

GENETIC PARAMETERS AND LAMBDA VALUES FOR POST-WEANING PRODUCTION TRAITS IN MERINO SHEEP

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SUMMARY

Appropriate genetic parameters are essential for accurate selection of animals with improved genetic merit for economically important traits. In recent years, Merino breeders have tended to record animals earlier in life making it important to characterise post-weaning measurements. Additionally, genomic information is used in Australian Merino genetic evaluations to obtain more accurate estimations of genetic merit using single-step GBLUP, utilising a weighting factor to partition polygenic and genomic variance, hereby referred to as lambda (λ). This study aimed to estimate genetic parameters and lambda values for production traits measured at the post-weaning stage in Merino sheep. Phenotypic records were obtained at the post-weaning stage for weight (PWT), eye muscle depth (PEMD), fat depth (PFAT), greasy fleece weight (PGFW), clean fleece weight (PCFW), fibre diameter (PFD), fibre diameter coefficient of variation (PDCV), and staple length (PSL). Genetic parameters were estimated with univariate and bivariate analyses, while a genomic REML analysis was performed to calculate the lambda value for each trait. Moderate to high heritability estimates were observed, ranging between 0.25 to 0.56. Genetic correlations were moderately positive between PWT and PCFW, PGFW, PFD, and PSL and negative for PDCV. Lambda values were on average (0.64) slightly higher than the current value used for genomic evaluation ($\lambda = 0.5$) and ranged from 0.51 to 0.90. Genetic parameters reported in this study are generally consistent with previous studies and will be used to update the genetic parameters used by Sheep Genetics for the MERINOSELECT analyses.

INTRODUCTION

The Australian sheep industry has significantly improved sheep production through the establishment of breeding programs. Genetic parameters are essential to accurately estimate breeding values and to predict the genetic and economic gain of the traits in breeding programs. Previous studies have shown that heritability increases as the age of measurement increases (Brown *et al.* 2013; Mortimer 2017), raising the need to estimate genetic parameters for each relevant stage of the developmental period. Previous studies estimated genetic parameters for live weight, ultrasound fat and muscle and wool traits at different stages in Merino sheep. Heritability estimates for wool traits were moderate for the yearling, hogget, and adult stages (Greeff *et al.* 2008, Brown *et al.* 2013, Mortimer *et al.* 2017), high for ultrasound traits (Mortimer *et al.* 2017) and moderate for live weight (Greeff *et al.* 2008; Mortimer 2017). However, Sheep Genetics recently revised the methods used to classify traits to each stage and redefined more accurate intervals for birth, marking (days 1-39), weaning (days 40-149), post-weaning (days 150-299), yearling (days 300-449), hogget (days 500-659), and adult (days 660-6059). These changes influence how the data is used in the analysis and therefore, it is necessary to estimate new genetic parameters to be used especially for the post-weaning stage as more data are now available.

In recent years, more accurate estimations of the genetic merit have been achieved by including genomic information in a single-step genomic BLUP (ssGBLUP). The use of this method requires a lambda (λ) for partitioning pedigree and genomic information. Moreover, Gurman *et al.* (2021)

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reported lambda values higher than 0.5 for carcass traits were required for ssGBLUP pointing to the importance of further studies. This project aims to estimate the genetic parameters, including heritabilities, correlations and lambda values for live weight, ultrasound, and wool traits recorded at the post-weaning stage in Australian Merino sheep.

MATERIALS AND METHODS

Animals and traits recorded. Flocks with the most complete data recorded were selected from the MERINOSELECT database applying the following thresholds: age of dam known and less than 12 years; date of birth known and with multiple dates recorded within each flock and year; sex; birth type and rear type; more than 5 years of records; flocks with at least 75% of animals with full pedigree; and phenotypes recorded between 2000 and 2022. This selection resulted in 307,815 animals (Table 1) from 175 flocks with measurements at the post-weaning stage (P; between 150 to 299 days of age) for body weight (PWT; kg), live ultrasound eye muscle depth (PEMD; mm) and live ultrasound fat at the C site (PFAT; mm), greasy fleece weight (PGFW; kg), clean fleece weight (PCFW; kg), fibre diameter (PFD; μm), fibre diameter coefficient of variation (PDCV; %), and staple length (PSL; mm). Animals were the progeny of 6,748 sires and 148,420 dams with up to 5 generations of pedigree used in the analysis.

Table 1. Descriptive statistics for live weight, wool and ultrasound traits at the post-weaning stage in Merino sheep

| | PWT | PEMD | PFAT | PCFW | PGFW | PFD | PDCV | PSL |
|-----------------|---------|--------|--------|--------|--------|--------|--------|--------|
| Records | 210,832 | 60,363 | 60,148 | 77,584 | 73,755 | 44,424 | 43,233 | 23,085 |
| Genotype | 9,446 | 25,697 | 8,613 | 7,657 | 12,974 | 6,220 | 6,207 | 15,447 |
| Mean | 35.1 | 24.6 | 2.3 | 2.2 | 3.1 | 16.5 | 18.3 | 72.4 |
| SD | 4.7 | 4.3 | 0.5 | 0.4 | 0.6 | 1.0 | 2.6 | 14.3 |
| Min | 12.4 | 9.7 | 0.5 | 0.4 | 0.8 | 11.9 | 10.6 | 25 |
| Max | 63.6 | 42.7 | 5 | 4.4 | 6.7 | 21.9 | 32 | 140 |
| CV (%) | 13.5 | 17.3 | 22.2 | 19.2 | 17.9 | 6.3 | 14.4 | 19.8 |

* For the trait abbreviations, see text.

Genetic parameters. For the univariate analysis, a linear mixed animal model was fitted in ASReml v4.2 (Gilmour *et al.* 2015) with fixed effects as birth type (4 levels), rear type (4 levels), age, sex (female and male), age of dam (12 levels), contemporary groups (between 344 to 2,266 levels), and weight fitted for PFAT and PEMD. The random effects consisted of genetic groups (defined by flock and time period as per MERINOSELECT), animal genetic, maternal genetic and permanent environmental.

Genome-base restricted maximum likelihood (GREML). The variance components were estimated using only the animals with genotype information (imputed 60k SNP chip) in a univariate GREML via MTG2 software (Lee and van der Werf 2016). The model included adjusted phenotypes for fixed effects and contemporary groups, with random effects fitted for pedigree, genetic groups and genomic relationship matrices. Lambda was calculated as the ratio of $\lambda = \frac{\sigma_G}{\sigma_G + \sigma_{A22}}$; where σ_G is the genetic variance and σ_{A22} is the variance explained by the numerator relationship matrix.

RESULTS AND DISCUSSION

Genetic variances and heritabilities. Moderate to high heritabilities were estimated for live weight, ultrasound and wool traits ranging between 0.25 (0.01) and 0.56 (0.01) (Table 2). The

heritabilities for PFAT (0.25), PEMD (0.27) and PWT (0.32) were consistent with previously reported estimates for PEMD (0.20 to 0.25), PFAT (0.15 to 0.22) adjusted with weight and PWT (0.31) (Mortimer *et al.*, 2014 and 2017; Huisman *et al.* 2008). However, a lower permanent environmental effect was observed for PWT (0.05) compared with the 0.11 reported by Mortimer *et al.* (2017). The heritability estimates for post-weaning wool traits were moderate to high, ranging from 0.29 to 0.56, agreeing with the estimates reported previously at the hogget stage ranging between 0.27 to 0.60 (Greeff *et al.* 2008). Fibre diameter had a higher heritability at post-weaning (0.56; Table 2), similar to previous studies at hogget and yearly (0.60 to 0.61; Greeff *et al.* 2008; Brown *et al.* 2013) but lower than the reported by Mortimer *et al.* (2017) at the yearling stage (0.74). There was a low maternal permanent environment effect for PGFW and PCFW (0.04 to 0.05), which was also observed by Mortimer *et al.* (2017) at the yearling stage.

Table 2. Estimates of phenotypic (σ_p^2) variance, heritabilities (h^2) and ratios of maternal genetic (m^2) and maternal permanent environmental effect (Pe^2) variances, and the ratio of genetic group:additive variance ($\sigma_{GG:G}$) for live weight, wool, and ultrasound traits in Merino sheep (standard error)

| Trait | σ_p^2 | h^2 | m^2 | Pe^2 | $\sigma_{GG:G}$ |
|-------|--------------|------------|------------|------------|-----------------|
| PWT | 19.9(0.08) | 0.32(0.01) | 0.06(0.0) | 0.05(0.0) | 1.14(0.17) |
| PEMD | 3.69(0.02) | 0.27(0.01) | | | 0.18(0.08) |
| PFAT | 0.21(0.0) | 0.25(0.01) | | | 0.29(0.12) |
| PCFW | 0.15(0.0) | 0.29(0.02) | 0.03(0.01) | 0.05(0.01) | 0.27(0.08) |
| PGFW | 0.25(0.0) | 0.32(0.01) | 0.03(0.01) | 0.04(0.01) | 0.06(0.07) |
| PFD | 1.11(0.01) | 0.56(0.01) | | | 0.37(0.1) |
| PDCV | 4.3(0.03) | 0.29(0.01) | | | 0.04(0.04) |
| PSL | 69.45(0.82) | 0.47(0.02) | | | 0.65(0.21) |

* For the trait abbreviations, see text.

Table 3. Phenotypic (below diagonal) and genetic (above diagonal) correlations between live weight, wool and scan traits in Merino sheep

| | PWT | PEMD | PFAT | PCFW | PGFW | PFD | PDCV | PSL |
|------|-------|-------|-------|-------|-------|-------|-------|-------|
| PWT | | -0.03 | 0.05 | 0.21 | 0.23 | 0.25 | -0.17 | 0.14 |
| PEMD | 0.12 | | 0.48 | -0.13 | -0.13 | 0.09 | -0.16 | 0.12 |
| PFAT | 0.12 | 0.32 | | -0.17 | -0.16 | 0.12 | -0.29 | 0.06 |
| PCFW | 0.45 | -0.02 | -0.09 | | 0.89 | 0.38 | 0.11 | 0.55 |
| PGFW | 0.42 | -0.01 | -0.03 | 0.91 | | 0.34 | 0.08 | 0.40 |
| PFD | 0.21 | 0.07 | 0.11 | 0.25 | 0.26 | | -0.13 | 0.26 |
| PDCV | -0.13 | -0.09 | -0.09 | -0.01 | 0.02 | -0.10 | | -0.11 |
| PSL | 0.17 | 0.07 | 0.07 | 0.32 | 0.30 | 0.25 | -0.12 | |

* For the trait abbreviations, see text. Standard errors ≤ 0.01 and 0.02 to 0.05 for phenotypic and genetic correlations, respectively.

Genetic and phenotypic correlations. Among the wool traits, PGFW and PCFW were highly genetically correlated (0.89), while PGFW had a small genetic correlation with PDCV (0.08). Moderate and positive genetic correlations were observed between PWT with PCFW (0.21),

PGFW (0.23), and PFD (0.25), whereas PWT was negatively correlated with PDCV (-0.17). These genetic correlations suggest that selection for higher live weight will result in an increase in PCFW, PGFW and PFD, but a decrease in PDCV. Mortimer *et al.* (2017) reported higher genetic correlations between PWT with yearling GFW (0.46), CGW (0.46) and SL (0.21). Ultrasound traits (PEMD and PFAT) had moderate phenotypic (0.32) and genetic (0.48) correlations. Low negative genetic correlations were observed between ultrasound traits and PCFW, PGFW and PDCV, consistent with the negative correlations observed by Mortimer *et al.* (2014) and Huisman and Brown (2009) between yearling GFW and PFAT (-0.26 to -0.48) and PEMD (-0.06 to -0.26). The phenotypic correlations were higher for PWT with the other traits but lower for ultrasound and wool traits.

Genomic REML. Heritability and lambda values were also estimated for all traits (Table 4). Lambda values averaged 0.70 but ranged from 0.51 to 0.90. Heritabilities ranged from 0.28 to 0.56 for the traits slightly differing from the heritabilities estimated from the pedigree models. Overall, these results suggest that lambda of $\lambda = 0.5$ used in the routine analyses could be adjusted slightly, but this needs to be investigated further for a greater range of traits.

Table 4. Estimation of heritabilities, phenotypic variances and lambda for live weight, wool and scan traits in Merino sheep

| Trait | PWT | PEMD | PFAT | PCFW | PGFW | PFD | PDCV | PSL |
|----------------------|-------|------|------|------|------|------|------|-------|
| Lambda | 0.66 | 0.67 | 0.76 | 0.51 | 0.62 | 0.86 | 0.90 | 0.62 |
| σ_p^2 | 13.24 | 4.21 | 0.14 | 0.12 | 0.21 | 1.06 | 4.52 | 66.19 |
| h² | 0.34 | 0.28 | 0.33 | 0.44 | 0.47 | 0.56 | 0.30 | 0.39 |

* For the trait abbreviations, see text. σ_p^2 : phenotypic variance; h²: heritability.

CONCLUSIONS

This study provides estimates of genetic parameters and correlations between economically essential traits such as live weight, wool, and ultrasound traits at a post-weaning stage. The genetic parameters described in this study can be incorporated into the routine evaluation. Lambdas differed from 0.5, indicating that further research will be needed to investigate new strategies to incorporate this information in the ssGBLUP analysis, its impact on prediction accuracies and its use for multi-breed evaluations.

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