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GENOMIC MODELS FOR ESTIMATING GENETIC PARAMETERS FOR LIFETIME WOOL TRAITS IN MERINO SHEEP

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SUMMARY

Lifetime production is a key driver of the profitability of Merino flocks. While the genetic control and relationships between young and adult assessments have been evaluated previously, the conclusions have not been validated using data from a progeny test design, which extensively captures lifetime data from diverse sires and ewe bases. This paper estimated genetic correlations between lifetime age stages of greasy fleece weight, fibre diameter and body wrinkle, and between the traits. The results show that assessments for these three traits made at a young age have a moderate correlation (r_g>0.6) with adult performance, however, they are genetically different from adult assessments. These results suggest measurement of adult performance is beneficial. Genetic groups derived from admixture analysis using genotypes provided a good alternative to account for population diversity when the pedigree-derived genetic groups are challenging to define accurately. Further work is required on the other important traits which determine lifetime productivity.

INTRODUCTION

The Australian Merino breed has, over time, been bred and reared under different environments and production systems leading to a significantly admixed population (Swan *et al.* 2016). A genetic evaluation system has been developed over time to drive genetic gain through selection across flocks and Merino bloodlines (MERINOSELECT) (Brown *et al.* 2007). However, since lifetime traits can be difficult and expensive to measure, genetic evaluation has been dominated by early-age preselection measurements. The Merino Lifetime Productivity project was designed to capture lifetime data on the progeny of 134 diverse industry sires for both production and visual traits, allowing a comprehensive analysis of the genetic basis of lifetime production, and current genetic improvement strategies (Ramsay *et al.* 2019). This study evaluated the results of genetic evaluation models a) using pedigree versus genotypes to define genetic relationships, and b) alternative methods of accounting for population diversity using pedigree information versus genomics, for estimating genetic parameters for lifetime wool traits and body wrinkle.

MATERIALS AND METHODS

Data. Greasy fleece weight (GFW), fibre diameter (FD) and body wrinkle (BDWR) records from 5,464 fully pedigreed Merino ewes were used for this analysis. All the ewes were genotyped with a 50k SNP chip and were the progeny of 134 sires and 4,266 dams from the Balmoral, Macquarie, MerinoLink, New England, and Pingelly sites which were involved in the Merino Lifetime Productivity (MLP) project (Ramsay *et al.* 2019). All sites provided two cohorts of ewes with lifetime data up to seven years of age, however, for ease of presentation, this analysis only considered one record for the young stage (P) and four adult measurements up to five years of age (A2 – A5). The two cohorts in each site included were: animals born in 2015 and 2016 at Balmoral,

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2016 and 2017 at Pingelly and MerinoLink, and 2017 and 2018 at Macquarie and New England sites. Table 1 shows the number of records, means and standard deviation for these traits.

Table 1. Number of records, mean and standard deviations of lifetime trait measurements for greasy fleece weight, fibre diameter and body wrinkle

Trait	Model	Records, means and standard deviation				
		P	A2	A3	A4	A5
Greasy fleece weight	Records	5414	5283	5156	4898	4587
	Mean (sd)	2.89 (0.88)	5.69 (1.77)	5.31 (1.30)	5.29 (1.28)	5.00 (1.24)
Fibre diameter	Records	5441	5294	5169	4918	4638
	Mean (sd)	16.14 (1.43)	17.84 (1.71)	17.75 (1.80)	18.07 (1.94)	18.08 (2.03)
Body wrinkle	Records	5430	4636	4459	4884	4618
	Mean (sd)	2.36 (0.82)	2.39 (0.84)	2.47 (0.91)	2.66 (0.85)	2.56 (0.82)

P – first shearing/post-weaning; A2 – 2 years old; A5 – 5 years old

Statistical analysis. Data were analysed using a linear mixed model using ASReml software (Gilmour *et al.* 2015): $y = \boldsymbol{X}\hat{\beta} + \boldsymbol{Z}_1\boldsymbol{Q}g + \boldsymbol{Z}_1 a + \boldsymbol{Z}_2 m + e$, where y was a vector of the trait measurements, $\hat{\beta}$ a vector of fixed effects, g a vector of random genetic group effects, a a vector of additive genetic effects within genetic groups for animals in the pedigree, m a vector of maternal permanent environment effects (for post-weaning or first shearing traits only), and e a vector of residual effects. $\boldsymbol{X}, \boldsymbol{Z}_1, \boldsymbol{Q}$ and $\boldsymbol{Z}_2$ were design matrices for their corresponding effects. Fixed effects included contemporary group (67 groups defined by site, year of birth and management group), birth and rearing type (9) within sites and reproduction status (6) within sites for adult stages with age of dam as a covariate. Univariate and bivariate models were used to estimate (co)variances, variance ratios and genetic correlations. Models without genetic groups (NoG), with pedigree (PedG) and genomically (GenG) derived genetic groups were used to evaluate the effect of population structure on genetic parameters. The model PedG included 205 genetic groups derived using pedigree, flock and year of birth information, while GenG included five groups derived from an admixture analysis (Alexandri *et al.* 2025) using genotyped animals in the MERINOSELECT genetic evaluation system (Brown *et al.* 2007). Genetic relationships (60k SNPs) between animals were also independently derived using the pedigree (NRM) and genotypes only (GRM) (Vanraden 2008).

RESULTS AND DISCUSSION

Heritabilities from pedigree models were consistently higher than those estimated from genomic models for all traits (Table 2). This may be due to the GRM capturing relationships by both descent and state, accounting for relationships beyond the NRM. The heritabilities for the first (P) GFW and FD assessments were lower than those at the adult stages, which was also observed by Brown *et al.* (2013). However, the heritabilities estimated with our dataset were slightly higher than those reported by Brown *et al.* (2013) most likely due to the very diverse sires used in the project. The proportion of genetic group variance relative to the genetic variance ranged between 9 – 28% (GFW), 11 – 24% (FD), and 27 – 96% (BDWR), using pedigree models, and 3 – 24% (GFW), 3 – 20% (FD) and 24 – 75% (BDWR) using genomic models. The proportion of genetic group variance increased with age stages for the wool traits and declined with age stages for BDWR. This explains the differences in heritability estimates between the models when diversity was not accounted for. The genetic group effects were lowest or not significant for the first shearing wool traits hence the similar heritabilities across models. Moderate maternal permanent environmental effects were estimated for GFW (0.12) and were low for FD (0.03) and BDWR (0.05).

Table 2. Heritabilities for greasy fleece weight, fibre diameter and body wrinkle from models using pedigree (NRM) vs genomic (GRM) relationships with no genetic groups (NoG) vs pedigree derived (PedG) and genomically derived genetic groups (GenG)

Trait	Genetic groups	NRM					GRM				
		P	A2	A3	A4	A5	P	A2	A3	A4	A5
Greasy fleece weight	NoG	0.41	0.58	0.60	0.54	0.70	0.34	0.54	0.54	0.51	0.54
	PedG	0.37	0.57	0.59	0.52	0.61	0.33	0.54	0.53	0.50	0.52
	GenG	0.41	0.60	0.60	0.54	0.64	0.34	0.54	0.52	0.49	0.52
Fibre diameter	NoG	0.72	0.81	0.85	0.81	0.88	0.61	0.71	0.71	0.68	0.68
	PedG	0.63	0.73	0.71	0.80	0.78	0.59	0.68	0.69	0.65	0.66
	GenG	0.70	0.80	0.76	0.83	0.82	0.61	0.70	0.70	0.66	0.67
Body wrinkle	NoG	0.64	0.58	0.60	0.59	0.56	0.41	0.38	0.33	0.37	0.34
	PedG	0.46	0.43	0.45	0.45	0.38	0.37	0.33	0.27	0.31	0.28
	GenG	0.51	0.47	0.51	0.52	0.49	0.36	0.35	0.31	0.36	0.32

P – post-weaning/first shearing; A2 to A5: 2 to 5 years old; standard errors (se) ranged from 0.02 to 0.07

Genetic correlations between the early measurements and adult performance for GFW, FD and BDWR were positive and moderate to high, ranging from 0.63 to 0.89 (Table 3), similar to Brown *et al.* (2013). These moderate to high genetic correlations suggest that assessments of young animals for these three traits are a good genetic predictor of adult performance. The correlations were highest for young age (P) with the first adult performance, decreasing slightly across the older stages suggesting that the first shearing (P) traits are genetically different from adult assessments, hence the need for adult measurements. The phenotypic correlations for the wool traits (0.42 – 0.69) and BDWR (0.33 – 0.38) were moderate, indicating that these traits are moderately repeatable. The genetic correlations among the adult stages (not shown) were above 0.95, indicating that adult performance across adult stages is effectively the same trait genetically. However, these correlations were not 1, suggesting that some sires could express different production trajectories over time.

Table 3. Genetic and phenotypic correlations between measurements at first shearing (P) and adult stages (2 to 5 years; A2 to A5) for greasy fleece weight, fibre diameter and body wrinkle

Trait	Genetic groups	**Genetic** (se = 0.01 to 0.07)				**Phenotypic** (se = 0.01 to 0.02)			
		A2	A3	A4	A5	A2	A3	A4	A5
Greasy fleece weight (P)	NRM-PedG	0.80	0.76	0.75	0.76	0.55	0.46	0.45	0.44
	NRM-GenG	0.78	0.71	0.70	0.70	0.55	0.45	0.44	0.43
	GRM-PedG	0.76	0.72	0.66	0.67	0.54	0.45	0.44	0.43
	GRM-GenG	0.75	0.69	0.63	0.63	0.54	0.45	0.44	0.42
Fibre diameter (P)	NRM-PedG	0.85	0.79	0.75	0.75	0.69	0.64	0.61	0.58
	NRM-GenG	0.84	0.78	0.74	0.73	0.68	0.63	0.60	0.58
	GRM-PedG	0.89	0.83	0.81	0.78	0.68	0.64	0.61	0.58
	GRM-GenG	0.88	0.83	0.80	0.77	0.69	0.64	0.61	0.58
Body wrinkle (P)	NRM-PedG	0.85	0.80	0.73	0.73	0.38	0.38	0.36	0.34
	NRM-GenG	0.78	0.69	0.66	0.68	0.37	0.37	0.35	0.34
	GRM-PedG	0.80	0.79	0.72	0.73	0.36	0.36	0.34	0.33
	GRM-GenG	0.76	0.70	0.68	0.69	0.36	0.36	0.34	0.33

PedG – pedigree-derived genetic groups; GenG – genomically derived genetic groups; se – standard error

The genetic correlations between post-weaning BDWR and GFW were positive (0.22 to 0.51), and between post-weaning GFW and FD were negative (-0.16 to -0.41) (Table 4). That is, Merino sheep with higher degree of body wrinkle tend to have moderately higher wool production and finer wool (-0.10 to -0.33). Higher wool production is also associated with higher fibre diameter, which is antagonistic to selection for higher fleece value. Index selection has been shown to accommodate this to ensure desired genetic gains for all traits included (Swan *et al.* 2016). Lower phenotypic correlations among these traits were estimated in the same directions as the genetic correlations (not shown), as in the literature (Brown *et al.* 2013). Genetic correlations within the age stages and NRM and GRM models were not significantly different. The slight differences between correlations for early stages, are difficult to explain due to the high standard errors associated with the correlations.

Table 4. Genetic correlations between body wrinkle at post-weaning and greasy fleece weight and fibre diameter (standard errors: 0.04 to 0.14)

Trait (age)	**Model**	**Genetic groups**	**Greasy fleece weight**					**Fibre diameter**				
			P	A2	A3	A4	A5	P	A2	A3	A4	A5
Body wrinkle (P)	NRM	PedG	0.22	0.41	0.24	0.20	0.22	-0.23	-0.25	-0.20	-0.27	-0.27
		GenG	0.30	0.51	0.37	0.35	0.36	-0.24	-0.19	-0.10	-0.19	-0.18
	GRM	PedG	0.33	0.41	0.34	0.27	0.26	-0.33	-0.22	-0.23	-0.21	-0.23
		GenG	0.32	0.44	0.38	0.32	0.32	-0.30	-0.20	-0.18	-0.17	-0.19
Greasy fleece weight (P)	NRM	PedG						0.41	0.34	0.29	0.25	0.29
		GenG						0.26	0.23	0.23	0.19	0.23
	GRM	PedG						0.18	0.28	0.26	0.23	0.22
		GenG						0.16	0.23	0.23	0.20	0.19

CONCLUSION

Greasy fleece weight, fibre diameter, and body wrinkle assessments conducted at a young age are moderate genetic predictors of adult performance, but are genetically different from adult assessments and highlight the importance of obtaining adult measures to accurately select for lifetime productivity. Genomic relationships derived from genotypes accounted for part of the trait variation due to diversity unaccounted for using pedigree relationships. Genetic groups derived from admixture analysis using genotypes provide a good alternative to account for population diversity when the pedigree-derived genetic groups are challenging to accurately define. Further work is required on the other important traits which determine lifetime productivity.

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