

## Could faecal moisture score be used to help select against DAG score in sheep?

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Daginess in sheep is undesirable with the most important reason being increased risk of flystrike and subsequent management costs. Genetic selection against daginess is possible by recording dag score on animals and using resultant ASBVs to guide selection. However additional correlated trait information could add strength to genetic evaluation of animals for dag especially if the correlated trait is closely linked genetically. One potentially correlated trait is faecal moisture, as this is likely to affect the formation of dag in sheep. Faecal moisture is often scored when worm egg counts are performed and could also be assessed in animals not fully expressing dag due to environmental conditions. This study will assess the genetic relationship between dag score and faecal moisture score in Australian Sheep.

Phenotypes for daginess (dag) and faecal moisture (fmoist) were taken from animals in the Information Nucleus and MLA Resource Flocks (Van der Werf *et al.* 2010) from 2007-2018. Faecal moisture is a subjective score assessed on a 1 (normal pellets) to 5 (extremely watery) scale (Le Jambre *et al.* 2007). The breeds represented in the dataset include Merino, Dohne, Corriedales, South African Meat Merinos, Maternal and Terminals. Genetic parameters were estimated across weaning (W) and yearling (Y) stages through a series of bivariate analyses for all animals irrespective of breed and for a subset of the data including only Merino and Dohne progeny. Data were analysed using the ASReml software package (Gilmour *et al.* 2015).

Results for the analyses are presented below in Table 1 for all animals and for the Merino and Dohne subset. Heritability for the traits are slightly higher in the Merino and Dohne subset analysis compared to the all animals' analysis, and the dag traits are higher than the faecal moisture traits. For the Merino and Dohne Subset within age stage genetic correlations are very high between fmoist and dag 0.81 at weaning and rising to 0.91 at the yearling stage even across age stage the correlations remain high for example weaning moisture and yearling dag is 0.75.

Trait	n	$\sigma_p^2$	$h^2$	Sofa	Wdag	Wfmoist	Ydag	Yfmoist
<b>Merino and Dohne Subset</b>								
Wdag	8688	0.63(0.01)	0.16(0.02)	0.01(0.02)		0.22(0.01)	0.15(0.02)	0.09(0.02)
Wfmoist	11039	0.87(0.01)	0.11(0.01)	0.02(0.01)	0.81(0.10)		0.12(0.01)	0.15(0.02)
Ydag	6346	0.68(0.01)	0.16(0.02)	0.06(0.02)	0.60(0.13)	0.75(0.13)		0.20(0.02)
Yfmoist	3805	0.61(0.01)	0.13(0.02)	0.03(0.02)	0.65(0.16)	0.93(0.15)	0.91(0.16)	
<b>All Animals</b>								
Wdag	20528	0.61(0.01)	0.12(0.01)	0.03(0.01)		0.24(0.01)	0.15(0.01)	0.08(0.01)
Wfmoist	27058	0.85(0.01)	0.10(0.01)	0.03(0.01)	0.95(0.07)		0.12(0.01)	0.12(0.01)
Ydag	7980	0.65(0.01)	0.14(0.02)	0.05(0.02)	0.66(0.12)	0.74(0.12)		0.20(0.01)
Yfmoist	6254	0.60(0.01)	0.12(0.02)	0.03(0.02)	0.72(0.15)	0.95(0.14)	0.96(0.15)	

**Table 1: Number of records (n), phenotypic variance ( $\sigma_p^2$ ), direct heritability ( $h^2$ ) and sire by flock (SxF) ratio with phenotypic correlations (above the diagonal) and genetic correlations (below the diagonal). Standard errors in parenthesis.**

It should be noted that the heritability of the dag traits in this study are slightly lower than those observed in other Australian studies (Brown *et al.* 2010). Being able to utilise the trait fmoist that is recorded for another purpose could provide in the case of merinos between 15,000-20,000 records a year to improve breeding values for dag traits. Given this and the strong correlations especially within stage between dag and fmoist, faecal moisture would provide additional information to help select against DAG and could be considered as a possible new trait for ASBVs estimation. However further research is required to understand the best time to record the trait and understand correlations with other traits important to Australian sheep breeding objectives.

### References

- Brown DJ, Swan AA and Graser HU (2010) *Proceedings of the World Congress on Genetics Applied to Livestock Production*
- Gilmour AR, Gogel BJ, Cullis BR, Welham SJ and Thompson R (2015) 'ASReml User Guide Release 4.1' (VSN International Ltd: Hemel Hempstead)
- Le Jambre LF, Dominik S, Eady SJ, Henshall JM and Colditz IG (2007). *Veterinary Parasitology* 145, 108-115
- Van der Werf JHJ, Kinghorn BP and Banks RG (2010) *Animal Production Science* 50, 998-1003