted for 26% of the variation among sires in SS (adjusted multiple R^2). This was increased to 50% of the variation in SS accounted for by including the proportion of fibres >30 µm and the proportion of large blobs. The equation for predicting SS from these characteristics in this flock, including a constant of 148, was as follows:

SS = 148 - 1.78(CVfd) - 0.28(Fibres>30 m) - 59.2(%Large blob).

Each factor in this relationship was statistically significant when tested individually (P<0.05).

Variation within flocks

The impact of sire effects on SS was examined using the detailed measurements of the wools from Flock 2. The minimum FD made a greater contribution to the variation in SS than did the mean FD (Table 1). The effect of sire was significant, but when the interactions between sire and other characteristics were included in the model, sire itself was not significant as a main effect (Table 1). No other significant interactions were detected.

Characteristic	Sum of Squares	df	Р
Minimum FD	7645	1	0.000
Across fibre SD	5405	1	0.000
Mean FD	2509	1	0.000
Sire x mean FD	2134	16	0.003
Sire x SDacross	2062	16	0.01
Blob %	895	1	0.000
Along fibre SD	504	1	0.003
Yield	319	1	0.02

Table 1. Contribution of various factors to SS in Flock 2 (Adjusted multiple $R^2 = 0.52$)

The interaction between sire and mean FD indicates that FD had a greater impact on SS in some sires than in others. FD was more closely related to SS in sires in which SDacross the fibre was poorly related to SS (r = 0.50, P<0.05, Fig 1a). In other words, SDacross had a greater effect on SS in those progeny groups in which FD did not have a large effect. SDacross itself was poorly correlated with SS if the SDalong was large (r = 0.54, P<0.05, Fig 1b). The results indicate that FD, SDacross and SDalong differed in their relative importance for SS in each progeny group.

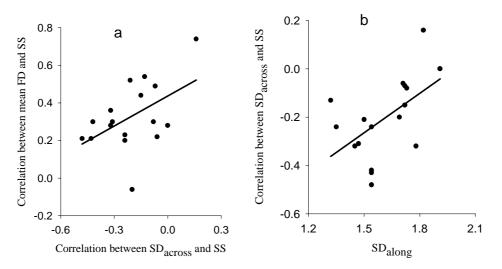


Figure 1. Relationships among factors contributing to SS for each of the 17 sire groups in Flock 2. SS was affected by either FD or SD_{across} , but not both (a), while SD_{across} affected SS if SD_{along} was low (b)

DISCUSSION

The consistent and substantial effect of CVfd (or its components FD and SD) on differences between progeny groups in SS confirms previous studies, and indicates the potential to use CVfd to make genetic gains in SS. However, there were also substantial differences among sires in SS that were not accounted for by CVfd (Table 1), as also reported by Masters *et al.* (2000). These were not due to a biased measurement of SS by factors such as yield, point of break or staple length which have been observed previously to affect SS (Adams *et al.* 2000; Mata *et al.* 2000). However, sire effects could be attributed to other factors measured in the present study, so that the prediction of differences among progeny groups in Flock 2 was substantially improved by including the proportion of fibres >30µm and %blobs. These results need to be tested in other environments to determine the extent to which they can be generalised, although it is reassuring that other trials associated with Flock 1 have found that the proportion of fibres with a diameter more than 10 m greater than the mean (the 'coarse edge') has value, together with CVfd, in predicting SS (unpublished data).

The proportion of fibres >30 m may reflect both variation in fibre length and fibre-to-fibre interactions. The CVfd is related to SS in part because it reflects the variation in length of fibres within the staple, which affects the synchronicity with which fibres break under strain (deJong *et al.* 1985) and so affects SS (Schlink *et al.* 2001). Fibre-to-fibre interactions were also described by deJong *et al.* (1985) as having a major effect on SS. The total magnitude of these interactions must be driven in part by the number of fibres in the staple, which is a function of FD and CVfd. Interestingly, in the analysis displayed in Table 2 the square of diameter was less closely associated with SS than the mean diameter, suggesting that fibre circumference had the greater effect on SS than fibre cross-sectional area. Fibre circumference would affect interactions among fibres, while cross-sectional area would determine the resistance to break.

The mechanism underlying the relationship between SS and blob measurement is not clear. The blob measurement was developed to estimate residual grease in the wool sample, but it actually measures all causes of unevenness in diameter along a short section of fibre (Brims 1997). Some of the unevenness relates to grease that was not removed by cleaning, but Schlink *et al.* (2000) using the 35 S technique showed that there are also normally very large changes in FD along short lengths of fibre. Unevenness in FD is associated with the strength of individual fibres (Woods *et al.* 1990), but to date there has been no simple way to measure this characteristic. The wools in the present study should have contained little grease because they were washed 3 times in solvent, so the results suggest that further work to clarify the source of short-term variations in FD measured by the OFDA2000 may prove rewarding.

Table 1 indicates that the relative importance of the components of CVfd (the FD, SDalong and SDacross) differed among sire progeny groups. For example, Figure 1a indicates that the major components of CVfd, FD and SDacross, trade off in their relative importance for SS; if FD had a large impact on SS, then SDacross has a lesser impact. Figure 1b indicates that the effect of SDacross on SS was greater when SDalong was low. The genetic parameters of these components of CVfd undoubtedly differ, and additional genetic variation would be provided by other contributors to SS, such as the variation in fibre length described above. It is therefore not surprising that interactions between genotype and environment for SS have been described (Hill and Ponzoni 1999). The predictability of genetic differences in SS might be improved by a better knowledge of the relative importance of the different components required to improve SS in a particular management situation.

The results show that genetics and management affect SS in quite different ways. As reported initially by Howe *et al.* (1991), and confirmed in progeny tests by Masters *et al.* (2000), SDacross fibres made a greater contribution to genetic differences in SS than SDalong. This is the opposite for comparisons among flocks in different environments (Mata *et al.* 2000). Minimum FD had a greater effect on SS than variation in diameter in the present study, again the opposite of studies examining management treatments (Mata *et al.* 2000). Therefore, definition of the causes of difference in SS due to management has only limited application in determining the genetic components of SS.

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