

Genotype by environment interaction for Merino sheep in New Zealand and Australia for a range of traits.

A.J. McMillan¹, M.B. Ferguson² & D.J. Brown¹

¹*Animal Genetics Breeding Unit*, University of New England, New South Wales, Australia
amcmill4@une.edu.au (Corresponding Author)*

²*The New Zealand Merino Company Limited, Christchurch, New Zealand*

Summary

In this study, we examined the significance of genotype by environment interactions for Merino type animals under Australian and New Zealand production systems, for a range of traits, with data sourced from the MERINOSELECT database. Bivariate analysis of traits between Australia and New Zealand with the genetic correlations giving an estimate of genotype by environment interaction. Models with and without sire by flock-year effects was examined to address practical problems associated with Industry data. The variance components and heritabilities were generally similar between both countries and between models including and excluding sire by flock-year effect. Genetic correlations were generally high between countries when sire by flock-year effect was fitted with only three of the traits having correlations < 0.8. These traits were yearling clean fleece weight (0.56 ± 0.22), yearling greasy fleece weight (0.74 ± 0.12) and yearling fibre diameter (0.73 ± 0.09), however, only ycfw was actually < 0.8 based on standard errors. By accounting for the sire by flock-year effect, genetic correlations for traits between Australia and New Zealand increased. With the high level of genetic correlation between countries, ram breeders can use MERINOSELECT ASBVs to select animals regardless of the country in which those animals were born.

Keywords: sire by flock-year interactions, international evaluation

Introduction

Genotype by environment interaction occurs when genotypes are expressed differentially in environments, with either re-ranking of merit or differential expression between environments without re-ranking. In terms of genetic evaluation of animals, re-ranking is of particular concern because selection decisions are compromised, especially if the re-ranking is large (Falconer, 1981).

Genotype by environment interactions are often considered biologically important when the genetic correlation is less than 0.8 (Robertson, 1959). However at that threshold it should be noted that 20% of potential genetic gain could be lost if relatives have no performance across environments with that falling to 10% and 4% with the recording of half-sibs and progeny respectively (Mulder *et al.*, 2005). Genotype by environment interaction has previously been examined across most of the major livestock species including cattle, sheep and pigs for a wide

* AGBU is a joint venture of NSW Department of Primary Industries and University of New England

variety of traits using a variety of methods (Hayes *et al.*, 2016).

The MERINOSELECT analysis (Brown *et al.*, 2007) contains data for animals with performance recorded under a range of environments. While the majority of animals in this data are recorded in Australia over the last decade, over 150,000 animals have been recorded in ram breeding flocks from New Zealand and the potential for genotype by environment interaction was investigated using the approach by Falconer (1952). Ten traits from the MERINOSELECT database were investigated including; weaning weight (wwt), yearling fat (ycf), yearling eye muscle depth (yemd), yearling greasy fleece weight (ygf), yearling clean fleece weight (ycfw), yearling fibre diameter coefficient of variation (ydcv), yearling curvature (ycuv), yearling staple length (ysl), yearling fibre diameter (yfd) and number of lambs weaned (nlw).

Data

Pedigree and performance data were extracted from the Sheep Genetics MERINOSELECT database (Brown *et al.*, 2007). This database consists of pedigree and performance records submitted by Australian and New Zealand Merino ram breeders and is used for industry genetic evaluation purposes. The database also contains information from the Sheep CRC Information Nucleus Flock (Fogarty *et al.*, 2007), MLA Resource Flocks and the New Zealand Merino Central Progeny Test flock (Walkom *et al.*, 2017).

From these data, all animals which have a sire which is a New Zealand Merino type animal within 4 generations and born since 1990 were included. Data were extracted from the database for traits of interest with contemporary groups transformed to a common mean within each group as is routine for Sheep Genetic analyses (Brown *et al.*, 2007). Two traits were generated, one for animals with records in Australia and a second for those recorded in New Zealand.

The pedigree was built using all ancestral information available. This resulted in pedigree files comprising between 64,088 and 387,321 animals for the dataset depending on the trait being analysed. A summary of the number of records available for each trait and sire in across country is shown in Table 1. Trans-Tasman sires are sires which have progeny in both countries. Australian son used in New Zealand are sires which don't have a New Zealand Merino sire but have progeny in New Zealand but not in Australia. Conversely, New Zealand Sons used in Australia are sires which have a New Zealand Merino Sire and have progeny in Australia but not New Zealand.

Parameters were estimated in a bivariate animal model analyses for each trait in ASReml (Gilmour *et al.* 2006), with Australian and New Zealand performance considered as two separate traits. For all traits, the fixed effects of contemporary group, birth type, rearing type, age of dam, and animal's age at measurement were fitted. For carcass traits, the fixed effects of contemporary group and the animal's live weight at measurement (as quadratic) were fitted. The contemporary group was defined as flock, year of birth, sex, date of measurement, management group subclass. A random term for the direct genetic effects was modelled for all traits. A maternal genetic effect and permanent environment effect were also fitted as random for the weight and fleece weight traits. Additionally, a second set of parameters were estimated with the inclusion of the random term for sire by flock-year. This term is used routinely in the Sheep Genetics evaluations (Brown *et al.*, 2007) as including this term provides significant improves to the fit of the models for traits especially with the use of industry data where data recording and structure are often not optimal.

Table 1. Summary of the records used by trait and a breakdown of Sire usage across country

| Trait | Records | | n | Trans Tasman Sires | | Aus Son Used in NZ | | NZ Son Used in Aus | |
|-------------|---------|--------|----|--------------------|---------|--------------------|--------|--------------------|------|
| | Aus | NZ | | Aus Prog | NZ Prog | n | Prog | n | Prog |
| wwt | 304,051 | 64,694 | 57 | 18,647 | 6,128 | 404 | 26,650 | 3 | 49 |
| ycf | 71,457 | 6,346 | 32 | 2,971 | 898 | 170 | 3,174 | 0 | 0 |
| yemd | 71,639 | 6,984 | 32 | 2,918 | 905 | 173 | 3,243 | 0 | 0 |
| ygfw | 214,418 | 77,325 | 73 | 16,400 | 6,024 | 663 | 33,511 | 5 | 43 |
| ycfw | 113,845 | 43,425 | 37 | 6,618 | 2,521 | 380 | 16,713 | 4 | 68 |
| ydcv | 214,941 | 69,076 | 64 | 15,278 | 5,286 | 588 | 29,080 | 4 | 41 |
| ycuv | 154,158 | 14,175 | 19 | 3,564 | 694 | 193 | 6,500 | 4 | 90 |
| ysl | 67,601 | 47,862 | 34 | 3,581 | 2,638 | 399 | 19,531 | 1 | 22 |
| yfd | 218,247 | 76,124 | 69 | 16,262 | 5,759 | 658 | 32,737 | 4 | 41 |
| nlw | 48,460 | 24,608 | 21 | 2,116 | 1,200 | 291 | 7,587 | 2 | 23 |

Results and Discussion

Genetic parameters estimated for Australian and New Zealand animals for the model including sire by the flock-year term are presented in Table 2. Genetic parameters for the model excluding the sire by flock-year term were not significantly different, except for the genetic correlations which are presented below for both models.

Differences in phenotypic variance between countries can be seen for some traits and are most pronounced for ysl. The reason for this difference could be due to the presence of some crossbred animals in the New Zealand data which have much longer fleece than pure breeds. An analysis run on a reduced dataset excluding all but Merino animals for the staple length trait resulted in similar genetic parameter estimates for both countries with a reduced phenotypic variance for New Zealand animals and a slightly increased genetic correlation (but not significantly so results not presented).

Heritability estimates between countries for this dataset are in general similar with some small differences seen for specific traits.

Sire by flock-year effect estimates shows no difference between the Australian and New Zealand. With the effect being between 1% and a 7%, although standard errors were large and generally larger for New Zealand than for Australia. While sire by flock-year effects was generally small, not including them in the model had a large impact on genetic correlation estimates. The Sire by flock-year term helps to deal with non-genetic factors such as preferential treatment of animals and data with sub-optimal data structures which are present in industry data. Four of the traits, wwt, ydcv, ysl and yfd had significantly different estimates resulting in a reduced genetic correlation when sire by flock-year effect was ignored.

Table 2. Summary of phenotypic variance (σ^2_p), heritability (h^2) and sire by flock year (S^2) for the model containing a sire by flock-year term (s.e. in parenthesis). Genetic correlations (r_g) are presented for models with (S^2) and without the sire by flock-year term (No S^2).

| | σ^2_p | | h^2 | | S^2 | | r_g | |
|-------------|------------------|-------------------|----------------|----------------|----------------|----------------|----------------|----------------|
| | Aus. | N.Z. | Aus. | N.Z. | Aus. | N.Z. | S^2 | No S^2 |
| wwt | 19.75 (0.45) | 21.39 (1.39) | 0.31 (0.02) | 0.26 (0.07) | 0.05 (0.02) | 0.07 (0.07) | 0.92 (0.08) | 0.49 (0.12) |
| yfc | 0.29 (0.00) | 0.27 (0.02) | 0.16 (0.01) | 0.19 (0.06) | 0.03 (0.01) | 0.01 (0.06) | 0.88 (0.21) | 0.83 (0.17) |
| yem | 4.51 (0.06) | 3.72 (0.07) | 0.21 (0.02) | 0.33 (0.03) | 0.03 (0.01) | 0.02 (0.02) | 0.93 (0.11) | 0.90 (0.09) |
| d | | | | | | | | |
| ygfw | 0.43 (0.01) | 0.40 (0.02) | 0.21 (0.03) | 0.16 (0.06) | 0.06 (0.03) | 0.06 (0.06) | 0.74 (0.12) | 0.63 (0.09) |
| yfcw | 0.25 (0.01) | 0.25 (0.02) | 0.18 (0.04) | 0.13 (0.10) | 0.04 (0.04) | 0.05 (0.10) | 0.56 (0.22) | 0.40 (0.16) |
| ydcv | 5.34 (0.07) | 3.81 (0.11) | 0.29 (0.01) | 0.38 (0.03) | 0.02 (0.01) | 0.01 (0.03) | 0.93 (0.05) | 0.83 (0.07) |
| ycuv | 100.09 (3.80) | 119.81 (16.34) | 0.28 (0.04) | 0.27 (0.14) | 0.02 (0.04) | 0.01 (0.14) | 0.84 (0.16) | 0.82 (0.14) |
| ysl | 112.35 (5.02) | 204.19 (18.55) | 0.26 (0.05) | 0.22 (0.09) | 0.05 (0.04) | 0.03 (0.09) | 0.88 (0.12) | 0.60 (0.14) |
| yfd | 1.75 (0.06) | 2.44 (0.22) | 0.40 (0.03) | 0.34 (0.09) | 0.03 (0.03) | 0.03 (0.09) | 0.73 (0.09) | 0.62 (0.10) |
| nlw | 0.40 (0.00) | 0.41 (0.01) | 0.04 (0.01) | 0.06 (0.03) | 0.01 (0.01) | 0.01 (0.03) | 0.97 (0.38) | 0.86 (0.35) |

Not accounting for the sire by flock-year effect would lead to wwt, ygfw, ysl and yfd all being considered to have a biologically significant genotype by environment interaction. However, when sire by flock-year is included in the model, only yfcw shows a biological important genotype by environment interaction with most traits either greater than 0.8 or not different than unity.

Conclusions

Yearling clean fleece weight had a biologically important genotype by environment interaction that would lead to re-ranking or re-scaling of animals between environments, although the standard error was high. For all the other traits investigated, by accounting for the sire by flock-year effect resulted in higher genetic correlations between countries. This allows ram breeders

regardless of location to select animals based on MERINOSELECT ASBVs without needing to be concerned about problems associated with genotype by environment interaction.

Acknowledgements

This work was funded by Meat and Livestock Australia, Australian Wool Innovation, the Cooperative Research Centre for Sheep Industry Innovation, made possible through the support of the Australian sheep industries. The authors acknowledge the contributions of the Sheep CRC Information Nucleus, MLA Resource Flock, the Australia Merino Sire Evaluation Association and industry-funded research flocks. The authors also wish to acknowledge the contribution of New Zealand Merino staff for the development and management of the Central Progeny Test. The New Zealand Merino Incorporated and ministry for primary industries for the funding of the central progeny test. The authors also wish to acknowledge the industry flocks from both countries for their contribution of phenotypes and pedigree information without which this work could not be carried out.

List of References

- Brown, D.J., Huisman, A.E., Swan, A.A., Graser, H-U, Woolaston, R.R., Ball, A.J., Atkins, K.D. & Banks, R.G. 2007. Genetic evaluation for the Australian sheep industry. Proc. Conf. Assoc. Anim. Breed. Genet. 17:187–194.
- Brown, D.J., Swan, A.A., Boerner, V., Li, L., Gurman, P.M., McMillan, A.J., Van der Werf, J.H.J., Chandler, H., Tier, B., & Banks, R.G. 2018. Single step genetic evaluations in the Australian sheep industry. Proc 11th World Congr Genet Appl Livest Prod.
- Falconer, D.S., 1952. The Problem of Environment and Selection. The American Naturalist. (86): 293-298.
- Falconer, D. S., 1981. Introduction to Quantitative Genetics, Ed. 2. Longmans Green, London/New York. 340pp.
- Gilmour A.R., Gogel B.J., Cullis B.R. and Thompson R. (2009) ASReml User Guide Release 3.0
- VSN International Ltd, Hemel Hempstead, HP1 1ES, UK.
- Hayes, B. J., Daetwyler, H. D., Goddard, M.E. 2016; Models for Genome X Environment Interaction. Examples in Livestock. Crop Science 56
- Mulder, H. A. and Bijma, P. 2005; Effects of genotype x environment interaction on genetic gain in breeding programs. Journal of Animal Science (83): 49-61.
- Robertson, A. 1959. The Sampling Variance of Genetic Correlation Coefficient. Biometrics 15
- Walkom, S.F., Ferguson, M.B., Gibson, W., Brown, D.J., & Bunter, K.L. 2017; Accommodating variable disease challenge on breeding value prediction for sires – using footrot as an example. Proc. Ass. Adv. Anim. Breed. Genet. 22.