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Inheritance of loose wool bulk

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ABSTRACT

An assortative breeding programme was carried out in 4 industry Perendale flocks and at Whatawhata using Cheviot, Perendale, Romney and Coopworth sheep. Within the industry flocks rams of high and low loose wool bulk were progeny tested. At Whatawhata Cheviot and Perendale rams of high, medium and low loose wool bulk were mated to ewes of equivalent bulk type within their own breed. High and low loose wool bulk Cheviot and Perendale rams and high loose wool bulk Romney rams were also mated to randomly allocated groups of Romney and Coopworth ewes.

Progeny data provided an estimate of the phenotypic correlation between loose wool bulk measured at lamb and hogget shearing of 0.5. Breed effects on hogget loose wool bulk were essentially additive and complementary to the effects of sire selection within breeds.

Statistical methods for evaluating heterogeneity of within-family variance of loose wool bulk at hogget shearing were used to investigate the possibility of a major gene influencing loose wool bulk. These methods could not confirm the hypothesis of a major gene controlling loose wool bulk.

Offspring-parent relationships were consistent with previously published heritability estimates of around 0.5.

Keywords Inheritance; loose wool bulk; Cheviot; Perendale; Romney; Coopworth

INTRODUCTION

Loose wool bulk is a characteristic of unprocessed wool that influences the texture and handle of yarn and subsequent end products. It appears a desirable feature of wool to be used in carpets (Carnaby *et al.*, 1984). There are large between breed differences in loose wool bulk with differences greater than 15% between lines of wool producing detectable differences in yarn bulk (Carnaby and Elliott, 1980). As a result of these effects, loose wool bulk is one of the 6 key characteristics that have been considered in the development of computer blending technology associated with the manufacture of woollen and semi-worsted yarns (Elliott, 1986).

Price advantages for bulky wools may result from increasing use of objective loose wool bulk measurements at auction. It may thus be financially worthwhile for crossbred wool growers to increase the bulkiness of their clip through breeding.

There are good prospects of improving bulk through selection. The distribution and the high estimates of heritability for loose wool bulk in the Perendale suggest that genes with large effect may be involved in the expression of loose wool bulk in breeds and crosses of Cheviot ancestory (Bigham *et al.*, 1985).

This paper reports the results of an assortative mating programme to further evaluate the inheritance of loose wool bulk.

EXPERIMENTAL

Two assortative mating trials were carried out in which Cheviot, Perendale, Romney and Coopworth rams and ewes of either high (H), medium (M), low (L) or random (R) loose wool bulk were interbred. Individual sheep were allocated to their respective loose wool bulk grouping on the basis of measurement (Bigham *et al.*, 1984) of a mid-side fleece sample taken at hogget shearing.

Fleeces of the progeny of the experimental matings were weighed and sampled in the mid-side region for loose wool bulk measurement at both lamb and hogget shearing.

TABLE 1 Mean (SD) loose wool bulk (cm^3/g) of the high (H) and low (L) bulk Perendale sire groups as hoggets and the mean (SD) loose wool bulk (cm^3/g) of their progeny as both lambs and hoggets on each farm in Trial 1. Perendale dams were selected at random.

Farm	Bulk type	Sire		Progeny		
		No. of sires	Mean bulk as hogget	No. of Progeny	Mean bulk as Lamb	Mean bulk as Hogget
1	H	1	34.0	16	26.5(2.6)	32.6(3.1)
	L	1	20.9	20	23.4(2.3)	27.3(3.8)
Signif. of diff. (H-L)					***	***
2	H	2	34.0(0.4)	35	25.2(2.4)	28.7(3.2)
	L	2	21.1 (0.7)	30	24.8(3.0)	27.6(4.1)
Signif. of diff. (H-L)					NS	NS
3	H	2	33.8(0.4)	35	26.0(2.8)	27.0(4.0)
	L	2	20.4(0.5)	33	24.0(1.8)	23.2(3.2)
Signif. of diff. (H-L)					**	***
4	H	2	33.1 (1.5)	20	24.0(2.2)	29.3(4.0)
	L	2	17.9 (0.5)	21	22.8(2.4)	25.9(3.5)
Signif. of diff. (H-L)					*	***

Trial 1

In each of 4 industry Perendale flocks a minimum of 80 mixed-age ewes were allocated at random for single sire matings among 4 rams (Table 1). These comprised 2 pairs of half-sibs, each pair being the rams with the highest and lowest loose wool bulk within their respective half-sib family group established by Bigham *et al.* (1985) in their Trial 3. One of the selected rams on Farm 1 died prior to mating. His half-sib mate was not used.

Trial 2

The mating programme carried out at Whatawhata Research Centre is summarized in Table 2. A total of 6 H, M and L loose wool bulk Perendale rams and 8 H, M and L loose wool bulk Cheviot rams from within the Perendale and Cheviot flocks maintained at Whatawhata were single sire mated to groups of ewes of equivalent bulk type within their breed. In addition the H and L Perendale and Cheviot rams and 2 H Romney rams, selected from a Landcorp flock, were single sire mated to groups of Romney and Coopworth ewes selected at random. Two randomly selected Romney rams were single sire mated to groups of Romney ewes selected at random and 4 randomly selected Coopworth rams, bred in industry flocks, were mass mated to a group of Coopworth ewes also selected at random.

RESULTS AND DISCUSSION

Phenotypic Correlations

The pooled correlation (repeatability) between loose wool bulk samples taken at lamb and hogget shearing was 0.5. Estimates ranged between 0.3 and 0.6 with no significant effect of breed cross. Variation in loose wool bulk within each subgroup was considerably less at lamb shearing than at hogget shearing 10 months later (Tables 1 and 2). These low correlations do not favour early measurement of lamb fleece samples for prediction of loose wool bulk in adults.

Genetic Variation

Mean loose wool bulk of Romney (24.1 SD 3.5) and Coopworth (24.0 SD 3.4) hoggets were similar (Trial 2). Cheviot hoggets had a higher (29.0 SD

TABLE 2 Mean (SD) loose wool bulk (cm^3/g) of the high (H), medium (M), low (L) and random (R) bulk sire and dam groups as hoggets and the mean (SD) loose wool bulk (cm^3/g) of their progeny as both lambs and hoggets for the various breed crosses developed between the Coopworth (Coop), Cheviot (Chev), Perendale (Peren) and Romney (Rom) in Trial 2.

Sire				Dam			Progeny		
Breed	Bulk type	No. of sires	Mean bulk as hogget	Breed	Bulk type	Mean bulk as hogget	No. of progeny	Mean bulk as Lamb	Mean bulk as Hogget
Chev	H	3	37.9 (0.9)	Chev	H	-	21	27.0(2.1)	32.7 (4.1)
				Rom	R	20.8 (3.0)	40	24.8(2.5)	28.3 (4.7)
				Coop	R	20.9 (3.6)	24	25.4(1.9)	28.0 (4.1)
	M	3	32.2 (0.9)	Chev	M	-	40	26.1(2.4)	29.6 (4.2)
	L	2	27.6 (0.4)	Chev	L	-	18	24.6(2.2)	24.6 (2.9)
				Rom	R	19.5 (2.1)	24	23.1(1.5)	22.8 (2.1)
				Coop	R	21.4 (2.9)	33	25.1(2.4)	25.2 (3.6)
Peren	H	2	33.3(0.7)	Peren	H	31.9 (1.9)	34	26.4(2.7)	31.0 (4.7)
				Rom	R	20.5 (3.3)	27	24.0(1.7)	27.6 (3.8)
				Coop	R	19.8 (3.4)	29	24.7(2.9)	27.6 (3.6)
	M	2	25.7 (0.1)	Peren	M	26.9 (1.8)	80	25.3(2.5)	27.8 (3.9)
	L	2	20.6(1.6)	Peren	L	22.2 (1.6)	45	23.4(2.7)	25.0 (3.9)
				Rom	R	21.3 (2.3)	21	21.9(1.8)	24.2 (3.6)
				Coop	R	21.0 (3.6)	36	22.5(2.8)	24.0 (3.5)
Rom	H	2	27.4 (0.6)	Rom	R	20.7 (3.0)	31	23.2(3.5)	25.7 (4.5)
	R	2	22.3(0.3)	Rom	R	20.6 (2.2)	26	21.2(2.2)	22.4 (3.5)
Coop	R	4	-	Coop	R	21.2 (2.5)	41	22.3(2.3)	24.0 (3.4)

4.8) loose wool bulk than Perendales (27.9 SD 4.6). There was no significant sire-breed x dam-breed interaction on hogget loose wool bulk in Trial 2. Relative to Coopworth sires, Romney, Perendale and Cheviot sires increased bulk by 0.3, 1.8 and 2.3 cm^3/g. Similarly Romney, Perendale and Cheviot dams increased bulk by 0.1, 1.9 and 3.1 cm^3/g respectively relative to Coopworth dams.

Sire and dam breeds combined additively in their effects on the loose wool bulk of their progeny. This equivalent responsiveness within the Romney, Coopworth and Perendale, has commercial significance in that it appears equally possible to increase the loose wool bulk of the 3 main breeds growing crossbred type wool in New Zealand through genetic selection and crossbreeding (Figs 1, 2 and 3).

The possibility of a major gene influencing loose wool bulk was investigated. The regression approach of Fain (1978) was used to compare the relationship between the variance of half-sib families and their mean for loose wool bulk. Given the presence of a major gene, the variance of families of half-sibs where heterozygotes are frequent should be greater than those containing homozygotes and the quadratic term should be significant in the regression of the variance on the mean. Similar trends were obtained to those reported by Bigham *et al.* (1985) with a significant linear relationship between the variance and mean for Trial 2 but no significant quadratic relationship. In Trial 1 there was no significant relationship between the variance and mean. Bartlett's test of homogeneity of variance was also used. This test was significant at the 0.1% level in Trial 2 for hogget loose wool bulk giving some indication that a main gene may be acting. It was not significant for hogget fleece weight. No breed differences were apparent. When applied to the Trial 1 data the test was not significant for either loose wool bulk or fleece weight measured at hogget shearing.

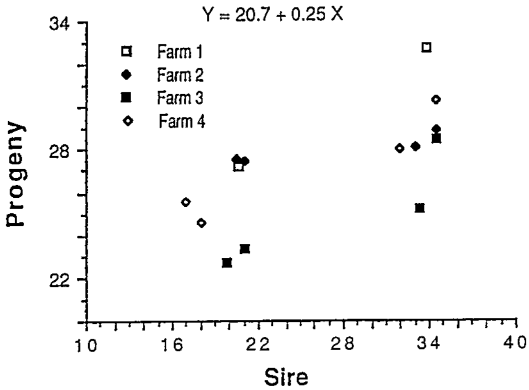

FIG. 1 Relation between loose wool bulk (cm^3/g) of Perendale sires as a hogget and the mean loose wool bulk (cm^3/g) of their progeny as hoggets when mated to Perendale ewes selected at random on 4 farms in Trial 1.

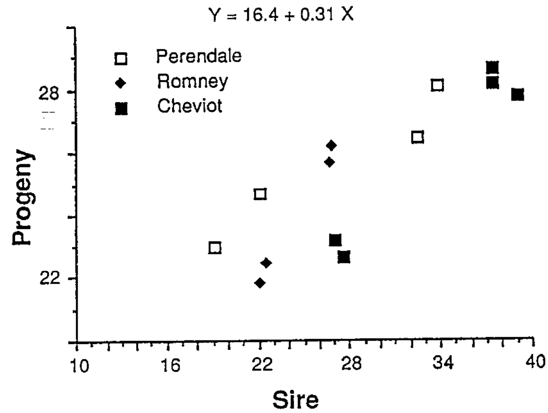

FIG. 2 Relation between loose wool bulk (cm^3/g) of Cheviot, Perendale and Romney sires as a hogget and the mean loose wool bulk (cm^3/g) of their progeny as hoggets when mated to Romney ewes selected at random in Trial 2.

These methods rely primarily upon the detection of differences in within sibship variance from segregation of a major gene as distinct from segregation of many genes each having a small effect. Although they are useful exploratory tests, there is a need to further investigate the possibility of using more complex segregation analyses in the Trial 2 data. Maximum likelihood techniques, which use all the information in the data, have been used in human genetics to discriminate among modes of inheritance. This approach is however computationally demanding with problems about how to proceed when major gene effects are masked by environmental influences and has not yet been tackled for animal breeding data.

Heritability

Differences in loose wool bulk among progeny of selected sires were consistent with previous published heritability estimates of around 0.5 (Bigham *et al.*, 1985).

Offspring-sire relationships for the Trial 1 data are shown in Fig. 1. The within-farm regression of offspring on sire was 0.25, indicating a heritability of 0.5. Slopes were similar on all farms. For the Trial 2 data the average slope for Romney ewes was 0.31 (Fig. 2) and for Coopworth ewes was 0.19 (Fig. 3). There were no significant sire or dam breed effects. An overall value for Trial 2 based on the regression of progeny on mid-parent (parental values repeated) was 0.58 ± 0.05. Pooled over dam breeds, the value for Cheviot sires tended to be higher (0.74) than for Perendale (0.53) and Romney (0.53) sires. No estimate was able to be calculated for the Coopworth as the sires were not measured for loose wool bulk as hoggets.

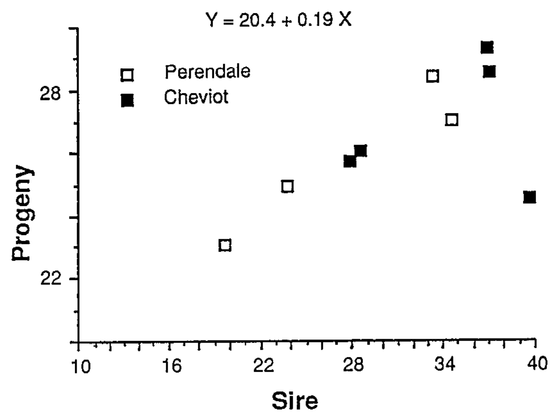

FIG. 3 Relation between loose wool bulk (cm^3/g) of Cheviot and Perendale sires as a hogget and the mean loose wool bulk (cm^3/g) of their progeny as hoggets when mated to Coopworth ewes selected at random in Trial 2.

CONCLUSION

These trials confirm the high heritability of loose wool bulk and previous knowledge of breed effects on this trait. The assortative mating design was unable to conclusively confirm or refute segregation of a major gene influencing loose wool bulk. The presented graphs show breed effects were essentially additive and complementary to the effects of sire selection within breeds. Consequently both selection and cross breeding using these breeds may be employed to change the loose wool bulk characteristics of hogget wool. Different breeds however may have different consequences in terms of associated changes in fleece weight.

Further selection for and against loose wool bulk will be used to differentiate the flocks for further analytical and biological study of the inheritance of loose wool bulk.

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