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GENOTYPING REDUCES PRESELECTION BIAS ON MERINOSELECT ASBVS IN MERINO FLOCKS

B.E. Clarke[1], D.J. Brown[2], P. Bradley[3] and A.A. Swan[2]

[1] Centre for Animal Production and Health, Murdoch University, Murdoch, WA, 6150
Australia
[2] Animal Genetics Breeding Unit*, University of New England, Armidale, NSW, 2351
Australia
[3] Meat and Livestock Australia, University of New England, Armidale, NSW, 2351 Australia

SUMMARY

Preselection of breeding animals to reduce the costs of phenotyping can lead to selection bias resulting in the loss of accuracy of Australian Sheep Breeding Values (ASBVs). This paper used a subset of data from the MERINOSELECT database to quantify the effects of selection bias in flocks with varying methods of preselection including random and selected phenotyping both with and without genotype information. Results show that genotyping all animals in combination with phenotyping the top 50% of animals based on genotype provided the most accurate individual and sire ASBVs. However, whilst this was the most accurate scenario, it still involved loss of ASBV accuracy and selection bias that varied according to trait when compared with the current model that includes genotyping and measuring all animals prior to selection.

INTRODUCTION

Accuracy of Australian Sheep Breeding Value (ASBV) prediction has increased with the implementation of single step genomic BLUP, with the largest increases in accuracies coming from genotyped animals (Brown *et al.* 2018). The MERINOSELECT analysis has seen an exponential increase in the number of genotypes since the introduction of single step genomic BLUP, with more than half of the 2023 born animals entering the analysis with a genotype. This increased uptake of genomics has led to higher costs for Merino ram breeders. To maintain a large selection pool, breeders produce and evaluate significantly more animals than are necessary for sale or breeding purposes. One approach to reducing both phenotyping costs and the costs associated with raising animals until phenotyping, is to preselect animals using either limited phenotype data or genomic information (Jibrali *et al.* 2020). While this preselection reduces the need to measure all animals from a cohort, it may also limit the information available for evaluating the preselected animals later, which can result in selection bias (Jibrila *et al.* 2021). The objective of this study was to establish the correlations between ASBVs calculated with different levels of phenotype and genotyping recording as well as to quantify the loss of selection advantage with differing levels of preselection within Merino flocks.

MATERIALS AND METHODS

Data. To quantify the effects of selection bias, a reduced dataset was extracted from the MERINOSELECT database. Extracted data came from 13 Merino flocks with a high proportion of genotyping. This resulted in a dataset of 273,896 animals of which 77,780 animals had genotypes.

Analyses. ASBVs were calculated for all animals in the extract using single-step genomic BLUP (ssGBLUP) methodology from the routine MERINOSELECT analysis (Brown *et al.* 2018). The dataset was then edited by taking out the 2023 drop of animals one flock at a time and removing

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different combinations of phenotype and genotype data and rerunning the ssGBLUP. Analyses were carried out on a subset of 15 traits from which four key traits, with the most data and covering all trait categories, are reported in the results (yearling weight, yearling eye muscle depth, yearling greasy fleece weight and yearling fibre diameter).

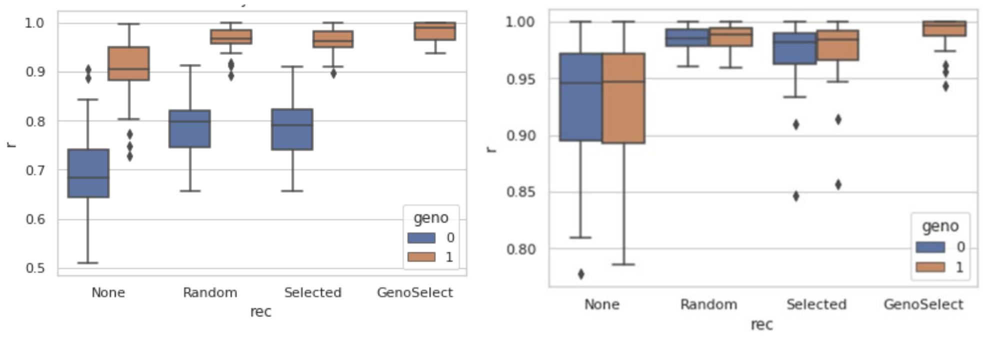
The following scenarios examined included different levels of phenotypic recording both with (geno = 1) and without (geno=0) genotyping on the 2023 drop.

1. None – no phenotype recording of animals
2. Random – phenotype recording of a random 50% of animals
3. Selected – phenotype recording the heaviest 50% of animals at weaning
4. GenoSelect – phenotype recording the top 50% of animals based on their ssGBLUP midparent value for the Merino Production Plus index (MP+).

The full MERINOSELECT analysis of the 13 Merino flocks was assumed to provide the true breeding value (TBV) for these comparisons. Correlations were calculated between the TBV and estimated ASBVs for both individual animals born in 2023 and the sires of these animals. Comparisons were also made between the bias in mean ASBV compared to the TBV as well as the proportion of selection advantage (difference between average of flock and top 10% of flock) achieved relative to the full analysis across all flocks.

RESULTS AND DISCUSSION

Correlations. The correlations between ASBVs calculated with different levels of recording and an animals TBV varied from 0.70 to 0.98 depending on the level of recording and whether genotype information was included (Figure 1a) when averaged across all flocks and all traits. Correlations between individual ASBVs and TBVs varied by trait (Figure 2), but each scenario had a similar range. The impact of different levels of recording on the ASBVs of sires of the 2023 drop was less, with the range reducing to 0.93-0.99 (Figure 1b). This again varied by trait (Figure 2) with no phenotype recording having the largest impact. The impact of genomic information was also reduced on the sires ASBVs across all traits and within individual traits. There was an advantage by the addition of genotype data to all the phenotype only scenarios in correlations between individual TBVs and ASBVs for all 15 traits and for the four yearling traits (Figures 1a and 2). This advantage was not evident in the sire TBV and ASBV correlations (Figure 1b).



(a) (b)

Figure 1. Correlations (r), with standard errors, between ASBVs and True Breeding Values calculated with four different data recording scenarios (rec) that either include (geno = 1) or don't include (geno = 0) genotype information across 13 Merino flocks and 15 traits for both individuals (a) and sires (b)

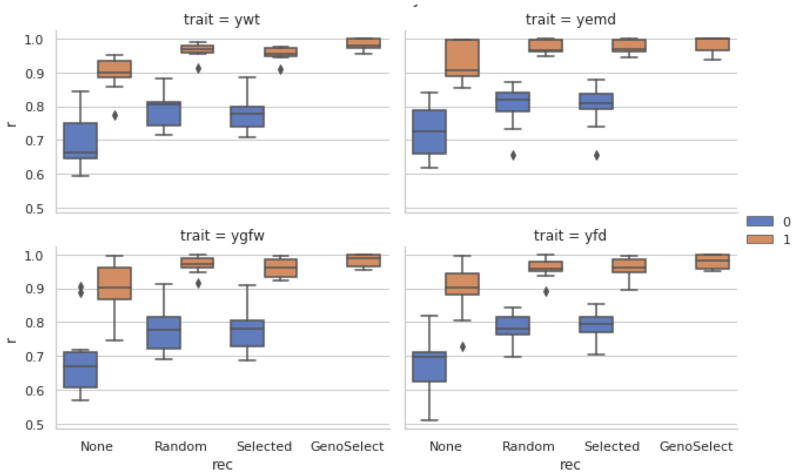


Figure 2. Correlations (r), with standard errors, between individual ASBVs and True Breeding Values calculated with four different data recording scenarios (rec) that either include (geno = 1) or don't include (geno = 0) genotype information across 13 Merino flocks for four yearling traits: weight (ywt), eye muscle depth (yemd), greasy fleece weight (ygfw) and fbre diameter (yfd)

Bias in mean ASBV. The bias in ASBVs estimated for individuals (Figure 3) varied by trait, with genotyping have a large impact on reducing both the range and average bias in individual ASBVs. This trend was the same for bias in mean sire ASBVs.

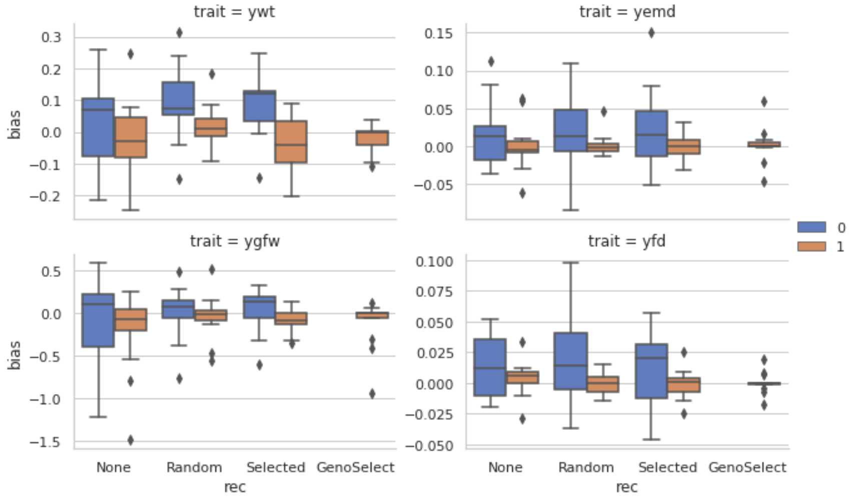


Figure 3. Bias in mean individual ASBVs from the full analysis across all flocks, with standard errors, between ASBVs and True Breeding Values calculated with four different data recording scenarios (rec) that either include (geno = 1) or don't include (geno = 0) genotype information across 13 Merino flocks for four yearling traits: weight (ywt), eye muscle depth (yemd), greasy fleece weight (ygfw) and fbre diameter (yfd)

Selection advantage. In all scenarios tested, genotyping allowed for above 90% of the selection advantage of the full analysis to be realised (Figure 4). The impact of genotyping was greater for the no phenotype scenario than for reduced phenotyping and no genotyping. Preselection based on genotype information (GenoSelect) achieved the highest proportion of selection advantage which has been shown to be due to the genotypes of preculled animals helping to more accurately reduce the bias caused by selected animals being a better-than-average subset (Jibrali *et al.* 2021).

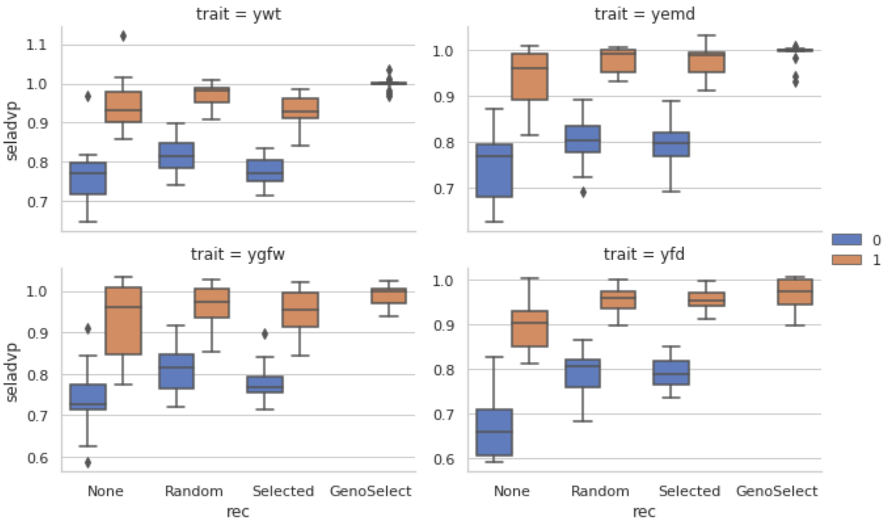


Figure 4. Proportion of selection advantage (seladvp) achieved relative to the full analysis across all flocks, with standard errors, for four different data recording scenarios (rec) that either include (geno = 1) or don't include (geno = 0) genotype information across 13 Merino flocks for four yearling traits: weight (ywt), eye muscle depth (yemd), greasy fleece weight (ygfw) and fbre diameter (yfd)

CONCLUSION

Genotyping and preselection based on genotype only ASBVs provides higher correlations with TBVs and less selection bias than preselection based on other variations of phenotyping examined in this paper. This study only looked at the effect of preselection on the ASBVs of the current generation. Further research is required to quantify the impact of the preselection on genetic gain in subsequent generations and the cost savings of this approach. This includes the long-term impact of selective recording on the reference population for individual flocks and the entire reference population. In addition, the impact of preselection on reproduction traits also needs to be examined.

REFERENCES

Brown D.J., Swan A.A., Boerner V., Li L., Gurman P.M., McMillan A.J., van der Werf J.H.J, Chandler H.R., Tier B. and Banks R.G. (2018) *Proc. World Cong. Genet. Appl. Livest. Prod.* **11**: 1.

Jibrali I.Ten Napel J., Vandenplas J., Veerkamp R.F. and Calus M.P.L. (2020) *Genet. Sel. Evol.* **52**: 42.

Jibrila I., Vandenplas J., Ten Napel J., Veerkamp R.F. and Calus M.P.L. (2021) *J. Anim. Breed. Genet.* **138**: 432.