ACCOUNTING FOR EWE SOURCE EFFECTS IN GENETIC EVALUATION OF MERINO FLEECE TRAITS

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SUMMARY

The significance of ewe bloodline sources and their interactions with sire effects were examined for Merino fleece traits recorded on progeny of Macquarie Merino Sire Evaluation and Merino Lifetime Productivity sites. Ewe source effects significantly influenced fleece traits expressed at post weaning, hogget and adult ages. Sire x ewe genotype interactions on fleece traits across ages were generally unimportant i.e. consistent sire rankings, accounting for small amounts of the phenotypic variation (less than 2%) in the fleece traits. These results support the methods to account for these effects that are used routinely in MERINOSELECT genetic evaluations.

INTRODUCTION

Models used in MERINOSELECT genetic evaluations account for possible sire by ewe genotype effects by fitting a sire by flock-year interaction (Li *et al.* 2015). That is where the flock-year component encompasses both flock environment and ewe genotype effects (G by E and G by G respectively). The procedure removes bias from across-flock genetic evaluations and means that MERINOSELECT breeding values (ASBVs) reflect average genetic merit of sires across all environments and ewe genotypes across which they are used. Mortimer and Casey (2015) reported that sire by ewe bloodline interactions were important for some post weaning (PW) fleece traits of Merinos. However, they highlighted the need for further studies using suitable data (without confounding of sire and other effects). This paper further investigates the importance of sire by ewe bloodline source effects on the genetic evaluation of sires in fleece traits expressed at several ages. Analyses are extended to incorporate later age assessments from the Macquarie Merino Sire Evaluation (MSE) site (hogget, H, and adult, A, traits), together with PW fleece data from the 2017 and 2018 drops of Merino Lifetime Productivity (MLP) progeny from the Macquarie site.

MATERIALS AND METHODS

A detailed description of the design of the Macquarie MSE and the data collection procedures for the progeny were given by Mortimer and Casey (2015). Briefly, progeny were born in 2012 and 2013 following AI of dams drawn from 3 bloodline sources, designated as MSE1, MSE2 and MSE3. Post weaning traits were assessed at shearing at average ages of 8 (2012 drop) and 8.6 months (2013 drop). Later assessments on the 2012 drop were conducted when the sheep were 16 (H) and 25 months of age (A), with 9 months wool growth at both assessments. For the 2013 drop, H traits were assessed at 17.5 months (8 months wool growth) while A traits were assessed at 26.5 months (9 months wool growth). Traits included greasy fleece weight (GFW, kg), clean wool yield (YLD, %), 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).

Data were also available from the 2017 and 2018 drop progeny of the Macquarie MLP site (PW assessments), which is also run according to the requirements of the Australian Merino Sire Evaluation

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Association (AMSEA) (AMSEA 2018). Briefly, the progeny were born following AI mating of 15 industry sires in late 2016 and of 16 sires in late 2017 to foundation ewes sourced from commercial flocks. Two flock sources, designated as MLP1 and MLP2, represented a bloodline selected for increased wool production and body size. Three flock sources, designated as MLP3, MLP4 and MLP5, represented a dual-purpose bloodline, where selection aimed to improve wool, fertility and growth traits. Approximately 90 ewes were inseminated to each sire. All ewes were at their second or later lambing opportunity and were allocated to each sire so they were balanced across the ewe flock sources. Foundation ewes were pregnancy scanned and run in separate management groups for single and multiple bearers. Before lambing, ewes were drafted into lambing groups based on AI week and litter size (but not lambed in sire groups). Lambs were tagged approximately 14 days after the end of lambing. DNA samples, derived from ear tissue samples, were collected for determination of parentage. Lambs were weaned at an average age of 119 (2017 drop) and 99 days (2018 drop). Birth type and rearing type were inferred from dam pregnancy scan results and the DNA parentage results, which were obtained through the Australian Innovation Company. Animals were shorn for PW assessment of GFW, YLD, CFW, FD, FDCV, CURV, SL and SS at an average age of 9 months (9 months wool).

Data were available for PW fleece traits from 988 and 996 animals of the MSE for GFW and FD respectively, while 2,017 and 2,021 animals contributed data for GFW and FD respectively from the MLP project (Table 1). Similar record numbers were available at later MSE assessments.

Table 1. Descriptive statistics for fleece traits in Macquarie MSE and MLP data

Trait	Mean	SD	Range	Trait	Mean	SD	Range
GFW (kg)				*YLD (%)*			
PW MSE	3.4	0.73	1.4 - 6.0	PW MSE	68.7	4.67	52.6 - 81.0
PW MLP	3.7	0.73	1.6 - 6.1	PW MLP	63.5	7.09	38.9 - 81.8
H MSE	6.0	0.85	3.7 – 9.0	H MSE	62.8	7.20	39.8 - 78.8
A MSE	6.3	0.95	3.1 - 9.3	A MSE	73.1	4.35	52.6 - 84.0
CFW (kg)				*FD (µm)*			
PW MSE	2.3	0.53	0.9 - 4.2	PW MSE	17.1	1.25	13.6 - 23.0
PW MLP	2.4	0.51	1.0 - 4.2	PW MLP	17.2	1.38	13.1 - 22.2
H MSE	3.8	0.70	1.9 - 6.2	H MSE	19.2	1.40	14.9 - 24.5
A MSE	4.6	0.77	2.2 - 7.1	A MSE	20.0	1.39	15.8 - 25.2
FDCV (%)				*CURV (°/mm)*			
PW MSE	18.1	1.89	13.0 - 25.7	PW MSE	90.4	7.62	65.7 - 117.5
PW MLP	18.8	2.33	12.2 - 28.7	PW MLP	61.1	9.47	32.0 - 111.0
H MSE	17.1	1.93	12.0 - 25.0	H MSE	89.0	7.65	57.8 - 126.8
A MSE	16.7	1.90	11.2 - 25.5	A MSE	89.3	8.00	61.0 - 114.6
SL (mm)				*SS (N/ktex)*			
PW MSE	66.6	9.15	40.0 -96.0	PW MSE	35.4	14.09	10.1 - 73.5
PW MLP	80.0	10.08	49.0 - 120.0	PW MLP	25.0	9.08	4.0 - 61.0
H MSE	78.8	8.82	55.0 - 106.0	H MSE	61.7	13.39	10.0 - 88.9
A MSE	87.0	7.64	63.0 - 112.0	A MSE	42.2	19.70	8.3 - 88.9

For both data sources, analyses were performed using ASReml (Gilmour *et al.* 2015). Significance of fixed effects was first tested in models that fitted a random effect of sire. For the MSE data, fixed effects were as described by Mortimer and Casey (2015), while for the MLP data the fixed effects examined included ewe source within bloodline (5 sources), birth type (single, twin, triplet), rearing type (single, twin, triplet) and dam age (3, 4, 5, 6 and 7 year old at mating), as well as a management

group effect. The importance of the interaction of sire with ewe source within bloodline was tested by fitting it as an additional random effect in a second model for each trait. The interaction effect was considered significant (P<0.05) if its inclusion increased significantly the log-likelihood between models.

RESULTS AND DISCUSSION

The ewe source effect influenced significantly (P<0.05) both fleece weights, FD and CURV at PW ages in both data sets (Table 2 for MSE results, Table 3 for MLP results). The ewe source effect also influenced (P < 0.001) H and A records of the MSE progeny for these traits, as well as SS. Larger ranges in fleece weights across ewe bloodline sources at PW assessment were observed for the MLP progeny (0.70 kg for GFW; 0.31 kg for CFW) than for the MSE progeny (0.17 kg for GFW; 0.06 kg for CFW). For FD at this youngest age, the ranges across estimates were similar in both data sets. The range across estimates of ewe bloodline sources for the MSE progeny were similar at H (0.73 kg for GFW; 0.33 kg for CFW) and A (0.78 kg for GFW; 0.37 kg for CFW) assessments, but the range for adult FD was smaller than for hogget FD (1.05 versus 2.08 μm).

Table 2. Significance of ewe source effects[1] and their estimates[2] for post weaning, hogget and adult fleece traits in the Macquarie Merino Sire Evaluation site and percentage of phenotypic variation accounted for by sire x ewe bloodline interaction

	GFW	YLD	CFW	FD	FDCV	CURV	SL	SS
Post weaning traits (Source: Mortimer and Casey 2015)								
Ewe source	*	n.s.	*	***	*	***	***	n.s.
MSE2	-0.09 (0.03)		-0.06 (0.02)	0.35 (0.08)	-0.32 (0.12)	-3.10 (0.51)	3.15 (0.73)	
MSE3	0.08 (0.09)		-0.02 (0.07)	-1.25 (0.21)	-0.19 (0.34)	0.43 (1.42)	-2.44 (1.99)	
Sire x ewe bloodline (%)	0 n.s.	0 n.s.	0 n.s.	4.0 *	2.8 *	1.6 n.s.	2.5 *	2.9 *
Hogget traits								
Ewe source	***	***	***	***	***	***	***	n.s.
MSE2	-0.46 (0.07)	-0.78 (0.32)	-0.33 (005)	0.57 (0.09)	-0.65 (0.13)	-2.28 (0.50)	0.61 (0.75)	
MSE3	0.27 (0.18)	-2.63 (0.91)	-0.07 (0.13)	-1.51 (0.24)	-0.47 (036)	-0.23 (1.43)	0.33 (2.08)	
Sire x ewe bloodline (%)	1.8 n.s.	0 n.s.	0.4 n.s.	0.9 n.s.	3.3 *	0.9 n.s.	4.1 n.s.	0 n.s.
Adult traits								
Ewe source	***	***	***	***	***	***	***	n.s.
MSE2	-0.41 (0.06)	-1.09 (0.26)	-0.37 (0.04)	0.54 (0.09)	-0.65 (0.12)	-1.96 (0.52)	1.90 (0.54)	
MSE3	-0.78 (0.14)	-1.23 (0.64)	-0.12 (0.11)	-0.51 (0.21)	-1.42 (0.30)	0.57 (1.25)	4.34 (1.31)	
Sire x ewe bloodline (%)	0.3 n.s.	0 n.s.	0.5 n.s.	0 n.s.	1.8 n.s.	3.5 *	0.4 n.s.	1.0 n.s.

[1] *, P < 0.05; **, P < 0.01; ***, P < 0.001; n.s., not significant.
[2] Estimates expressed as the deviation from the MSE1 ewe source estimate for each of the MSE2 and MSE3 ewe sources. Standard errors are in brackets.

For the wool production traits at all assessment ages, sire x ewe bloodline source interactions were generally not significant and accounted for less than 2% of the phenotypic variance across both data sets (Tables 2, 3). In contrast to the findings of Mortimer and Casey (2015), the interaction was not

significant for wool quality traits at PW assessments in the MLP data, where the interaction accounted for less than 2% of the phenotypic variance for these traits. At later assessments in the MSE data, sire x ewe bloodline source interaction was significant only for FDCV at H assessment and CURV at A assessment, accounting for 3.3 to 3.5% of the phenotypic variation in these traits. Using data on yearling Merino fleece traits from the Information Nucleus flock, Swan *et al.* (2016) reported that sire by site interaction effects were small (1% of the phenotypic variation in CURV) to moderate (6% of the phenotypic variation in CFW).

Table 3. Significance of ewe source effects[1] and their estimates[2] for post weaning fleece traits in the Macquarie Merino Lifetime Productivity progeny and percentage of phenotypic variation accounted for by sire x ewe bloodline interaction

	GFW	YLD	CFW	FD	FDCV	CURV	SL	SS
Post weaning traits								
Ewe source	***	n.s.	***	***	***	*	n.s.	*
MLP2	0.70 (0.12)		0.31 (0.05)	0.69 (0.08)	0.20 (0.17)	1.34 (0.69)		0.92 (0.52)
MLP3	0.70 (0.12)		0.18 (0.05)	-0.73 (0.08)	-1.08 (0.16)	0.21 (0.67)		1.21 (0.51)
MLP4	0.22 (0.17)		0.15 (0.06)	-0.85 (0.09)	-0.91 (0.18)	-0.49 (0.76)		0.57 (0.57)
MLP5	0.68 (0.18)		0.29 (0.08)	-0.44 (0.11)	-0.25 (0.22)	2.14 (0.92)		-0.76 (0.69)
Sire x ewe bloodline (%)	1.5 n.s.	0.3 n.s.	1.8 *	0.1 n.s.	0 n.s.	0.4 n.s.	0.8 n.s.	1.8 n.s.

[1] *, $P < 0.05$; **, $P < 0.01$; ***, $P < 0.001$; n.s., not significant.
[2] Estimates expressed as the deviation from the MLP1 ewe source estimate for each of the MLP2, MLP3, MLP4 and MLP5 ewe sources. Standard errors are in brackets.

CONCLUSIONS

Sire x ewe genotype interactions were generally unimportant and accounted for minor amounts of phenotypic variation in Merino fleece traits across age expressions, indicating that rankings of the sires for fleece traits would be consistent for evaluations conducted across differing ewe genotypes. This study supports the methods adopted by MERINOSELECT genetic evaluations that routinely fit this interaction and account for ewe source effects (Li *et al.* 2015).

ACKNOWLEDGMENTS

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