

# Impact of ewe genotype on sire breeding values in genetic evaluation of Merino visual traits

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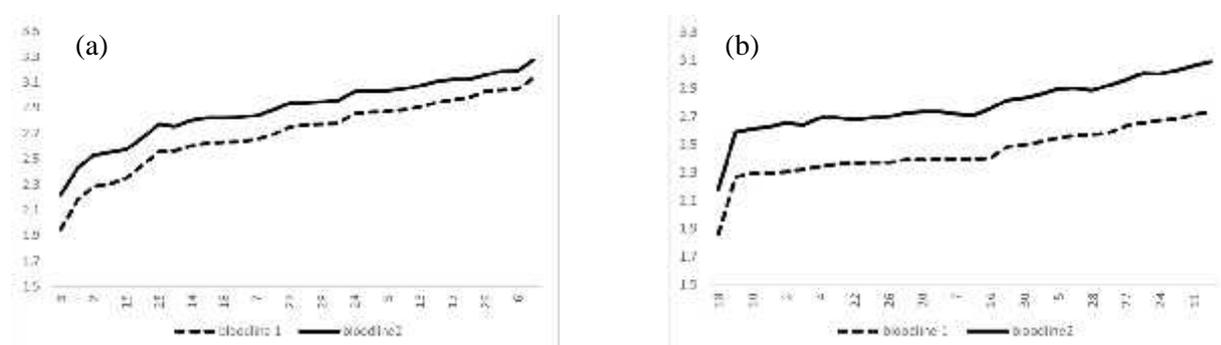
Merino ram breeders often place significant emphasis on visually assessed fleece traits within their breeding programs. There are concerns among Merino breeders that anecdotally Australian Sheep Breeding Values (ASBVs) of sires do not always predict performance when sires are used in a different genetic background, or in other words, when joined to different ewe genotypes (often referred to as “bloodlines”). Egerton-Warburton *et al.* (2019) reported that sire rankings for fleece traits were consistent across ewe genotypes, and that sire x ewe genotype interactions accounted for less than 2% of phenotypic variation.

Using data collected from the Merino Lifetime Productivity (MLP) progeny run at the Trangie Agricultural Research Centre (a co-investment with AWI and AMSEA), this study evaluated the relationship between predicted sire progeny means for visually assessed fleece traits recorded in progeny from mating’s to two different ewe bloodlines. A multivariate method (Gilmour *et al.* 2015) where the expressions within the progeny of each ewe bloodline were treated as individual traits was employed. With sires fitted as random effects, the correlation between sire effects is an estimate of the genetic correlation between performance in each bloodline. Visual traits included wool colour (COL), staple structure (SSTRC), wool character (CHAR) and body wrinkle (BDWR) and were collected on progeny born in 2017 and 2018. Visual scores were collected at post-weaning, hogget and adult age stages. Data structures were described by Egerton-Warburton *et al.* (2019). The analysis accounted for fixed effects of sex (body wrinkle only), birth type, rearing type and management group whilst fitting a random sire effect. Adult expressions were adjusted for reproduction (conception).

Estimated genetic correlations between ewe bloodlines were generally greater than 0.90 (Table 1; Figure 1).

**Table 1. Correlations ( $\pm$  SE) estimated between visual fleece traits assessed in two different ewe bloodlines.**

	COL	SSTRC	CHAR	BDWR
Post-weaning	0.94 $\pm$ 0.30	0.96 $\pm$ 0.27	0.99 $\pm$ 0.48	0.99 $\pm$ 0.05
Hogget	0.92 $\pm$ 0.13	0.88 $\pm$ 0.24	0.98 $\pm$ 0.14	0.97 $\pm$ 0.10
Adult	0.97 $\pm$ 0.29	0.97 $\pm$ 0.41	0.98 $\pm$ 0.29	0.97 $\pm$ 0.18



**Figure 1. Predicted sire progeny means at the post-weaning stage for each ewe bloodline for (a) body wrinkle and (b) staple structure.**

When sires were joined to these ewe bloodlines, their progeny generally maintained their relative ranking across a range of objective and visual wool traits, and across the age stages. This investigation of genotype x genotype interaction within an environment has demonstrated that limited re-ranking occurs across ewe bloodlines for visual wool traits. These results suggest that Australian Sheep Breeding Values for these traits will reliably predict performance when sires are mated to ewes from different genetic backgrounds.

## References

Egerton-Warburton KL, Mortimer SI and Swan AA (2019) Proceedings of the Association for the Advancement of Animal Breeding and Genetics. 23, 520-523.

Gilmour AR, Gogel BJ, Cullis BR, Welham SJ and Thompson R (2015) ‘ASReml User Guide Release 4.1 Functional Specification’. VSN International Ltd, Hemel Hempstead, UK.

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