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Genetic effects in GrowBulk sheep

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ABSTRACT

GrowBulk sheep are a strain of long-wool type sheep growing high bulk wool developed by introgressing high-bulk genes from Texel and Dorset rams into Romney ewes. Progeny selection was planned to minimise decreases in clean fleece weight. Rams have been released to four multiplier flocks. Genetic effects were evaluated in the nucleus and multiplier flocks using a restricted maximum likelihood animal model. Heritability estimates were 0.46 ± 0.05 for bulk and 0.30 ± 0.05 for clean fleece weight with a genetic correlation of -0.48 ± 0.09 . The crossbred genotypes represented in the nucleus flock showed a range in average breeding merit for bulk of 27 to 31 cm³/g, their weighted mean genetic superiority over contemporaneous Romneys being 5.3 cm³/g. The first crop of commercial progeny by rams from this flock showed an average genetic superiority in bulk over their dams of approximately 4 cm³/g. Genetic trends indicate that selection has been able to maintain the bulk advantage of the crossbreds while at the same time improving their fleece weight.

Keywords: wool bulk; genetic parameters; selection responses; outcross performance.

INTRODUCTION

Wool bulk is defined as the specific volume of a known mass of fibre under a set load expressed as cm³/g. Bulk is a desirable attribute closely associated with the crimp (Sumner *et al.*, 1993) imparted to fibres during growth and retained through processing. It is sought by interior textile and knitting yarn processors as both processing and end-product performance are improved by increased wool bulk (Sumner *et al.*, 1991, Maddever and Wuliji, 1993). Wool bulk is strongly inherited in Perendale sheep (Sumner *et al.*, 1995) where there is the suggestion that it may be controlled by relatively few genes of large effect. Fleece weight and bulk are however negatively correlated, especially clean fleece weight and at the genetic compared to the phenotypic level (Sumner *et al.*, 1995; Clarke *et al.*, 1999). In order to develop a long wool, polled and non-pigmented sheep growing high bulk wool, high bulk Poll Dorset and Texel rams were crossed with high fleece weight Romney ewes. The progeny were selected and interbred to produce GrowBulk sheep. GrowBulk rams have recently been disseminated to commercial crossbred wool-type ram breeding flocks.

This paper presents genetic trends estimated by best linear prediction methods (BLUP) from a combined analysis of the performance of base, nucleus and multiplier flocks.

MATERIALS AND METHODS

Sheep

The animals were bred at the Whatawhata Research Centre and the Gore Research Station as described by Sumner *et al.*, (1998). Dorset x Romney first-crosses (DR1) and interbreds (DR2) were produced at Whatawhata during 1992 to 1994 and 1994 to 1997, respectively. Texel x Romney first-crosses (TR1) and interbreds (TR2) were produced at Gore during 1991 to 1994 and 1994 to 1997 respectively, although only records from 1994 were available for these analyses. The Romney dams for these crosses

were screened from high fleece weight institutional (Texel matings) or industry (Dorset matings) flocks. Rams of the base sire breeds were selected from industry flocks for their high bulk wool and above average fleece weight. In any one year and location the same selected first-cross rams were used to generate DR2 (or TR2) and TR x DR (or DR x TR) progeny. First-cross DR and TR rams were transferred across locations from 1994 to 1995, to generate TR x DR progeny at Whatawhata (or DR x TR progeny at Gore). This design served to genetically link the genotypes derived at the two locations. Rams were chosen on an index of high bulk and high clean fleece weight. All animals were brought together into a single flock in the North Island in 1997, and are now located at Whatawhata alongside descendants of the original Romney dams to monitor the changes resulting from crossbreeding and selection. Composite GrowBulk rams were released to 4 industry ram-breeding flocks (4 Romney and 1 Coopworth) in 1997. These multiplier flocks were located in the King Country, Manawatu, Canterbury and Southland. Their progeny were evaluated for the first time at hogget shearing in 1998.

Data collection and analysis

The data analysed comprise clean fleece weight and bulk records for 3171 hoggets born between 1992 and 1997. Lambs were shorn at 3 months and again at 12 months of age when in addition to greasy fleece weights a mid-side fleece sample was taken, scoured and weighed for determination of clean fleece weight. Core bulk was measured using standard procedures (Standards Association of New Zealand, 1994).

Statistical analysis

Genetic trends were analysed by fitting a univariate animal model using ASREML (Gilmour, 1997). Significant fixed effects associated with birthday, birth-rearing rank and a covariate defining dominance expectations of heterosis from Dorset and Texel versus Romney crosses, were included in the model for analysis of clean fleece weight,

while for bulk the significant effect of age of dam only was included. In addition to a random animal effect to estimate breeding values using the genetic relationship matrix, a random litter effect was also fitted for clean fleece weight. This effect, representing the non-genetic similarity of litter mates, was not significantly different from zero for bulk. Genetic group effects, representing the average genetic merit of base animals (unmeasured purebred parents of the animals being analysed), were fitted through their inclusion in the pedigree file defining genetic relationships among animals (Gilmour, 1999). Groups were defined to represent the introgressed Texel and Dorset rams, the Romney ewes to which they were mated (1992-1994) and the industry ewes generating commercial progeny in 1997. Univariate breeding value solutions were summarised by genotype and year of birth to provide estimates of genetic trends. Bivariate analyses were undertaken to estimate the genetic correlation between the traits.

RESULTS

Genetic parameters

Fixed effect and variance components estimated by univariate and multivariate analyses gave the genetic and phenotypic parameters summarised in Table 1. Also shown are the genetic group effects for the base genotypes contributing to the composite population.

TABLE 1: Estimates of phenotypic and genetic parameters for bulk and clean fleece weight.

	Bulk (cm ³ /g)	CFW (kg)
Mean	28.4	2.07
Univariate		
Phenotypic variance	6.69	0.116
Direct heritability	0.46±0.05	0.30±0.05
Litter environment*	-	0.10±0.04
Heterosis effect (kg)	-	0.24±0.07
Genetic Group Means		
Base Romney	24.1±0.37	2.98±0.08
Dorset	34.8±0.62	1.97±0.16
Texel	32.1±0.83	2.11±0.18
Industry dams	22.1±0.71	2.84±0.12
Bivariate		
Direct heritability	0.47±0.05	0.33±0.05
Genetic correlation	-0.46±0.09	
Phenotypic correlation	-0.22±0.02	
Direct heritability	0.47±0.05	0.30±0.05
Litter environment*	-	0.12±0.04
Genetic correlation	-0.48±0.09	
Phenotypic correlation	-0.22±0.02	

* as a proportion of phenotypic variance

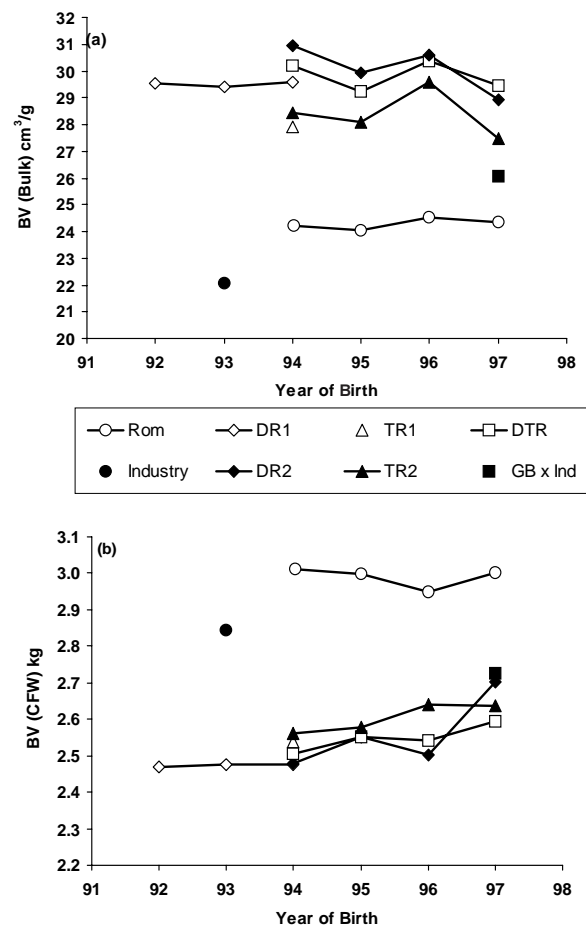
Litter effects were important for CFW only, accounting for 10% of the phenotypic variation. The bivariate model, expected to better account for selection effects on genetic parameters gave similar heritabilities to the corresponding univariate models from which genetic trends were estimated. The estimated genetic correlation was -0.48 ± 0.09 in contrast to the phenotypic correlation of -0.22 ± 0.02 . Estimates of the phenotypic and genetic parameters are in agreement with those published for these flocks by Sumner *et al.* (1998) for animals born up to and including 1995,

with the exception of the more strongly negative genetic correlation (-0.48 ± 0.09 vs -0.35 ± 0.06) found here. This genetic association is also more antagonistic than most published estimates (Sumner *et al.*, 1998). The estimate of heterosis for clean fleece weight was similar to most published estimates being 11% of the mean.

Genetic trends

Estimates of genetic trends derived from univariate estimates of breeding value are presented graphically in Figure 1.

FIGURE 1: Genetic trends in hogget fleeces for: (a) bulk and (b) clean fleece weight (refer text for genotype abbreviations; Rom = Romney; GB x Ind = GrowBulk x Industry matings).



Bulk

As shown in the upper set of graphs in the figure (Figure 1a) the average genetic trend in wool bulk for Romney hoggets was close to zero (0.03 ± 0.04 mm cm³/g per year), as expected in the absence of selection in this reference group established to monitor changes in the other genotypes with time. The average genetic trend for the DR1 (-0.01 ± 0.07 cm³/g per year), DR2 (-0.09 ± 0.09 cm³/g per year), TR2 (0.17 ± 0.11 cm³/g per year) and DTR genotypes (-0.15 ± 0.04 cm³/g per year) was also close to zero ($+0.05 \pm 0.02$ cm³/g per year). DTR were 4 to 7 cm³/g higher in bulk than the base Romneys from which the crossbred nucleus flock was established. Their genetic mean is at the level expected from the average of the genetic group effects of the base breeds (Table 1) from which they were

derived. The performance of the first crop of hoggets in multiplier flocks (born 1997) is also shown in Figure 1a (solid square), along with the genetic group effect (solid circle) for hoggets representing the base ewes from which they were produced (taken from Table 1). The latter is set at the 1993 birth year, reflecting the approximate average year of birth of these animals. As expected in the absence of heterosis effects, this first crop of industry progeny fell midway between the two parental levels (26 cm³/g).

Clean fleece weight

The genetic trend in clean fleece weight (Figure 1b) in the unselected Romney hoggets was not significantly different from zero (-9±8 g per year). For the crossbred genotypes in the breeding flock, it ranged from 3±6 g per year in DR1 to +33±8 g per year in TR2, averaging +24±2 g per year for all crossbred genotypes. The high fleece weight Romneys from which the nucleus ram breeding flocks derived had a genetic clean fleece weight superiority of about 0.14 kg over the industry ewes (mainly Romney) used to produce the first crop of progeny in multiplier flocks in 1997.

DISCUSSION

The crossbred genotypes representing the nucleus ram breeding flock showed a range in average breeding merit for bulk of 28 to 31 cm³/g. Their average merit of approximately 30 cm³/g was 5.3 cm³/g higher than contemporaneous Romneys. The first crop of commercial (multiplier) progeny by rams from this flock showed a genetic superiority in bulk over their industry dams of approximately 4 cm³/g. Unexpectedly, the high fleece weight Romney ewes from which the nucleus ram breeding flock was derived and which were screened from recorded industry and research flocks had a breeding merit for bulk which was on average about 2 cm³/g higher than the industry ewes (mainly Romneys) generating the first crop of commercial progeny in 1997. Their 0.14 kg superiority in clean fleece weight was less than expected from the responses that have been demonstrated for long-term institutional selection flocks (Clarke and Johnson, 1993).

CONCLUSIONS

The genetic trends indicate that selection has been able to maintain the bulk advantage of the crossbred hoggets comprising the nucleus ram breeding flock while at the same time improving their fleece weight at a reasonable rate - approximately 20 g per year since 1994. This response in fleece weight is about one third the rate expected for single trait responses to selection for clean fleece weight in Romney sheep (Clarke and Johnson, 1993). Thus selection has been effective in maintaining the bulk advantages introduced by crossbreeding while at the same time countering some of the expected decline in clean wool production, despite the more pronounced genetic antagonism estimated for this flock ($r_g \approx -0.5$) in contrast to those published recently for Romneys ($r_g \approx -0.2$; Morris *et al.*, 1996, Wuliji *et al.*, 1998).

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