

## GENETIC BENCHMARKING OF MATERNAL SHEEP FLOCKS USING GENOMIC TESTING

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### SUMMARY

This study aimed to examine the predictive ability of the “Flock Profile” genomic benchmarking method in maternal sheep flocks, estimated from the Maternal LAMBPLAN analysis. Data from this analysis was used in a validation study to test the accuracy of predicting mean flock performance for reproductive traits. For each validation flock, the pedigree, genotypes and performance data were removed for the entire flock and then its Flock Profile result was estimated from genomic predictions based on estimated SNP marker effects from single step genomic BLUP analyses (ssGBLUP). The Flock Profile results were then compared to the original Australian Sheep Breeding Values (ASBVs) from the full analysis. The accuracy of ranking of mean flock performance was high ( $r > 0.85$ ) for all traits except ewe rearing ability. However, the Flock Profile results were generally over-dispersed and thus had more variation compared to their ASBVs. Genomic predictions for individual animals were also highly correlated to the full ASBVs. This initial study supports further investment into the development of these products, with the potential to offer commercial producers new genetic tools to foster ongoing improvement in on-farm profitability.

### INTRODUCTION

The Flock Profile test is successfully used to genetically benchmark commercial Merino flocks (Swan *et al.* 2018). While the average Australian Sheep Breeding Value (ASBV) of rams purchased is often the most accurate metric of genetic merit, it is not available to commercial flocks from outside of Sheep Genetics when sourcing rams. Thus, Flock Profile tests are an important tool for those breeders without any knowledge of their current genetic benchmark. At present, these are only commercially available in purebred Merino flocks and does not include reproduction traits. However, dissemination of genetic gain made in the seedstock sector would be enhanced across industry if similar products were available for other breeds, and in particular for commercial crossbred flocks. Brown *et al.* (2022) conducted a preliminary validation in terminal sire breeds for carcase traits, which demonstrated that genomic flock profiling accurately predicted their true ASBV mean. Another application under consideration is a Flock Profile product to support the marketing of maternal replacements, allowing purchasers to value sale lots on more accurate genetic benchmarks for all the key traits rather than relying on visual appraisal alone. In addition to flock benchmarking, the methodology could also be used to perform genomic prediction on individual animals.

This study aimed to examine the predictive ability of the Flock Profile test for reproductive traits in maternal sheep breeds, estimated from the maternal LAMBPLAN analysis (Brown *et al.* 2007).

### MATERIALS AND METHODS

Data from the reproductive component trait analysis for Maternal LAMBPLAN (as described by Bunter *et al.* 2019) were utilised for this study. Reproductive data and genotypes were identified for 14 selected seedstock flocks within this analysis, chosen based on volume and quality of data. The

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flocks consisted of Border Leicester, Coopworth and composite breeds. The data available for each trait are illustrated in Table 1. To generate an independent ASBV analysis, all the phenotype data, pedigree and genotypes from these 14 flocks were removed sequentially and 14 special Maternal LAMBPLAN analyses conducted. Using the genotypes only, ASBVs were estimated for each animal using the back-solve methods described by Swan *et al.* (2018) and these were then averaged for each flock to estimate the Flock Profile result. The Flock Profile results were then compared to their true ASBV means from the full LAMBPLAN analysis using all data. A key aspect of the Flock Profile method is the projection of genetic group effects using a regression of genetic group coefficients on genomic relationships between reference animals in the ssGBLUP and the animals targeted for prediction. Genetic groups in Maternal LAMBPLAN are defined at the breed level, and an important difference between Merino and Maternal LAMBPLAN ssGBLUP analyses is that the latter uses a genomic relationship matrix which accounts for breed structure (Gurman *et al.* 2019) while the Merino analysis does not. The current Maternal LAMBPLAN analysis uses a breed-adjusted genomic relationship matrix (G) and a lambda of 0.5. In an attempt to capture breed effects in the Flock Profile prediction in this study, back-solving was conducted using genomic relationships without accounting for breed structure. In addition, a “lambda” value of 1 was used i.e. variance fully explained by markers with no residual polygenic variation.

The component reproduction traits analysed included conception rate (CON: 0=failed to conceive, 1=conceived) litter size (LS: 1 to 4 lambs born) and ewe rearing ability (ERA: lambs surviving/lambs born for ewes which lambed). All three traits have yearling and adult expressions separated. Additional correlated traits included maternal behaviour score (MBS: from 1: good to 5: poor) and, pre-joining weight (AWT) and condition score (CS) recorded within the 30 days before joining. Body composition and development traits also included in the analysis were post-weaning body weight (PWT), carcass fat (PFAT) and eye muscle depth (PEMD), along with post-weaning (PSC) or yearling (YSC) scrotal circumferences.

**Table 1. Descriptive statistics of the data used in the validation for each trait.**

Trait	Flocks	Animals	Genotyped	Mean	SD
PWT	14	94,176	14,632	45.50	9.54
PCF	14	94,095	14,616	3.33	1.26
PEMD	14	94,145	14,628	26.52	3.95
AWT	13	65,016	19,790	68.80	11.58
PSC	10	31,029	1,449	28.88	4.44
YSC	7	15,075	269	28.49	2.90
MBS	11	26,845	19,320	1.82	0.92
CS	12	33,976	15,542	3.49	0.64
CON	14	102,562	17,447	0.92	0.27
LS	14	154,410	25,279	1.76	0.60
ERA	14	108,618	19,415	0.85	0.30
YCS	6	4,859	3,580	3.41	0.55
YCON	12	43,130	13,963	0.66	0.47
YLS	14	37,854	10,231	1.51	0.55
YERA	14	28,719	7,707	0.78	0.36

## RESULTS AND DISCUSSION

The accuracy of ranking of flocks was high ( $r > 0.85$ ) for all traits except ewe rearing ability. However, the ASBV means and variation between flocks were significantly different between the full ASBV and Flock Profile results (Table 2). The difference in the variation between flocks and

slope values significantly less than 1 indicate that the Flock Profile results were generally over-dispersed compared to their ASBVs. This over-dispersion maybe due to the use of the unadjusted G and lambda of 1.0 in this study and further research is required to study the impact of these factors.

**Table 2. Relationship between Flock Profile (n=14) results and ASBV means from the full Maternal LAMBPLAN analysis**

Trait	Flock Profile mean	ASBV mean (SD)	Slope	Corr	RMSE <sup>#</sup>
PWT	-0.50 (3.89)	2.76 (1.61)	0.39 (0.04)	0.95	0.49
PCF	0.27 (0.13)	0.35 (0.13)	0.85 (0.14)	0.87	0.06
PEMD	0.33 (2.09)	2.21 (1.00)	0.44 (0.06)	0.92	0.40
AWT	-1.31 (1.47)	0.80 (1.13)	0.70 (0.09)	0.91	0.47
PSC	-0.56 (1.97)	1.10 (0.93)	0.44 (0.05)	0.94	0.33
YSC	-1.05 (1.70)	0.71 (0.87)	0.49 (0.04)	0.96	0.25
MBS	-0.10 (0.04)	-0.11 (0.05)	0.92 (0.19)	0.81	0.03
CS	0.13 (0.08)	0.13 (0.05)	0.47 (0.12)	0.75	0.03
CON	0.00 (0.04)	0.03 (0.01)	0.33 (0.07)	0.83	0.01
LS	-0.18 (0.25)	0.08 (0.11)	0.41 (0.05)	0.92	0.04
ERA	0.01 (0.02)	0.02 (0.01)	-0.02 (0.14)	-0.03	0.01
YCS	0.15 (0.10)	0.24 (0.08)	0.73 (0.10)	0.91	0.03
YCON	0.01 (0.16)	0.19 (0.06)	0.36 (0.05)	0.91	0.03
YLS	-0.11 (0.20)	0.11 (0.08)	0.36 (0.07)	0.85	0.04
YERA	0.01 (0.03)	0.03 (0.01)	0.28 (0.05)	0.86	0.01

# RMSE: Root mean square error

The results of the back-solved breeding values at the level of individual animal are shown in Table 3. These results highlight that the Flock Profile methodology could accurately predict the ranking of ASBVs within the flocks tested with correlations generally greater than 0.7 for most traits and regression slopes of close to 1.0. The relationships across all animals and flocks were lower with correlations ranging from 0.34 to 0.96. Further research is required to refine the methodology to more accurately partition flock and breed effects.

It should be noted that unlike most commercial flocks, the flocks used in this analysis were seedstock breeders with stronger genetic links to other breeding and reference flocks in the Maternal LAMBPLAN analysis and some descendants of these flocks would have existed in other flocks that remained in the analysis. Thus, the correlations observed here may be higher compared to those observed in less related commercial flocks in industry that are the target of Flock Profile products.

The longer-term challenge for the development of a commercial Flock Profile test for industry flocks is to accommodate their crossbred structure. Lamb production flocks generally incorporate breed components from the 3 major breed types of Merino, maternal and terminal, each of which are analysed separately by Sheep Genetics in their MERINOSELECT, Terminal LAMBPLAN and Maternal LAMBPLAN evaluations. Therefore, the results would need to be aligned relative to each of these 3 different ASBV analyses. One difficulty of alignment across analyses not covered in this study is the potential effects of heterosis in commercial crossbred ewes, which is one of the key benefits of using these maternal sheep, for example in the Border Leicester x Merino production system. This requires further consideration. Another technical challenge is that the LAMBPLAN analyses are multi-breed, with genomic information corrected for breed effects (Gurman *et al.* 2019). One of the motives of this study was to investigate this issue and ensure breeds effects could be accommodated in the Flock Profile method. Aside from addressing the technical challenges associated with breed structure and heterosis, Flock Profile testing should be expanded to cover more of the traits that influence profitability in sheep enterprises, including reproduction and ewe

efficiency, product quality and disease resistance.

**Table 3. Relationship of the genomic only animal level breeding values to the ASBV from the full Maternal LAMBPLAN analysis both across and within flocks**

Trait	Flock Profile mean (SD)	Across all flocks			Average of within flock		
		ASBV mean (SD)	Slope	Corr	RMSE <sup>#</sup>	Corr	Slope
PWT	1.59 (3.34)	3.69 (2.02)	0.51 (0.00)	0.85	1.06	0.87 (0.03)	0.88
PCF	0.30 (0.25)	0.35 (0.26)	0.93 (0.00)	0.89	0.11	0.90 (0.03)	0.95
PEMD	1.49 (1.73)	2.69 (1.13)	0.54 (0.00)	0.83	0.64	0.86 (0.04)	0.90
AWT	-0.84 (2.88)	1.05 (2.84)	0.89 (0.00)	0.90	1.21	0.88 (0.03)	0.92
PSC	0.64 (1.63)	1.77 (1.03)	0.54 (0.00)	0.86	0.52	0.87 (0.06)	0.93
YSC	-0.01 (1.47)	1.30 (0.96)	0.58 (0.00)	0.89	0.44	0.86 (0.06)	0.92
MBS	-0.09 (0.13)	-0.12 (0.14)	0.96 (0.00)	0.87	0.07	0.90 (0.03)	1.00
CS	0.09 (0.12)	0.12 (0.12)	0.81 (0.00)	0.85	0.06	0.90 (0.03)	0.96
CON	0.02 (0.03)	0.04 (0.02)	0.34 (0.00)	0.49	0.02	0.58 (0.19)	0.76
LS	-0.04 (0.21)	0.16 (0.14)	0.55 (0.00)	0.83	0.08	0.68 (0.13)	0.79
ERA	0.01 (0.02)	0.01 (0.02)	0.39 (0.01)	0.35	0.02	0.64 (0.12)	0.92
YCS	0.20 (0.10)	0.27 (0.10)	0.86 (0.00)	0.85	0.05	0.87 (0.04)	0.98
YCON	0.10 (0.13)	0.23 (0.09)	0.46 (0.00)	0.65	0.07	0.65 (0.18)	0.75
YLS	-0.01 (0.17)	0.17 (0.13)	0.57 (0.00)	0.78	0.08	0.70 (0.14)	0.84
YERA	0.03 (0.03)	0.04 (0.03)	0.52 (0.00)	0.57	0.02	0.66 (0.15)	0.81

# RMSE: Root mean square error

## CONCLUSIONS

The results of this study demonstrate accurate ranking of flocks, but more work is required to produce accurate ASBV benchmarks for all traits. This initial study supports further investment into the development of Flock Profile products, which has the potential to expand the range of genetic tools available to the sheep industry to foster ongoing improvement in on-farm profitability.

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