EWE GENOTYPE EFFECTS IN GENETIC EVALUATION OF MERINO FLEECE TRAITS ACROSS AGES

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SUMMARY

The significance of ewe genotype and its interactions with sire effects were examined for Merino fleece traits recorded between post weaning and adult stages of progeny at the Macquarie site of the Merino Lifetime Productivity project. Across post weaning, hogget and 3 adult expressions, ewe bloodline effects significantly influenced fleece traits, particularly fleece weight and fibre diameter. Sire X ewe genotype interactions on fleece traits across ages were generally unimportant, accounting for small amounts of the phenotypic variance (less than 1%). Correlations between sire progeny performances were generally greater than 0.70. These results support the methods used routinely to account for these effects in MERINOSELECT genetic evaluations.

INTRODUCTION

Atkins *et al.* (1999) concluded that for across-flock genetic evaluation of Merino sires, though sire X dam source interactions were small, the influence of heterosis on some Merino traits may also need to be included in evaluation models. This has been addressed by the fitting of a sire X flock-year interaction in the model; its component of a genotype X genotype interaction allows the MERINOSELECT genetic evaluation system to account for potential sire X ewe genotype interactions (Li *et al.* 2015).

In the context of central test sire evaluation and on-farm progeny testing, it is usual to have the sires mated to an even line of ewes selected to meet a breeding objective that differs from that of the majority of the sires. Anecdotally, some Merino breeders have concerns that these genetic benchmarking systems will be biased by heterosis as sires are mated to ewes of a different genetic background, with these concerns greater for assessments at later ages. Several recent studies have shown that these sire X ewe bloodline interactions are unimportant for measured fleece traits (Egerton-Warburton *et al.* 2019), visually assessed wool traits (Mortimer *et al.* 2021b) and body composition and reproduction traits (Mortimer *et al.* 2021a) recorded at post weaning, hogget and/or a first adult shearing. At most, the interaction effect in those studies accounted for less than 2% of the phenotypic variance. Using data recorded on progeny at the Macquarie site of the Merino Lifetime Productivity (MLP) project, this study extends the findings of Egerton-Warburton *et al.* (2019) by examining the influence of sire X ewe bloodline interaction on fleece traits recorded at hogget and 3 adult shearings.

MATERIALS AND METHODS

Data were available from the progeny born in 2017 and 2018 at the Macquarie MLP site. The site's establishment at the Trangie Agricultural Research Centre has been outlined by Egerton-Warburton *et al.* (2019), while the overall design of the MLP project has been described by Ramsay *et al.* (2019). Briefly, each drop was generated by AI matings of industry sires (30 sires in total, including a link sire) to foundation ewes, which had previously lambed, of 2 bloodlines sourced

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from representative commercial flocks. Bloodline 1 (B1) was selected to meet a dual purpose objective, where selection aimed to improve wool, fertility and growth traits. The breeding objective of bloodline 2 (B2) was set to increase wool production and body size. The allocation of ewes to sires was balanced across the ewe flock sources. The progeny were assessed at post weaning (average age of 280.6 days), hogget (average age of 533.7 days), first adult (average age of 899.3 days), second adult (average age of 1,273.7 days) and third adult (average age of 1,659.2 days) shearings. Animals were shorn for assessment of greasy fleece weight (gfw, kg), clean fleece weight (cfw, kg), mean fibre diameter (fd, μm), coefficient of variation of fd (fdcv, %), fibre curvature (curv, degrees/mm), staple length (sl, mm) and staple strength (ss, N/ktex). Birth type and rearing type of the progeny were inferred from parentage determination based on DNA samples and the dam's pregnancy scan results. Fleece traits recorded on the ewe progeny have been used for this study, except for the post weaning assessment where the records were available for both drops on wethers only. From the post weaning assessment, records were available from 529 (52% of records) and 495 animals for B1 and B2 respectively, with these proportions maintained across the later assessments. Mean performances for each trait of each bloodline are shown in Table 1. Coefficients of variation were similar for each combination of bloodline and trait within an assessment (results not shown).

Table 1. Means (standard deviations) for fleece traits of bloodline 1 (B1) and bloodline 2 (B2) for post weaning to third adult assessments of fleece traits

		Post weaning	Hogget	First adult	Second adult	Third adult
gfw	B1	3.6 (0.72)	5.1 (0.72)	7.5 (1.30)	6.8 (1.12)	6.8 (1.17)
	B2	3.5 (0.69)	5.1 (0.68)	7.7 (1.29)	7.4 (1.11)	7.4 (1.19)
cfw	B1	2.4 (0.54)	2.8 (0.49)	4.5 (0.89)	4.7 (0.94)	4.8 (0.98)
	B2	2.4 (0.53)	2.9 (0.54)	4.9 (0.84)	5.4 (0.92)	5.6 (1.01)
fd	B1	16.5 (1.12)	18.0 (1.33)	18.3 (1.29)	18.9 (1.44)	19.5 (1.49)
	B2	17.5 (1.34)	19.0 (1.45)	19.5 (1.40)	20.5 (1.59)	21.2 (1.70)
fdcv	B1	18.3 (2.20)	15.8 (2.35)	16.5 (2.36)	15.8 (2.00)	15.3 (1.83)
	B2	19.2 (2.26)	17.2 (2.60)	17.8 (2.55)	16.9 (2.22)	16.0 (1.98)
curv	B1	60.1 (10.02)	63.1 (10.80)	61.6 (11.4)	62.5 (12.29)	62.9 (12.68)
	B2	60.4 (8.85)	63.1 (10.62)	61.5 (10.52)	60.5 (11.63)	60.0 (12.21)
sl	B1	77.3 (9.77)	81.3 (10.02)	115.3 (11.28)	115.8 (10.41)	108.6 (10.36)
	B2	77.1 (8.79)	79.4 (9.90)	112.6 (10.51)	114.7 (9.76)	108.6 (9.68)
ss	B1	26.9 (8.03)	44.3 (9.29)	28.7 (9.41)	34.9 (11.13)	38.5 (12.47)
	B2	26.6 (9.58)	48.3 (10.11)	30.6 (9.51)	37.2 (10.92)	40.0 (12.74)

Analyses were performed using ASReml (Gilmour et al. 2021). Initially, the significance of ewe bloodline fitted as a fixed effect was tested in univariate models that fitted other fixed effects and a random effect of sire. Those fixed effects included birth type (single, twin, triplet), rearing type (single, twin), dam age (3, 4, 5, 6 and 7 years old at mating), current reproduction (adult traits only) and contemporary group. Fixed effects were excluded from the model when not significant. Then, to this model a sire X ewe interaction was added to test if it increased significantly ($P < 0.05$) the log-likelihoods between models. Treating the performances of the progeny of each ewe bloodline as individual traits, a multivariate approach also was used to evaluate the correlation between predicted sire effects as a measure of the genetic correlation between performance in each bloodline.

RESULTS AND DISCUSSION

In general, the ewe bloodline effect was significant ($P < 0.001$) for the fleece weights and mean and variability of fd (Table 2). Bloodline 1 cut less clean wool than B2 at hogget (0.45 kg) and adult

shearings (0.9 to 1.1 kg) and grew finer fleeces at all shearings (from 0.5 μm to 1.9 μm at post weaning and third adult shearings respectively) which were of more uniform diameter. The results were consistent with the breeding objectives described for the bloodlines and agreed with the findings for post weaning fibre diameter traits reported earlier from the Macquarie data (Egerton-Warburton *et al.* 2019). The ewe bloodline effect also influenced curv at later shearings, sl at hogget and first adult shearing and ss at the hogget and the first and second adult shearings.

In agreement with Egerton-Warburton *et al.* (2019), the sire X ewe bloodline interaction was significant for cfw at the post weaning shearing, accounting for 4.6% of the phenotypic variation (Table 2), versus 1.8% in the earlier study. Previously, Mortimer and Casey (2015) had found the interaction to be not significant for both clean and greasy fleece weights, accounting for negligible amounts of phenotypic variance. Otherwise, the interaction was unimportant for fleece traits recorded at later stages, where it tended to account for less than 1% of the phenotypic variation, particularly for traits recorded at hogget and later adult shearings. For yearling Merino fleece traits recorded on the Information Nucleus flock, sire by site interaction effects have been shown to be at most moderate, accounting for 6% of the phenotypic variation in cfw (Swan *et al.* 2016).

Table 2. Significant ewe bloodline effects[1], and their estimates (deviation from bloodline 2), for post weaning to third adult fleece traits and percentage variation accounted for by sire X ewe bloodline interaction

	Post weaning	Hogget	First adult	Second adult	Third adult
Ewe bloodline effect					
gfw	0.02 (0.13)***	ns	-0.83 (0.21)***	-0.92 (0.21)***	-1.07 (0.22)***
cfw	ns	-0.45 (0.09)***	-0.87 (0.16)***	-0.89 (0.17)***	-1.07 (0.18)***
fd	-0.48 (0.24)***	-1.56 (0.25)***	-1.46 (0.26)***	-1.82 (0.29)***	-1.89 (0.32)***
fdcv	-0.21 (0.46)***	-1.81 (0.48)***	-1.14 (0.47)***	-1.67 (0.42)***	-1.32 (0.40)***
curv	ns	ns	ns	2.29 (2.25)**	5.09 (2.42)***
sl	ns	2.10 (1.43)***	0.84 (2.07)***	ns	ns
ss	ns	-3.35 (1.79)***	-6.49 (1.95)**	-3.85 (2.17)**	ns
Sire X ewe bloodline (%)					
gfw	3.6	0	1.7	0.7	0
cfw	4.2*	0.5	2.6	0.7	0
fd	1.7	0	0	0.7	0.5
fdcv	0	0	2.0	0	0
curv	0	0	0	0	0
sl	2.7	0	0	0	0
ss	0.7	0	2.5	0	0.9

[1] ns, not significant; *, $P < 0.05$; **, $P < 0.01$; ***, $P < 0.001$.

Correlations between predicted sire progeny means across the stages for each bloodline for both greasy and clean fleece weights were generally around 0.80 (Table 3). While the sire X ewe bloodline interaction was not significant for post weaning gfw, the correlation was 0.36. At this assessment, progeny of B1 ewes produced more greasy wool than progeny of B2 ewes in contrast to the trend observed across later assessments. Most sire progeny means for post weaning gfw of B1 and B2 were not significantly different from each other, but significantly different means were detected where the sire progeny means were at the higher end of the range for B1. Reasonably high correlations, usually greater than 0.70, were also estimated for mean and variability of fd across assessments. For fd, there tended to be at least half the sire means of B1 and B2 detected to be significantly different from each other.

Table 3. Correlations between predicted sire progeny means for post weaning to third adult fleece traits in 2 different ewe bloodlines

	Post weaning	Hogget	First adult	Second adult	Third adult
gfw	0.36	0.77	0.90	0.80	0.78
cfw	0.79	0.88	0.79	0.81	0.79
fd	0.77	0.90	0.86	0.79	0.71
fdcv	0.75	0.85	0.82	0.78	0.67
curv	0.72	0.87	0.82	0.90	0.86
sl	0.54	0.97	0.87	0.77	0.85
ss	0.96	0.91	0.35	0.93	0.61

CONCLUSION

Although ewe bloodline effects influenced the fleece traits across stages, sire X ewe genotype interactions were generally unimportant and accounted for minor amounts of phenotypic variation in Merino fleece traits. Rankings of sires for fleece traits would be reasonably consistent for evaluations conducted across different ewe genotypes. This study supports the methods adopted by MERINOSELECT genetic evaluations that routinely fit this interaction to account for ewe bloodline source effects (Li *et al.* 2015).

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