Final report

Developing genomic prediction tools for commercial Merino sheep

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Abstract

The project aim was to obtain experience and validation of the value of genomic testing in commercial Merino flocks. The number of samples submitted for genotyping totalled 10,238 across 19 different flocks. Animal Genetics & Breeding Unit (AGBU) has adapted the pipeline for predicting breeding values for animals with only genotype information, based on the method that was previously developed for Flock Profile. A validation of Genomic Breeding Values (GBVs) against phenotypes showed estimated correlations for Fibre Diameter, Fleece Weight and Body Weight equal to 0.49, 0.23 and 0.26, implying an accuracy of genomic testing of 0.6, 0.4 and 0.5, respectively. Two online workshops were held with breeders, with four detailed case studies on producers' application of this testing within their flock summarised in this report. A modelling study was performed to estimate cost-benefit and breakeven costs of genotyping. For a moderately accurate genomic test, the break-even cost of genotyping males in a multiplier flock for use as sires in a commercial flock was approximately $250 and the break-even cost of selecting ewes in the multiplier flock using genomic testing is approximately $100. The break-even cost of selecting replacement ewes in a commercial flock is between $10 and $15. These results indicate that there is opportunity for cost-effective genotyping in commercial Merino flocks.

Executive summary

Background

Genomic testing has rapidly been adopted in the seedstock industry, with the number of genotyped animals in the Merino Sheep Genetics database now above 500,000. The accuracy of genomic prediction is increasing due to the number of animals with measured phenotypes that can be linked to genotype information is rapidly growing. While most of the genomic testing completed is currently in seedstock breeder flocks, there is potential to extract value from genomic testing in commercial flocks. Genomic predictions have already been used to predict genetic merit of animals at a flock level, such as the current flock profile prediction for commercial Merino flocks. The Flock Profile benchmarks against industry and helps producers make more informed ram selection decisions for genetic progress. Individual prediction of genetic merit of commercial sheep without recorded phenotypic information could be useful when ranking animals within flock, e.g. for decisions around culling or mating of ewes for flock replacement, or for selecting ewes or rams in the multiplier flocks to improve the genetic merit of sires used in commercial flocks. Genotyping of commercial cattle is already utilised in the beef and dairy industries, but the value proportion has not been explored in sheep.

Therefore, this project aims to develop a pipeline for genomic breeding value prediction of individual commercial Merino sheep and develop validation and value propositions where both accuracy and benefit of such predictions will be evaluated to underpin potential adoption of the technology in the sheep industry.

Objectives

The project had the following objectives:

1. Genotype 10,000 commercial Merino sheep that have recorded performance data.
2. Develop a pipeline for genomic prediction of genetic merit of individual Merino sheep that have no phenotypic information.
3. Validate genomic predictions based on the rank correlation with phenotypic data within flocks.
4. Evaluate user experience of how producers use genomic predictions within their flock and develop case studies for broader extension purposes. Hold two workshops to discuss and validate value propositions with project participants.
5. Undertake a cost-benefit analysis to support value propositions of genotyping individual commercial Merino sheep.

Methodology

The project collected genotypes from 10,000 commercial Merino sheep that have recorded performance data. These genotypes were aimed to be collected via collaboration with around 20-30 flocks with approximately 300-500 ewes genotyped per flock. Based on genotype information from individual animals, genomic predictions were generated using a backsolving strategy (Swan et al., 2018). Genomic predictions were aligned with performance data to validate and demonstrate the predictive accuracy of the genomic test, both within flocks and between flocks. For example, flocks currently using RAMPOWER, were targeted as they have both data and an interest in ranking their animals within flocks. Where sire teams are available pedigree can be assigned and the genomic test results compared to sire ASBVs.

The value of using genomic prediction in decision making was modelled based on these observed accuracies. A modelling study was performed to estimate cost-benefit and break-even costs of genotyping. Selection index theory was used to predict selection differentials of selected ewes or rams, using either the Merino Lamb (ML) index or the Sustainable Merino (SM) index as an objective. Selection accuracy was compared for three different information sources, 1) a postweaning phenotype for weight, fibre diameter and clean fleece weight, 2) a moderately accurate genomic test, similar to the current expected accuracy and 3) a more accurate genomic test, as to be expected in the next few years. A deterministic geneflow method was used to predict future expression of selection superiority of ewes or rams in their descendants, or of their own phenotype. Deterministic modelling was validated with results from stochastic simulation.
Discussion forums were held with producers and genotyping service providers and four specific case studies were developed with producers that breed their own rams.

Results/key findings

The total number of participating producers in the project was 19, with 19 flocks, providing 10,238 DNA samples for genotyping by one of the three service providers (Neogen, Xytovet and Weatherbys). The average number of samples per flock was 465 with a range from 46 to 1071 samples. Genomically estimated breeding values (GBVs) were provided to all participants and 11 flocks provided phenotypic information on their genotyped animals. The validation study suggests a reasonable correspondence between individual animal performance and its genomic prediction with estimated correlations for fibre diameter (FD), fleece weight (FW) and body weight (WT) equal to 0.49, 0.23 and 0.26, implying an accuracy of genomic test of 0.6, 0.4 and 0.5 respectively. Overall, participants were excited about the availability of a tool to genomically rank animals. Some challenges were encountered on how to use the ranking in the yards to make selection decisions when previously visual selection plus a RAMPOWER index ranking (which is based on the animals' phenotype) were used. Two flocks have shown that the GBV ranking lined up well with the RAMPOWER ranking while for some other flocks it was not reflective. This posed the question about how accurate or well linked the flock(s) were to the genomic reference population, which is required to be researched further. The modelling study estimated that for a moderately accurate genomic test, the break-even cost of genotyping males in a multiplier flock for use as sires in a commercial flock was around $250 and the break-even cost of selecting ewes in the multiplier flock is around $100. The break-even cost of selecting replacement ewes in a commercial flock is between $10 and $15. These results indicate that there is prospect for cost-effective genotyping in commercial Merino flocks.

Benefits to industry

Given the likelihood that genomic predictions of genetic merit will be increasingly accurate, there seems ample prospect to use genomic testing in commercial Merino flocks, especially for those cases where selected animals have an influence on a lot of offspring, such as selection of rams and ewes in a multiplier flock. If we assume that around 25% of sheep producers in Australia breed their own rams (DPIRD WA, 2023), there is a significant commercial market for new genomic products for commercial producers in Australia. This technology will therefore contribute to achieving a larger proportion of the Australian flock having higher genetic merit, especially for traits that are not easy to observe or measurable on-farm, e.g. lamb eating quality and sustainability traits.

Future research and recommendations

While prediction may be accurate for many commercial flocks, there is likely variation in the degree of linkage of flocks with the genomic reference populations, and therefore accuracy of genomic prediction may vary between flock. It is recommended to invest in methods that can give an indication of industry linkage and accuracy of specific genomic predictions. Further application of genomic testing and ranking of individual sheep maybe be explored in future projects.

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1. Background

Currently, Sheep Genetics offer a genetic evaluation system to the sheep industry where breeders can submit phenotypic, pedigree and genomic data to get estimated breeding values for their sheep (ASBVs). The genomic information is most useful where there is limited trait recording, i.e. for traits hard to measure in the breeding flocks, or for traits where phenotypic information is not yet available for selection candidates. Overall genomic testing accelerates rates of genetic improvement, especially for hard to measure traits and for breeders trying to shorten generation intervals. The information derived from genomic testing depends on the size of the reference populations, and the accuracy of that information is expected to grow significantly over time.

Genomic testing has rapidly been adopted in the sheep seedstock industry, with the number of genotyped sheep in the Merino Sheep Genetics database now above 500,000 (Andrew Swan, Pers. Comm., November 2024). The accuracy of genomic prediction is increasing as the reference population, made up of animals with a genotype and phenotype, increases. While most of genomic testing is currently in seedstock breeder flocks, there is also potential to extract value by genomic testing in commercial flocks. Genomic predictions are currently used to predict the genetic merit of animals at a flock level, such as the current flock profile prediction for commercial Merino flocks, available through Sheep Genetics. This is used to benchmark commercial flocks on key traits to then assist with their sire selection and to gauge genetic progress.

Individual animal prediction of merit in commercial sheep with limited recorded information could be useful in other applications across industry. This might include trading stock such as lambs to meat supply chains or breeding ewes of unknown backgrounds. Access to genomics prediction of merit could be of use when ranking ewes within a flock for culling, mating, selecting replacement ewes or rams in multiplier flocks etc. The potential to combine with performance data from abattoirs for example could flow back into the database for more accurate future genomics predictions. Large scale genotyping of commercial animals could have benefits for traceability and linking to phenotypic data for an increased reference population, further increasing genomic prediction accuracies.

Genotyping of commercial cattle is already quite common in beef and dairy industries, but the value proposition has not been widely explored in sheep. This project aims to develop a pipeline for genomic prediction of individual commercial Merino sheep and develop validation and value propositions where both accuracy and benefit of such predictions will be evaluated to underpin adoption of the technology in the sheep industry.

2. Objectives

This project will

- Genotype 10,000 commercial Merino sheep that have also recorded performance data
- Develop a pipeline for DNA based prediction of genetic merit for commercial sheep that have no information on phenotype or pedigree.
- Validate genomic predictions on individual sheep
- Undertake cost-benefit analyses of investment in genotyping, under various scenarios
- Three case studies developed for broader extension and two value proposition workshops discussed and validated with project participants

The project will demonstrate the impact of within and across flock genetic differences and provide case study / real life examples for extension and adoption activities. The data from this project will clearly demonstrate the value of tracking ram team EBV averages and its ability to predict performance outcomes in progeny. Cost benefit analysis will be used to calculate breakeven costs of genotyping for ewe replacement in commercial flocks, or for ewe and ram selection in multiplier flocks that provide rams to commercial flocks. These new tools will further support adoption of ASBVs across the commercial sheep industry and provide a pathway for breeders not currently using ASBVs to access genomic prediction tools.

3. Methodology

The project developed DNA based prediction of genetic merit for commercial sheep to better enable informed decision-making regarding culling, selection, purchasing and management of sheep. The project aimed to genotype 10,000 commercial Merino sheep that have recorded performance data. Based on genotype information from individual animals, genomic predictions were generated using a back-solving strategy (Swan et al., 2018). Genomic predictions were aligned with performance data to validate and demonstrate the predictive accuracy of the genomic test, both within flocks and between flocks. For example, flocks currently involved in RAMPOWER, were targeted as they have both data and an interest in ranking animals within flocks. Individual genomic predictions were delivered alongside a flock profile result such that the genetic merit of the flock as well as the ranking of animals within flock can be assessed by the producer.

The value of using genomic prediction in decision making were modelled based on observed accuracies, and a cost-benefit analysis was developed for specific case studies of producers that breed their own rams, i.e. for within flock culling and mating decisions.
The benefit of selective culling was calculated as being dependent on:

1. The predicted difference, or the superiority, i.e. how much better are the animals that are kept.
2. The number of future expressions of that superiority, which in turn depends on
    - the number of future phenotypic expressions of the animals itself
    - the number of expressions in future offspring and their descendants
    - when these expressions are realised, as future benefits should be discounted for net present value

Selection index methodology was used to predict selection superiority of individual traits and of an overall index, assuming animals were ranked according to either the Merino Lamb (ML) index or the Sustainable Merino (SM) index. Future expression of selection superiority of selected parents was modelled with the GeneFlow method. Results were also validated using stochastic simulation. Selecting animals based on commonly measured phenotypes (weight, fleece weight and fibre diameter) were compared with selection based on a genomic test, which is either moderately accurate, like the current test, or more highly accurate, as it will be expected to be over the next few years. Moderate and accurate genomic tests were simulated to an equivalent accuracy of having five or twenty progeny measured for all traits. From the expected benefit of selection, the break-even cost of a genomic test was derived, considering three scenarios of selection. The first scenario is selection of replacement ewes in a commercial flock, the second is selection of males born in a multiplier flock, to be used as sired in a commercial flock, and the third scenario is selection of ewes within the multiplier flock.
Findings from these scenarios combined with the cost benefit analysis was discussed in forums with participating genotype service providers and producers. The cost-benefit propositions were discussed and validated with participating producers in individual case studies.

4. Results

4.1 10,000 commercial Merino ewes genotyped.

The total number of participating producers in the project was 19, with 19 flocks. Of the 19 flocks, 14 are from NSW, 3 from Victoria, 1 from Tasmania and 1 from South Australia. There were no participants from Western Australia or Queensland.

As of 15 October 2024, there were 10,238 samples collected and processed for genotyping. The average number of samples per flock was 465 with a range from 46 to 1071 samples.

Table 1 shows the number of samples collected and processed by the participating genotyping service providers. Note the differences between the labs was from participants indicating they were sending a certain number of samples and then sending more or less than initially budgeted on. This is the final number of samples as reconciled with all labs.

Table 1. Number of samples processed by each genotyping service provider

Neogen	3,380
Xytovet	3,161
Weatherbys	3,697
Total	10,238

A detailed list of participants and number of samples collected is shown in Appendix 1.

Two **online producer meetings** were held and recorded. These meetings were well attended by producers and also attended by MLA and GPS representatives. Prior to each of these, meetings with the GPS were held to update on progress and proposed delivery of results back to producers. Preliminary insights into the cost benefit of genotyping were discussed, along with different selection strategies, e.g. genotyping ewes for making decisions on ewe replacement, or genotyping multiplier males to make decisions on which males to use as sires in the commercial flock.

- 4th June 2024 - https://youtu.be/wQruEYFX7cA
    - **Agenda**
        - Validation of predictions.
        - Discussion of possible benefits of genotyping.
        - Discussion of methods to convey results to users.
        - Discussion of possible case studies and strategies to communicate results to the wider industry.

- 3rd October 2024 - https://youtu.be/_2Ql-9wY0nY
    - **Agenda**
        - Project update:
            - number of tests
            - results delivered to date
            - cost benefit analysis
            - draft case studies

- Feedback from participants:
    - results and how they are currently presented
    - do we need to look at including additional traits
- Delivery model - current structure and timelines
- Next phase of the project:
    - producer demonstration project concept
    - location of sites
    - feedback and questions producers would like answered
    - parallel project – accuracy GEBV and Flock Profile

Peta Bradley (Sheep Genetics) presented the MLA preferred model of reporting, that is via Sheep Genetics on a fortnightly basis. A draft timeline from sample collection to receiving results is estimated to be 6 to 7 weeks, as shown in Appendix 2.

Online workshops and meetings have been adopted for the project to accommodate the large geographic area that the project participants are located. Figure 1 is a map showing the spread of participants across NSW, VIC, SA and TAS.

Figure 1. Location of participating flocks in the project

The communication with project participants has been on a one-to-one basis to gauge progress on DNA sampling and data submission. Four participants have received their GBVs. Two participants have gone through the results and sheep to compare the GBV with their normal RAMPOWER within flock ranking tool. The difference between the two sets of results is still being assessed with a likelihood that producers will move to using the GEBV that tells how the animal will breed rather than how they will perform themselves.

On the delivery of results, a decision needs to be finalised regarding the technical name of the product. It is a genomic prediction of breeding value, so an abbreviation could be GEBV, but also GBV, or gEBV. This will be determined by follow up meetings between MLA and GPS about commercialisation of the product.

4.2 Genetic merit predictions delivered back to Merino producers

AGBU has modified the genotype processing pipeline to cater for this new test (GBVs). This will enable both reporting of the product through the analysis pipeline and reporting the monthly volume of test throughput back to MLA and the providers as is currently done for existing genomic products. The back-solve process to estimate Flock Profile reports (Swan et al, 2018) has been modified to cater for this new test. The approach used is to first estimate a standard flock profile and then generate a new ranking of individual within each flock for each trait. The process includes;

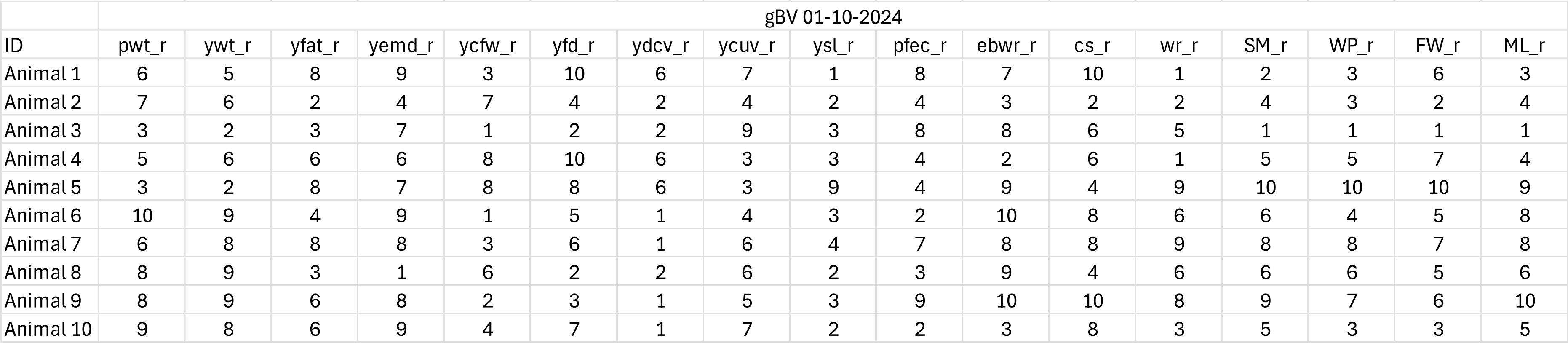
- Standardising GBVs for all traits so that they have a mean of zero and standard deviation of 1. This makes the results not comparable to ASBVs.
- Percentiles are then used to rank each animal for each trait and index from 1 to 10, with 1 being top 10% and 10 bottom 10% in the flock. This results in an even distribution with equal numbers of animals for each score. The order of ranks will be such that the best animals for each trait will always score 1. There have been some suggestions to reverse this, i.e. a higher number means a better GBV.

The current trait and index list being used is the same as that for the standard Flock Profile report, which include

Yearling Clean Fleece Weight (YCFW)
Yearling Fibre Diameter (YFD)
Yearling Fibre Diameter Coefficient of Variation (YFDCV)
Yearling Curvature (YCURV)
Yearling Staple Length (YSL)
Post Weaning Weight (PWT)
Yearling Weight (YWT)
Yearling Fat Depth (YFAT)
Yearling Eye Muscle Depth (YEMD)
Early Post Weaning Breech Wrinkle (EBWR)
Post Weaning Worm Egg Count (PWEC)
Merino Lamb Index (ML)
Wool Production Index (WP)
Sustainable Merino Index (SM)
Fine Wool Index (FW)
Condition Score (CS)
Weaning Rate (WR)

Results were presented back to breeders as a ranking according to a percentile band (within flock) for all of the traits and indexes currently reported in the Flock Profile. Breeders also received a Flock Profile report. An example of within flock ranking is presented below (Figure 2).

Figure 2. Example of within flock ranking of GBVs according to percentage band, for each trait and some indices. Note that 1 is top and 10 is bottom.



	gBV 01-10-2024															
ID	pwt_r	ywt_r	yfat_r	yemd_r	ycfw_r	yfd_r	ydcv_r	ycuv_r	ysl_r	pfec_r	ebwr_r	cs_r	wr_r	SM_r	WP_r	FW_r	ML_r
Animal 1	6	5	8	9	3	10	6	7	1	8	7	10	1	2	3	6	3
Animal 2	7	6	2	4	7	4	2	4	2	4	3	2	2	4	3	2	4
Animal 3	3	2	3	7	1	2	2	9	3	8	8	6	5	1	1	1	1
Animal 4	5	6	6	6	8	10	6	3	3	4	2	6	1	5	5	7	4
Animal 5	3	2	8	7	8	8	6	3	9	4	9	4	9	10	10	10	9
Animal 6	10	9	4	9	1	5	1	4	3	2	10	8	6	6	4	5	8
Animal 7	6	8	8	8	3	6	1	6	4	7	8	8	9	8	8	7	8
Animal 8	8	9	3	1	6	2	2	6	2	3	9	4	6	6	6	5	6
Animal 9	8	9	6	8	2	3	1	5	3	9	10	10	8	9	7	6	10
Animal 10	9	8	6	9	4	7	1	7	2	2	3	8	3	5	3	3	5

4.3 Validation of GBVs with phenotypic data

4.3.1 Materials and Methods

On-farm phenotype measurements were received from 11 flocks and could be used to validate Genomic Breeding Values (GBVs) based on within flock ranking. Phenotypic performance measured on farm were compared to the genomic predictions, determining how well they correlated for each trait.

A summary of the phenotypic data from all 11 flocks is shown in Table 2. A summary of the data for each flock is included in Appendix 3.

Table 2: Summary of total data used for each trait.

Trait	Number of records	Record Mean	Standard deviation
WT	1937	41.46	17.70
CFW	2090	2.87	0.66
FD	4185	18.06	1.65
SL	631	88.37	22.51
CV	3850	17.60	2.83
EBWR	94	2.07	1.07

The project ran bivariate linear regression in R to correct for differences between flocks and years for phenotypes and GBVs.

$$phenotype\ GEBV = \mu + yearflock + e$$

where phenotype is the measured trait value on farm, GBV is the estimated GBV, year-flock is the fixed effect for year and flock and e is the residual.

For individual flocks, when there were measurements across multiple years, the following was used:

$$phenotype\ GEBV = \mu + year + e$$

where year is the year of measurement. These results are presented in Appendix A

Once corrected for fixed effects, used the residual of these models and the mean to create corrected phenotypes and GBVs.

4.3.2 Results

Figures 3 and Figure 4 as well as Table 3 show the correlations between corrected phenotype and GBVs across all flocks (between animals and sire means).

Figure 3: Corrected phenotype vs GBV for six traits on all animals recorded in eleven flocks (estimated correlation is given in each trait-box).

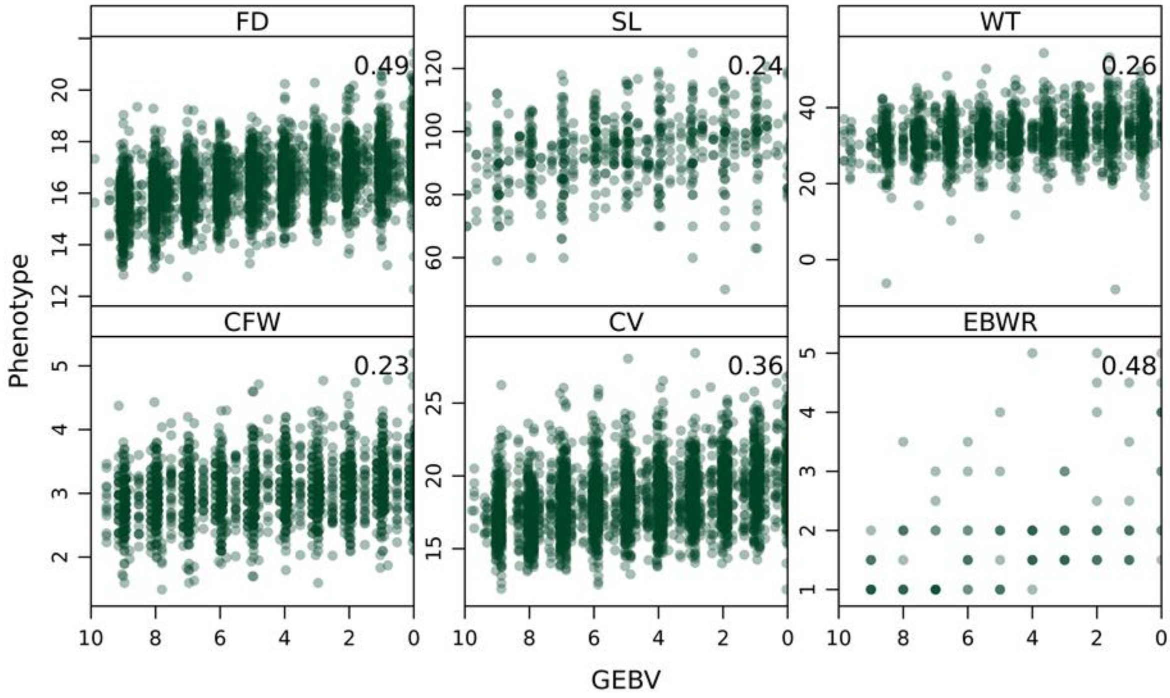


Figure 4. Sire averages of corrected phenotype vs GBV for six traits recorded in eleven flocks.

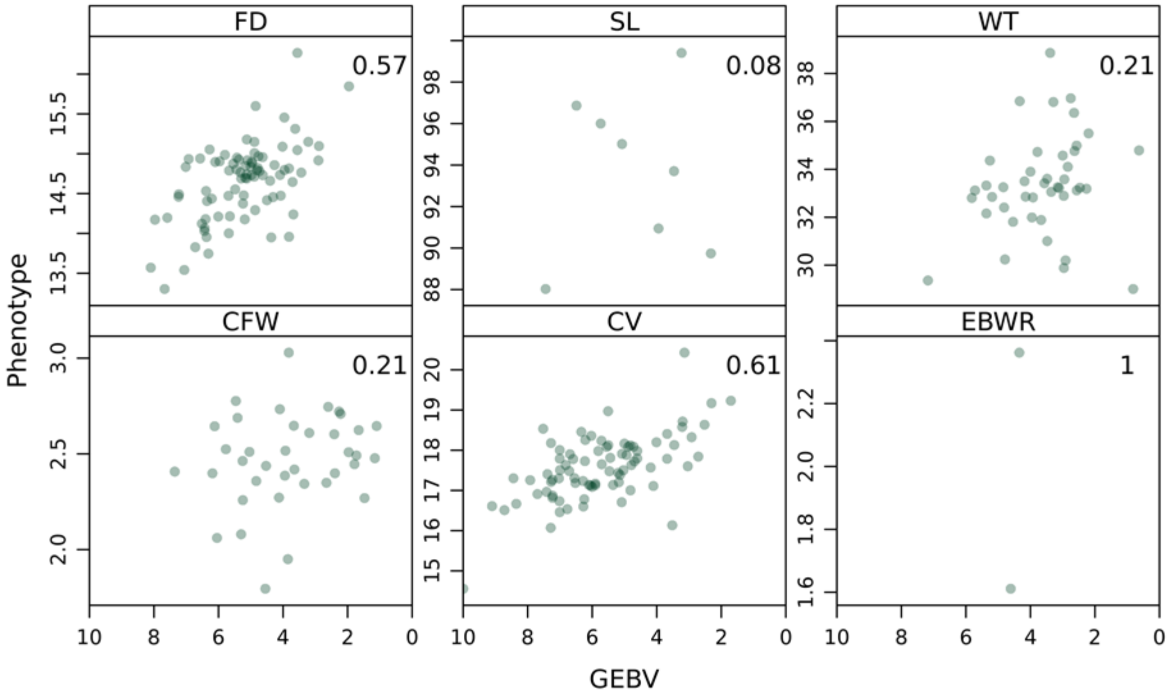


Table 3: Summary of correlations between corrected phenotypes and GBVs.

Trait	Sire means	Animals
WT	0.21	0.26
CFW	0.21	0.23
FD	0.57	0.49
SL	0.08	0.24
CV	0.61	0.36
EBWR	1.00	0.48

4.3.4 Conclusion on individual animal validation

Fibre diameter and early breech wrinkle had the strongest correlations between corrected phenotypes and GBVs (Figure 3). Sire average phenotypes were more correlated to genomic breeding values than animal phenotypes for some traits.

Generally, the correlation between phenotype and genomic breeding value increased as the heritability of the trait increased. This is logical because as heritability increases, more of the differences between animals can be explained by genetic differences. The expected correlation between EBV and phenotypes is equal to r.h, where r is the EBV accuracy and h is the square root of heritability (Figure 6)

4.3.5 Flock Profile validation

Genomic prediction in Flock Profile reports was also evaluated. This study examined the predictive ability of the “Flock Profile” genomic benchmarking method in Merino sheep flocks, estimated from the MERINOSELECT analysis. The Flock Profile is a product delivered to commercial Merino flocks providing a flock average benchmark compared to the flock average of the MERINOSELECT analysis. Results are delivered in ASBV terms and can be used to estimate where a flock sits in industry for traits of production and welfare importance. Data from this analysis was used in a validation study to test the accuracy of predicting mean flock genetic performance for reproductive traits. For each validation flock, the pedigree, genotypes and performance data were removed for the entire flock and then the 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 ($r > 0.79$) for all traits except Ewe Rearing Ability (see Figure 5 and Table 4). However, the Flock Profile results were slightly over-dispersed with an average regression slope across traits of 0.91 and thus had slightly more variation compared to ASBVs. Genomic predictions for individual animals were also highly correlated ($r>0.78$) to the full ASBVs. The analysis also demonstrated that there is variability in genomic connectedness to the reference population across flocks and traits and thus the development of an accuracy metric is important. More detail on the validation of flock profile predictions can be found in Appendix 3.

Figure 5. Accuracy of the Flock Profile (BSBV, n=42) results to predict the ASBV means from the full MERINOSELECT analysis

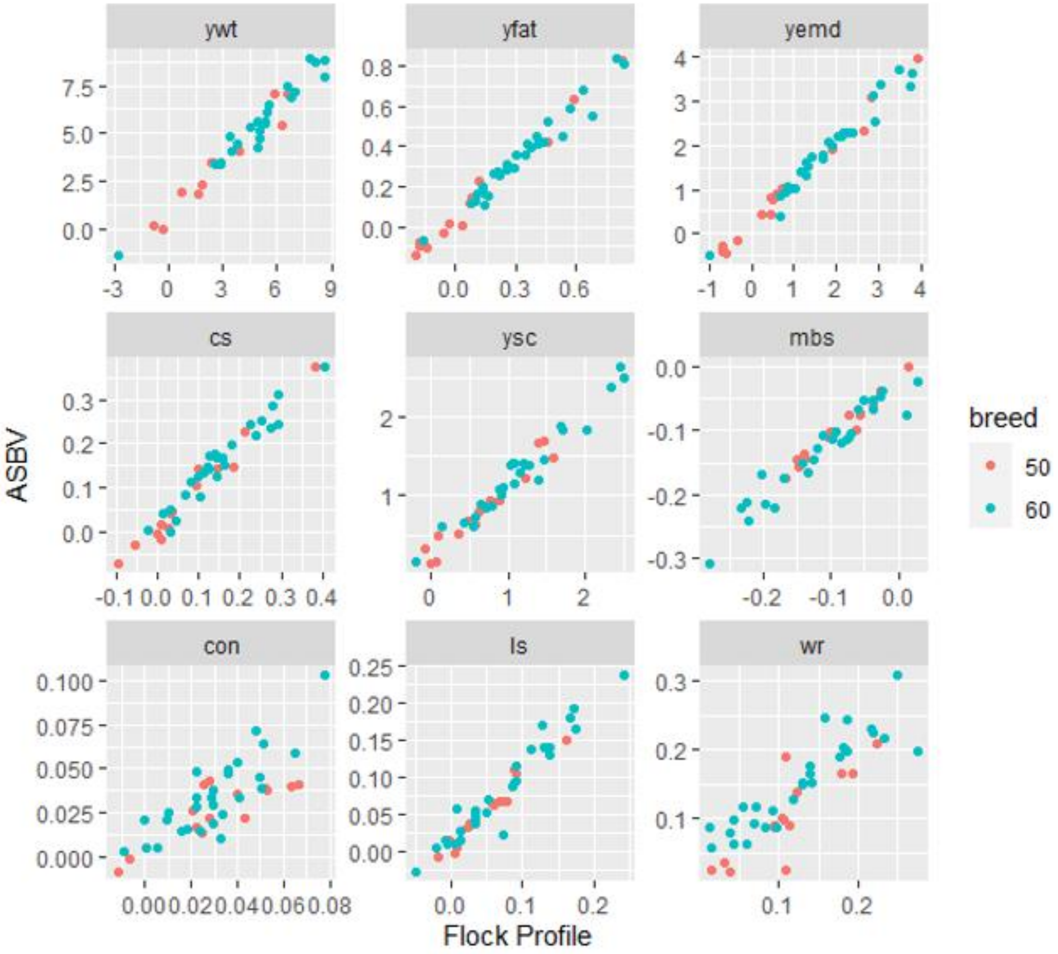


Table 4. Accuracy of the genomic only animal level breeding values to predict the ASBV from the full MERINOSELECT analysis both across and within flocks

	Across all flocks					Average of within flock	
Trait	Flock Profile mean (SD)	ASBV mean (SD)	Slope	Corr	RMSE#	Corr	Slope
PWT	3.34 (3.01)	3.93 (2.83)	0.89 (0.00)	0.95	0.87	0.94 (0.03)	0.87
YWT	4.58 (3.94)	5.27 (3.64)	0.88 (0.00)	0.95	1.09	0.94 (0.03)	0.87
AWT	5.20 (4.05)	5.83 (3.74)	0.88 (0.00)	0.95	1.14	0.94 (0.03)	0.86
PFAT	0.19 (0.33)	0.22 (0.30)	0.90 (0.00)	0.97	0.08	0.95 (0.03)	0.88
YFAT	0.24 (0.38)	0.28 (0.36)	0.91 (0.00)	0.97	0.08	0.95 (0.03)	0.88
PEMD	1.27 (1.45)	1.45 (1.37)	0.92 (0.00)	0.97	0.34	0.95 (0.04)	0.88
YEMD	1.40 (1.66)	1.57 (1.55)	0.91 (0.00)	0.97	0.37	0.95 (0.04)	0.87
CS	0.12 (0.16)	0.13 (0.15)	0.90 (0.00)	0.97	0.04	0.95 (0.03)	0.88
PSC	0.88 (1.20)	1.11 (1.12)	0.90 (0.00)	0.96	0.31	0.95 (0.02)	0.88
YSC	1.01 (1.26)	1.22 (1.16)	0.89 (0.00)	0.96	0.31	0.95 (0.02)	0.88
MBS	-0.10 (0.17)	-0.12 (0.16)	0.86 (0.00)	0.93	0.06	0.94 (0.04)	0.89
YCON	0.05 (0.12)	0.07 (0.11)	0.81 (0.00)	0.84	0.06	0.88 (0.11)	0.83
CON	0.02 (0.04)	0.03 (0.04)	0.76 (0.00)	0.79	0.02	0.78 (0.12)	0.75

YLS	0.01 (0.05)	0.01 (0.05)	0.90 (0.00)	0.88	0.02	0.88 (0.06)	0.88
LS	0.05 (0.11)	0.07 (0.11)	0.91 (0.00)	0.90	0.05	0.87 (0.06)	0.88
ERA	0.02 (0.03)	0.03 (0.03)	0.72 (0.00)	0.72	0.02	0.80 (0.10)	0.79
WR	0.10 (0.11)	0.12 (0.11)	0.87 (0.00)	0.84	0.06	0.83 (0.08)	0.83

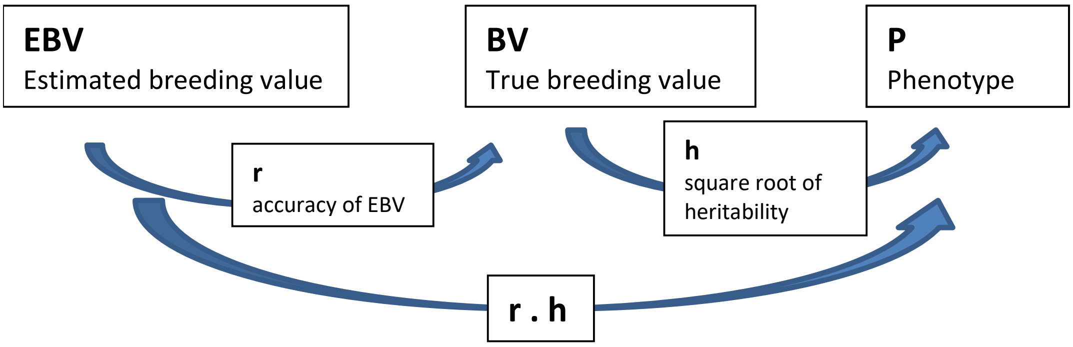
RMSE: Root mean square error

4.3.6 Discussion on validation analysis

Sire average phenotypes were more correlated to genomic breeding values than animal phenotypes. Fibre diameter (0.48, 0.76 and 0.51) had the highest correlation between phenotype and genomic breeding value. Flock 609423 has a low negative correlation for post weaning weight which contradicted the positive correlations in other flocks. The lowest correlation was between ranking based on class order (‘classing’) and the Fibre Production index. This suggests that ranking animals based on class order in this flock does not select the best animals to breed for the Fibre Production index.

Generally, the correlation between phenotype and genomic breeding value increased as the heritability of the trait increased. This is expected because as heritability increases, more of the differences between animals can be explained by genetics. Theoretically, it is expected that the correlation between and estimated breeding value and a phenotype (as deviation from the contemporary group mean) is equal to h.r (Fig 5), where h (square root of heritability) is the correlation between the true breeding value and phenotype and r (accuracy of EBV) is the correlation between the estimated breeding value and true breeding value. Hence for a trait with a heritability of 0.5 and an EBV accuracy of 0.6, the expected correlation between EBV and phenotype would be 0.3.

Figure 6. Expected relationship between estimated breeding value and phenotype.



The validation study suggests a reasonable correlation between individual animal performance and its genomic prediction. When dividing the observed correlation with the square root of the heritability we would obtain an estimate of the accuracy of genomic prediction, i.e. the correlation between the GBV and the true breeding value. These estimated accuracies would be around 0.5, 0.4 and 0.6 for body weight, fleece weight and fibre diameter, respectively, which is in line with the expected accuracy of genomic testing, based on experience in the evaluation by Sheep Genetics.

4.4 Participant reflection and individual case studies

Overall participants are excited about the availability of a tool to genomically rank animals individually within a flock. The project participants fell into two main categories, commercial breeders who were breeding their own rams (a multiplier structure) and looking to make better informed ram selections, and commercial breeders who purchased rams and were looking to use the GBV to select replacement ewes.

Some challenges have been understanding how to use the ranking in the yards to make selection decisions when in the past visual selection plus a within flock RAMPOWER index ranking (which is based on the animal's phenotype) has been used. The GBV ranking lined up well with the RAMPOWER ranking for some project participants, while others it was not as consistent with past selection tools. This posed the question about how accurate or well linked the flock(s) were to the genomic reference population. From this observation work is now being carried out to provide a relatedness value of a flock to the genomic reference population.

The price point of obtaining a GBV via a genomic test will also be a challenge to increase adoption for commercial sheep breeders. Currently the estimated cost of the GBV when commercialised will be between $30 and $40 per test equating to approximately 15-20% the value of a maiden Merino ewe, this compared to the cattle industry using a comparable tool known as HeiferSelect at 4-6% of the heifer value is a significant difference.

The GBV is seen to be a good segway into submitting data into Sheep Genetics. The project participants who breed their own rams felt that the process of using the GBV as an initial starting point provided the opportunity to obtain sire and in some instances dam pedigree, setting up their dataset to take the next step to submit data into Sheep Genetics to generate ASBVs.

Questions that have been asked by participants:

- Q - Can I just do the GBV and not worry about phenotyping anymore?
    - A – The GBV provides the opportunity to take a DNA sample and obtain a genomic ranking for key traits in a breeding objective without taking any phenotypic measurements. This approach requires the breeder to be confident that their flock is well linked to the genomic reference population and that selection processes used in the past have been superseded. Critical to adopting this approach is to continue to use some form of visual appraisal (for example visual scoring) as a selection tool for traits that are not yet captured and reported as GBVs.
- Q - How can I tell how accurate the GBV is for my flock?
    - A - This is a question that still needs to be answered, should new users of GBVs do a Flock Profile first before embarking on testing for GBVs (this question to be answered with the new work being done by AGBU – June 2025).
- Q - Can we compare doing GBVs vs ASBVs for a commercial ram breeding operation (multiplier)?
    - A - Cost benefit comparison – labour, timing of decision making – this question will be addressed with the Producer Demonstration phase of the project.
- Q - Will I be able to get year on year re-ranking of animals? e.g. so I can compare across years.
    - A - Yes. As more animals are tested their GBV will be able to be re calculated to provide across year rankings and a view of genetic progress. Examples of this concept can be seen in the 3 case studies associated with the project.

4.5 Cost-Benefit analysis: Predicting the effect of selecting better animals.

At culling, producers keep the better animals. Hence, there will be a difference in outcome, depending on how well we can select better animals. In general, we want to select animals to maximize future returns, and these returns are based on future performance of those selected animals and their offspring. In order to predict these future performances, we need information on current phenotypic performance and genetic merit of the selected animals. More information about a cohort will give a better prediction of future performance, which is expressed as a higher selection superiority of animals that are selected. Selective culling has a direct effect on the average performance of the flock. The animals will have better genetic merit, which will be passed onto their offspring. So, there are two types of benefit, the first depending on the phenotypic superiority of the animals that are kept, and the latter depending on their genetic superiority, as expressed in progeny.

The benefit of selective culling will depend on

1. the predicted difference, or the superiority, i.e. how much better are the animals that are kept.
2. the number of future expressions of that superiority, which in turn depends on
    - the number of future expressions of the animal itself
    - the number of expressions in future offspring and their descendants
    - when these expressions are realised, as future benefits should be discounted for net present value

4.5.1 Predicting selection superiority

Selected animals will be S_p units better in phenotype compared with unselected animals. And they will be S_g units better in breeding value. For multiple traits we can have a vector for S_p and S_g.

The phenotypic superiority in S_p is relevant for predicting future realisations of phenotype for the selected animals, referring to 2a, and the genotypic superiority in S_g is relevant for predicting future realisations of phenotype of their descendants (2b).

Note that P = A + E where A is the breeding value and E is the random residual (non-genetic/environmental) effect on phenotype. For descendants we can predict superiority in A but not in E. For the animals itself, we can also predict future E to some extent, as there are correlations between traits, both in A and in E, i.e. there is a genetic covariance as well as an environmental covariance between traits measured on the same animal.

The correlation between phenotype (P) and breeding value (A) is equal to the square root of heritability (h) when it concerns the same trait and it is $h.r_A$ when it concerns different traits. The correlation between subsequent phenotypes of the same trait on the same animal is equal to the square root of repeatability and in general, the correlation between phenotypes on the same animal is equal to the phenotypic correlation.

The superiority of selected animals (S) is their average value relative to the whole cohort, or equally, relative to a randomly selected group of the cohort. Phenotypic and genetic superiority can be predicted by regressing the relevant phenotypes and breeding values on information sources we select on. Superiority of selected animals can be predicted as:

$$S = i.r.\sigma$$

where *i* is the selection intensity, *r* is the accuracy of selection and σ is the standard deviation of a target variable. This target value can be a future phenotype or breeding value for a single trait, or, more commonly, it can be an overall profit value from an amalgamation of values for multiple traits and their economic value, i.e. multiple trait (breeding) objective. The accuracy of predicting the target value depends on the information used. When predicting future phenotype for the animal itself, repeatability and phenotypic correlations are relevant parameters. When predicting breeding value, heritability and genetic correlations are important (as well as phenotypic correlation if predicted directly from phenotypic information). Selection index theory can be used to predict selection superiorities, from the regression of the breeding objective on the information that is used to predict it. Let matrix P be the variance-covariance matrix between the information sources and G is a matrix between the information sources and the breeding objective traits; their breeding value if predicting S_g and their phenotype is predicting S_p, and v is a vector with economic values of these traits, then the regression is a vector $b = P^{-1}Gv$, and the accuracy of predicting the breeding objective is the square root of $b'Pb/vCv$, where C is the variance-covariance matrix of the (true) breeding values of the objective traits and the selection differentials are $b'G/\sqrt{(b'Pb)}$.

For the project predictions the MERINOSELECT parameters and economic values were used. The project compared the Merino Lamb (ML) and Sustainable Merino (SM) indexes. Currently the genetic and residual correlations between the new component reproduction traits and all other traits in MERINOSELECT are not yet fully estimated. Therefore used, number of lambs weaned (NLW) instead of the component reproduction traits. The project used the new indexes but had to estimate the economic value of NLW from the component reproduction traits. To do this the genetic correlations between the component reproduction traits and their economic values was utilised. The economic weightings used are in Table 5.

Table 5. Traits and parameters as well as economic values used for traits used in the CB analysis

Trait Name	Units	Phenotypic Stand. Dev	Herit ability	Economic Values	
				ML index	SM index
acfw	kg	0.57	0.37	0.60	0.53
afd	micron	1.35	0.59	-2.34	-2.39
ass	n	10.09	0.24	0.10	0.09
awt	kg	5.70	0.40	-0.51	-0.72
bwt	kg	0.75	0.17	0.00	0
ebwr	score	0.84	0.36	-9.00	-9
edag	score	1.00	0.15	0.00	-6
hcfw	kg	0.46	0.39	0.09	0.24
hfd	micron	1.27	0.62	-0.49	-1.24
hss	n	10.47	0.19	0.02	0.06
hwt	kg	5.20	0.41	0.00	0.2
imf	%	1.18	0.61	5.80	0
lmy	%	2.14	0.43	1.51	1.16
nlw	lambs	0.65	0.06	66.29	80
pcfw	kg	0.39	0.27	0.17	0.39
pfd	micron	1.06	0.56	-1.20	-2.37
pfec	worms	2.88	0.20	0.00	-0.13
pss	n	10.63	0.23	0.05	0.11
pwt	kg	4.82	0.27	1.09	0.97
wwt	kg	4.04	0.21	0	0

The superiority of the ewes selected for replacement can be calculated using selection index theory. There will be a selection differential (difference between selected group and the cohort), for each trait, both genetically and phenotypically. Genetic (S_g) and phenotypic (S_p) selection differential refers to the superiority of the expected breeding value and future phenotypes of the animals in the selected group. The genetic superiority will be expressed in future progeny and depends on the predicted breeding value of the selected animals. The phenotypic superiority will be expressed in future phenotypic expression of the selected ewes. When selection is based on early phenotypes, breeding values and future phenotypes can be predicted from the covariance between these early phenotypes with breeding value and future phenotypes, respectively. Both S_g and S_p are shown in Table 6 for adult traits, comparing these for selection on phenotype measured at postweaning age (pWT, pFD and pFW). The table shows a difference in predicted breeding value when selecting on a genomic test with moderate accuracy (equivalent to having 5 progeny for each trait). When selecting on estimated breeding values, as predicted from the genomic test, there is no difference in genetic and phenotypic superiority of the selected group of animals. Note that the values in Table 6 are for one unit of selection intensity, therefore the actual superiority of a selected group needs multiplication of these values with the selection intensity.

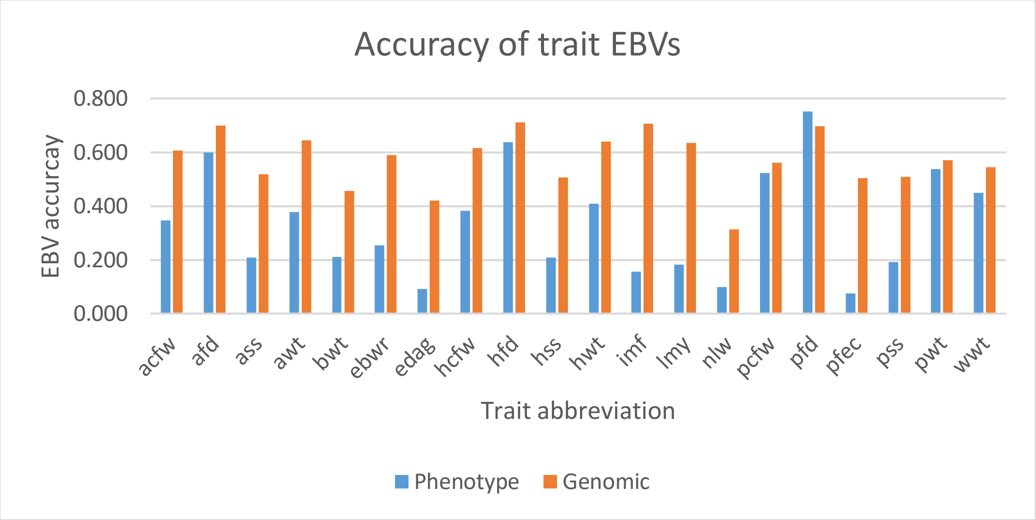
Table 6. Comparing genetic (S_g) and phenotypic (S_p) selection superiority for all traits (per unit of selection intensity) and selection accuracy of EBV of ewes selected base on either phenotypic information (postweaning WT, FD and CFW) or genomic information using the SM index (shaded traits are adult traits and nlw).

		Selection on Phenotype			Genomic Selection	
Trait	Units	Sg	Sp	EBV Accuracy	Sg	EBV Accuracy
SM Index	$	3.942	4.448	0.244	7.183	0.444
acfw	kg	-0.077	-0.053	0.345	-0.082	0.606
afd	micron	-0.426	-0.374	0.599	-0.291	0.698
ass	n	-0.633	-0.565	0.208	-0.317	0.518
awt	kg	0.489	0.904	0.377	0.454	0.644
bwt	kg	0.040	0.045	0.212	0.017	0.455
ebwr	score	-0.014	-0.024	0.255	-0.183	0.590
edag	score	-0.035	-0.033	0.093	-0.061	0.420
hcfw	kg	-0.065	-0.060	0.384	-0.066	0.616
hfd	micron	-0.430	-0.380	0.637	-0.274	0.711
hss	n	-0.585	-0.520	0.208	-0.288	0.506
hwt	kg	0.474	0.619	0.408	0.523	0.641
imf	%	0.052	0.037	0.157	-0.032	0.707
lmy	%	0.166	0.188	0.182	0.244	0.634
nlw	lambs	0.011	0.012	0.100	0.040	0.314
pcfw	kg	-0.059	-0.055	0.524	-0.039	0.561
pfd	micron	-0.377	-0.330	0.753	-0.208	0.697
pfec	worms	0.025	0.026	0.075	-0.094	0.503
pss	n	-0.635	-0.573	0.191	-0.255	0.508
pwt	kg	0.611	1.493	0.537	0.490	0.571
wwt	kg	0.348	0.775	0.450	0.300	0.545

When selecting on early phenotypes, it is generally expected to have better phenotypes in the selected animals at later ages, due to the phenotypic correlations with the trait selected for, i.e. more selection differential for phenotypes ($S_{p)}$) than for genotypes (S_g). However, there are unfavourable correlations between some wool traits, in particular fibre diameter and fleece weight, and as a result these differences are harder to predict. For example, in Table 6 the S_p value for weight (awt) is clearly higher than the S_g value but for fibre diameter and fleece weight the selection differentials in S_p are lower. The heritabilities for FD relative to FW are relatively higher that the ratio in repeatability or those traits, and as a result the accuracy of predicting breeding values is relatively higher for FD than the accuracy of predicting future phenotypes. Selection in EBV pulls harder on FD with a resulting slight negative response for FW, but when selecting on phenotypes, the pull on FD is slightly less hard, with as a result also less loss in FW.

The accuracy of prediction breeding values for all traits is shown in Figure 7, comparing selecting based on early phenotypes versus selection based on a genomic test.

Figure 7. Comparing accuracies of predicting genetic merit based on either phenotypic selection or genomic selection.



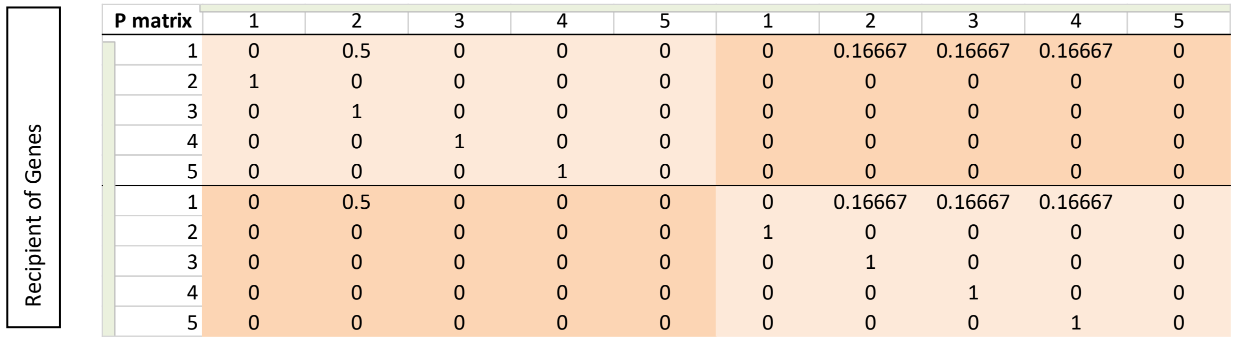
4.5.2 Future expressions of selection superiority

After predicting the phenotypic and genetic superiority of selected individuals we have to predict the future expressions of phenotypes of these selected individuals and expression of their breeding value in the phenotypes of their descendants.

Future expressions of progeny will depend on genetic relationships. How many of these expressions and when they will occur can be predicted deterministically using a *GENEFLOW* method. This method predicts the contribution of selected individuals to future generations. Alternatively, a stochastic simulation can be used to get more precise values. Deterministic simulation does not account for reduced variance after selection, inbreeding or complex family relationships in the population. The *GENEFLOW* method also does not account for the fact that the better animals within the cohort of selected parents will leave more genetic contributions in the future than others, as their progeny are more likely to be selected. But a deterministic method is easier to understand and can be useful to look at approximate figures.

The *GENEFLOW* method requires a matrix that specifies how genes are transmitted in a population from animals in different age classes. This is called a transition matrix P. For example, all newborn animals in age class 1 will receive half of their genes from selected dams, possibly from age classes 2, 3 and 4, and the other half from sires, possibly only from age class 2. Animals in all other age classes will receive their genes from the previous age classes through ageing. Therefore, a transition matrix can look like this, with the donors of genes in the column and the recipient age classes in the rows. Any age structure can be fitted, as well as more age classes. An example is given in Table 7.

Table 7. Example of geneflow within a nucleus, assuming sires are used only once, and dams for 3 matings (recipients of genes in rows, donors of genes in columns)



		Sire age classes					Dam age classes				
	P matrix	1	2	3	4	5	1	2	3	4	5
Recipient of Genes	1	0	0.5	0	0	0	0	0.16667	0.16667	0.16667	0
	2	1	0	0	0	0	0	0	0	0	0
	3	0	1	0	0	0	0	0	0	0	0
	4	0	0	1	0	0	0	0	0	0	0
	5	0	0	0	1	0	0	0	0	0	0
	1	0	0.5	0	0	0	0	0.16667	0.16667	0.16667	0
	2	0	0	0	0	0	1	0	0	0	0
	3	0	0	0	0	0	0	1	0	0	0
	4	0	0	0	0	0	0	0	1	0	0
	5	0	0	0	0	0	0	0	0	1	0

Now, if using one cohort of selected males in the nucleus, then a unit of selection superiority will flow through the nucleus population as follows in the next 10 years. This is shown in Table 8, where g_i refers to the vector of gene expressions in year i, and g_i values are shown for all five age classes of nucleus males. Each g_{i+1} is derived by multiplying the previous g_i by the transition matrix P, i.e. $g_{i+1} = P.g_i$ and g_0 is has a value of 1 placed in the first element, to reflect one unit of genetic superiority in a selected cohort of nucleus males (Table 8).

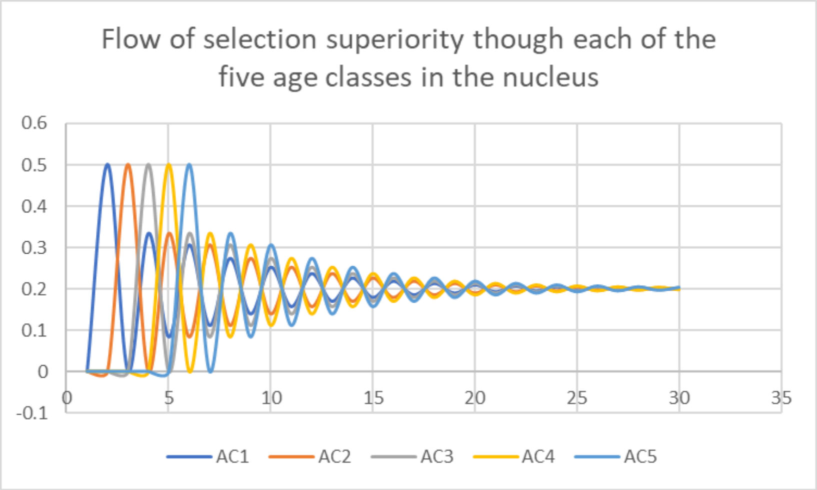
Table 8. Expression of genetic superiority in g_i in year I, in five different age classes in a nucleus

age class	g1	g2	g3	g4	g5	g6	g7	g8	g9	g10
1	0.00	0.50	0.00	0.33	0.08	0.31	0.11	0.27	0.14	0.25
2	1.00	0.00	0.50	0.00	0.33	0.08	0.31	0.11	0.27	0.14
3	0.00	1.00	0.00	0.50	0.00	0.33	0.08	0.31	0.11	0.27
4	0.00	0.00	1.00	0.00	0.50	0.00	0.33	0.08	0.31	0.11
5	0.00	0.00	0.00	1.00	0.00	0.50	0.00	0.33	0.08	0.31

The newborns in year 2 receive 50% of their genes from the selected sires. Note that the newborn animals in year 3 do not get the superiority as we look only at one round of selection and sires were only used once. The newborn in year 4 receive genes from the sons and daughters of initially selected males, i.e. grand-progeny of the selected sires. There is initially quite a bit of oscillation of when and where the selection superiority is expressed, but on the long term is converges to an equal value for all age classes (Figure 8). This value is 0.2 in our example, which is exactly the inverse of the sum of the male and female generation interval: $1/(L_m + L_f)$. This is also derived in the well-known response formula for genetic gain (dg) which is equal to selection superiority of selected parents divided by the generation interval:

dg = $(S_m + S_f)/(L_m + L_f)$, and the long term gain from one unit of superiority is $1/(L_m + L_f)$.

Figure 8. Expression superiority of select nucleus males in future years for various nucleus age classes



Multi-tier structure

In a typical production system, there is a nucleus, selling males to lower tiers, and the actual expression of genetic gain is in the commercial tier. In sheep and cattle, the nucleus consists of the breeding studs. Nucleus born animals receive their genes from selected nucleus parents. Sires used for the commercial tier are born in the nucleus, as in the diagram below, which represents a 2-tier system, or they could be from a multiplier tier. In the scheme below, we assume that nucleus born males are mated to breeding females in the commercial flocks. So, males born in the commercial tier are not used for reproduction.

Figure 9. Schematic diagram of cohorts in a 2-tier geneflow transition matrix

Sn<Sn	Sn<Dn	Sn<Sc	Sn<Cm	Sn<Cf	Sn	Sires of Nucleus		
Dn<Sn	Dn<Dn	Sf<Sc	Dn<Cm	Dn<Cf	Sf	Dams of Nucleus		
Sc<Sn	Sc<Dn	Sc<Sc	Sc<Cm	Sc<Cf	Sc	Stud born males to contribute to commercial		
Cm<Sn	Cm<Dn	Cm<Sc	Cm<Cm	Cm<Cf	Cm	Commercial born males		
Cf<Sn	Cf<Dn	Cf<Sc	Cf<Cm	Cf<Cf	Cf	Commercial born females		

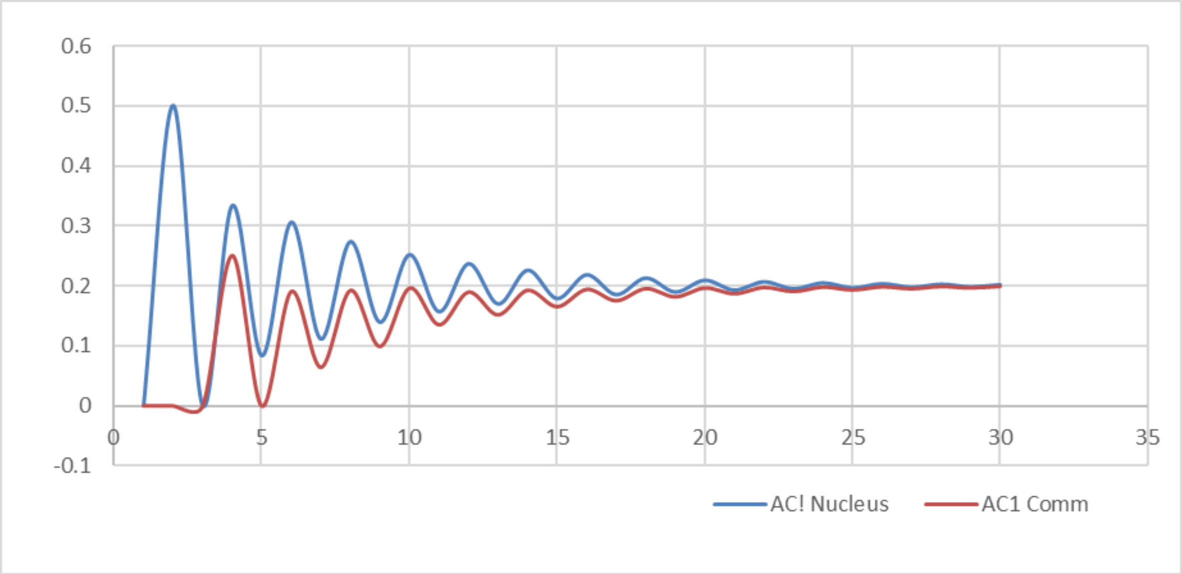
The flow of genes from sires selected for the nucleus is shown below. Assume that these sires get progeny at the age of 2 years and are only used once. The first age class in the nucleus (AC1) receive these genes, which make up 50% of their genetic makeup. Then, two years later the nucleus born animals retain 25% as these are grandsons of the sires originally selected. They also get some of this improvement via the dams, dams are used for 3 years, so 1/3 of 25% is added via the dam pathway. The newborn animals in the commercial flocks receive these improved genes somewhat later. Also, the pattern is slightly different as it is assumed that the sires used in the commercial flocks are used for 3 years.

Figure 10 Expression of genetic superiority in age class 1 (AC1) in nucleus and commercial tiers

Year	YR1	YR2	YR3	YR4	YR5	YR6	YR7	YR8	YR9	YR10
AC! Nucleus	0	0.5	0	0.333335	0.083335	0.305559	0.111114	0.273154	0.138893	0.25155
AC1 Comm	0	0	0	0.25	0	0.208334	0.083334	0.229169	0.104168	0.223383

Figure 10 shows the same geneflow, as a graph, as expressed in age class 1 (AC1) in the nucleus and commercial tiers. The superiority of selected nucleus males is expressed in the commercial tier a bit late, but ultimately gets equal benefit each year.

Figure 11. Expression of nucleus male selection superiority in newborn animals in the nucleus and the commercial tiers

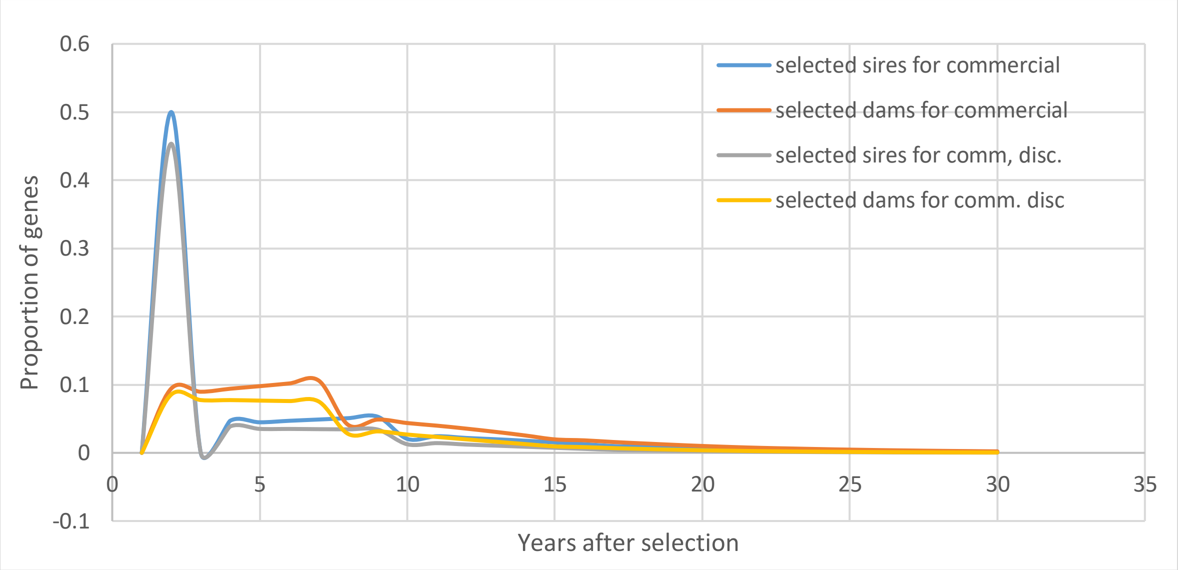


The superiority of nucleus sire and dam selection have stable contributions of $1/(L_m + L_f)$ in the long run to both nucleus and commercial tiers.

Figure 11 shows the expression of superiority of selecting better rams from the nucleus for the commercial flock and selecting replacement ewes for the commercial flock. Both graphs show that these contributions are only short term, as in the long term they will be taken over by new geneflow from the nucleus. Hence, superiority created in nucleus mating will last as it is ‘recycled’ in the nucleus and passed on to lower tiers. Superiority created below the nucleus will fade out. Think of using a Dorset ram once in a Merino stud. Within the stud a proportion of the Dorset will remain. However, when using only once a Dorset ram once in a commercial flock, the Dorset footprint in that flock will be completely wiped out after several years of using Merino rams again. Note that contributions of sires and dams in the commercial flocks are similar, but not equal, as dams are used over more years while the sires are used only once (in this example).

The total future contribution of selected animals is calculated as the sum of contributions over the years, basically the area under the curve. However, future contributions are discounted by a factor $1/(1+r)^n$ where r is the discount rate (inflation adjusted interest rate) and n is the number of years in the future. We call these contributions *Cumulative Discounted Expressions* (CDE). The expression will also depend on when a trait is expressed, and how often.

Figure 11. Expression and discounted expression of selected sires and commercial replacement females in the offspring in the commercial tier. Sires are used only once while the proportion of ewes in age class 2-7 is [18.9% 17.9% 17.0% 16.2% 15.4% 14.6%]



When calculating economic values of traits for a breeding objective, these economic values should consider the difference between traits in frequency and timing of expressing that trait. So, we will calculate CDE values as expressed in the first age class only.

Finally, the value of selecting better animals needs to consider the number of animals that express this. The easiest way to calculate that is to multiply the vector of expressions (which reflect the proportion of expressions in an age class) by the number of breeding ewes in the flock. This would give the total expression in a flock. Since economic values are calculated on a per ewe basis, we will multiply the expression in the females by the commercial flock size, i.e. number of breeding ewes. The total expression in the flock can then be divided by the number of selected animals to find the number of expressions per selected animal. Effectively this is the same as multiplying the expression of a single individual with the number of matings in an animal's lifetime. Table 9 shows how one unit of superiority of replacement dams will be expressed in the first female age class over a 10-year period, both without and without discounting, and the last row shows the total number of expression in a 1000 ewe flock. The flock age structure is such that ewes are distributed over age class 2-7 as 18.9%, 17.9%, 17.0%, 16.2%, 15.4%, and 14.6%, respectively. Note that the sum of the expressions is 0.76 being the sum of expression in direct progeny, grand progeny etc. After discounting this reduced to 0.578, and the total expression in a whole flock is 0.578 times the flock size. The benefit per selected ewe is then the total amount of expression divided by the number of ewes selected, i.e. 578/189 = 3.06. Each selected ewe will have 1000/189 = 5.29 matings as a breeding ewe and each mating will result in 0.578 expressions, which also leads to 5.29 x 0.578 = 3.06 expressions per selected ewe.

Table 9. Expression per individual, without and with discounting and the total number of expression per unit of selection superiority in selected ewe replacements in a 1000 ewe commercial flock.

Year	0	1	2	3	4	5	6	7	8	9	10	Sum
Expression	0.00	0.094	0.090	0.094	0.098	0.102	0.106	0.041	0.049	0.044	0.040	0.76
Disc.Expr	0.00	0.086	0.077	0.077	0.077	0.076	0.075	0.028	0.031	0.027	0.023	0.578
Total Expr	0	85.60	77.45	77.40	76.66	75.98	75.31	27.68	31.49	26.84	23.35	578

When we keep better replacement ewes, there will an advantage of having these as better animals in the flock This is due to a phenotypic superiority of the selected animal. Figure 12 shows the phenotypic and genotypic expressions of selecting better ewes. The phenotypic contribution equal to the proportion of selected ewes in the flock, e.g. 18.9% in the first year, but there is not benefit if all selected ewes have been culled, after 7 years (Figure 11). The genetic expression is through the offspring and is about half of the phenotypic expression, with smaller expressions in later descendants. The phenotypic expressions sum to 1 (Table 10) but after discounting the CDE of this expression in its own future phenotype is 0.81. The CDE of the genetic contribution to descendants is equal to 0.67 which is the sum of its contributions to offspring, grand-offspring etc., so a bit higher than 0.5.

Figure 12. Genetic and phenotypic superiority of selected ewes in a flock.

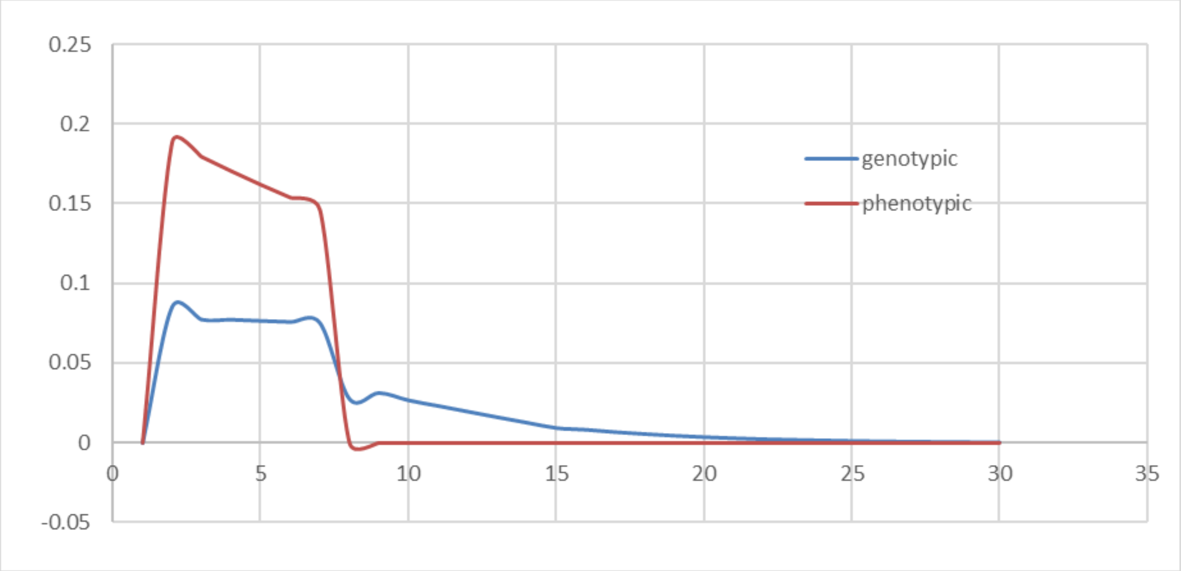


Table 10. Expression of phenotypic and genotypic superiority of selected replacement ewes in the commercial flock.

Year	YR1	YR2	YR3	YR4	YR5	YR6	YR7	YR8	YR9	YR10
genotypic	0.000	0.094	0.090	0.094	0.098	0.102	0.106	0.041	0.049	0.044
phenotypic	0.000	0.189	0.179	0.170	0.162	0.154	0.146	0.000	0.000	0.000

The sum of these expressions, when accumulated over 20 years and discounted, is equal to 0.81 and 0.67 for the phenotypic and genotypic components, i.e. $CDE_g = 0.67$ and $CDE_p = 0.81$. The total value for the commercial flock of selecting better female replacements is equal to:

$$i.(S_p * CDE_p + S_g CDE_g).\ EconVal$$

where i is the selection intensity, S_p and S_g are the phenotypic and genetic selection differential (per unit of selection differential), CDE_p and CDE_g are the phenotypic and genetic cumulative discounted future expressions of traits in the entire commercial flock (0.81 x 1000 and 0.67 x 1000, respectively), and EconVal is the economic value for each trait. We will use 20 traits, reflecting breeding objectives for the Merino Lamb (ML) index and the Sustainable Merino (SM) index. Hence, S_p and S_g as well as EconVal are vectors for 20 traits and the value can be accumulated over all traits, resulting in an overall dollar value per selected animal.

4.5.3 Value of selecting better replacement females

Flock Age structure.

Key Parameters

Nr. of breeding ewes in commercial flock:	1000
Weaning rate: lambs per breeding ewe	1.2
Attrition rate breeding ewes (per annum)	10%
Cast for age	7 years
Proportion of selection candidates genotyped	80%

Derived parameters

Age structure	(see Table 11)
replacement rate is	213/1000 = 21%
number of ewes selected as hogget age	237
number of selection candidates suitable (and genotyped)	432
selected proportion females	237 / 432 = 54%
selection intensity	0.72
number of breeding females expressing the benefit	213

Table 11 Example of flock age structure, assuming 1000 breeding ewes with a weaning rate of 1.2, an attrition rate of 10% p.a. and cast for age after 7 years (6 matings)

Age Class	Breeding females	Males	Females
0		600	600
1	237	540	540
2	213		213
3	192		192
4	173		173
5	156		156
6	140		140
7	126		126
8	0		
9	0		
10	0		
Sum AC2 -10	1000		

Selection superiority

We compare selection on phenotype measured at postweaning age (pWT, pFD and pFW) with selection based on a genomic test, either moderate accuracy (5p) or high accuracy (20p). The selection accuracies are the same as those in Table 12. The selection intensity is 0.72.

Table 12. Index selection superiority of selected ewes for flock replacement for varying amounts of information selected on[1]

Index selection superiority of selected replacement ewes	SM Index	ML Index
selection on phenotype	\$2.85	\$2.40
selection on genotype (5p)	\$5.19	\$4.85
selection on genotype (20p)	\$7.59	\$6.98

[1] Selection on phenotype measured at postweaning age (pWT, pFD and pFW) with selection based on a genomic test, either moderate accuracy (5p) or high accuracy (20p).

The phenotypic superiority of selected ewes based on phenotypic selection is \$3.21 based on the SM index, and \$2.87 based on the ML index.

The total value for the commercial flock of selecting better female replacements is equal to:

$$i.(S_p * CDE_p + S_g CDE_g).\ EconVal$$

where i is the selection intensity, S_p and S_g are the phenotypic and genetic selection differential, CDE_p and CDE_g are the phenotypic and genetic cumulative discounted future expressions of traits in the entire commercial flock (0.81 x 1000 and 0.67 x 1000, respectively), and EconVal is the economic value for each trait. We will use 20 traits, reflecting breeding objectives for the Merino Lamb (ML) index and the Sustainable Merino (SM) index. Hence, S_p and S_g as well as EconVal are vectors for 20 traits and the value can be accumulated over all traits, resulting in an overall dollar value per selected animal.

Table 13 shows the benefit of selection, expressed in dollar value per selected ewe. The table compares selection on early phenotypes, moderate accuracy in genomic selection (equivalent to 5 progeny per selected animal) and accurate genomic selection (equivalent to 20 progeny per selected animal). We assume the breeding objective is the SM index. The benefits are detailed for each trait group. In the example there are 213 selected ewes expressing the benefit while there was 432 that were genotyped. The break-even cost is therefore calculated as the profit per selected animal divided by the number of animals that had to be tested per selected animal (432/213) = 2.024.

Table 13 Benefit (per selected replacement ewe) per trait group and total benefit of three selection strategies for replacement females in a commercial flock, and the break-even cost of collecting the information used for selection, using 20 traits with economic values according to the SM Index.

Selection on phenotype	Phenotypic benefit	Genotypic benefit	Total benefit	Relative contribution
wool	$ 3.86	$ 5.33	$ 9.19	65%
repro	$ 2.95	$ 2.00	$ 4.95	35%
meat	-$ 1.62	$ 1.21	-$ 0.41	-3%
other	$ -	$ 0.47	$ 0.47	3%
total	$ 5.19	$ 9.01	$ 14.19	100%
Break-even measurement cost			$ 7.01	
Selection on genotype (5p)				
wool	$ 2.89	$ 6.91	$ 9.80	34%
repro	$ 10.03	$ 7.40	$ 17.43	61%
meat	-$ 0.68	$ 1.23	$ 0.55	2%
other	$ -	$ 0.87	$ 0.87	3%
total	$ 12.24	$ 16.41	$ 28.66	100%
Break-even genotype cost			$ 14.16	
Selection on genotype (20p)				
wool	$ 3.14	$ 8.57	$ 11.70	27%
repro	$ 17.18	$ 12.67	$ 29.84	68%
meat	-$ 0.61	$ 1.58	$ 0.97	2%
other	$ -	$ 1.18	$ 1.18	3%
total	$ 19.71	$ 23.99	$ 43.69	100%
Break-even genotype cost			$ 21.58	

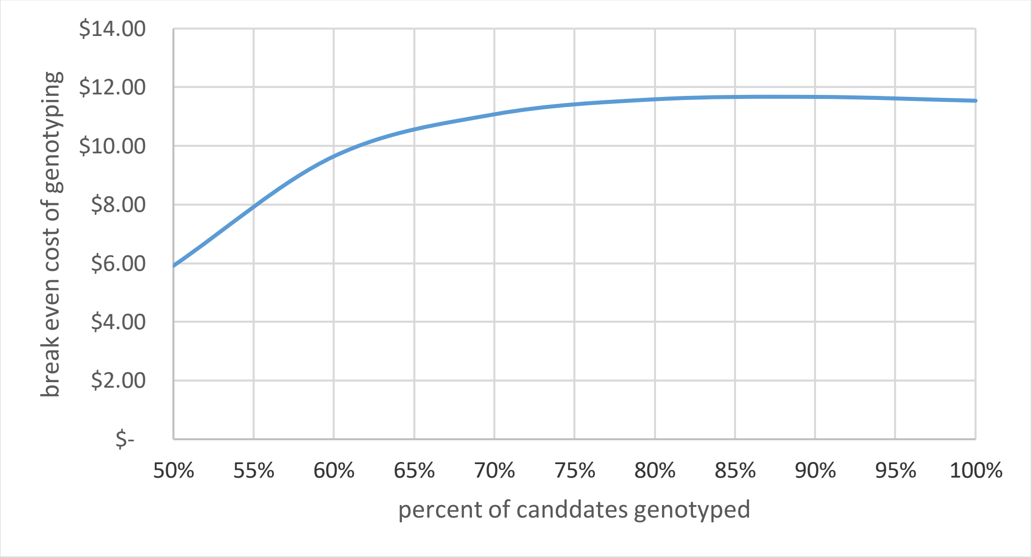
Note that the difference between phenotypic selection and genomic selection is not only the larger selection differential and benefit that can be obtained with genomic selection. There is also a shift towards more benefit for hard to measure traits, such as reproduction and other traits related to sustainability. In the ML index, there is more emphasis on meat traits with genomic selection.

Table 14. Benefit (per selected replacement ewe) per trait group and total benefit of three selection strategies for replacement females in a commercial flock, and the break-even cost of collecting the information used for selection, using 20 traits with economic values according to the ML Index

Selection on phenotype	Phenotypic benefit	Genotypic benefit	Total benefit	Relative contribution
wool	$ 2.35	$ 3.61	$ 5.96	56%
repro	$ 2.26	$ 1.70	$ 3.96	37%
meat	-$ 1.43	$ 2.19	$ 0.76	7%
other	$ -	$ -	$ -	0%
total	$ 3.18	$ 7.50	$ 10.68	100%
Break-even measurement cost			$ 5.28	
Selection on genotype (5p)				
wool	$ 2.01	$ 5.04	$ 7.05	30%
repro	$ 6.28	$ 5.19	$ 11.47	49%
meat	-$ 0.04	$ 4.98	$ 4.94	21%
other	$ -	$ -	$ -	0%
total	$ 8.25	$ 15.20	$ 23.46	100%
Break-even genotype cost			$ 11.59	
Selection on genotype (20p)				
wool	$ 2.05	$ 6.52	$ 8.57	24%
repro	$ 11.30	$ 9.35	$ 20.65	59%
meat	-$ 0.07	$ 5.99	$ 5.92	17%
other	$ -	$ -	$ -	0%
total	$ 13.28	$ 21.86	$ 35.14	100%
Break-even genotype cost			$ 17.36	

Overall, it seems that the value is generally not enough to cover costs of genotyping. The break-even cost is much lower than a typical cost of genotyping. The break-even cost depends on several assumed parameters, in particular weaning rate and replacement rate. If ewes are kept longer and have more offspring, the selection intensity will be higher. A higher weaning rate will also give a higher number of progeny per ewe. For example, a weaning rate of 1.5 would give a break -even cost of genotyping of $11.54 for the ML index, rather than $11.59 as in the Table 14 above (weaning rate 1.2) as the extra benefits per ewe are offset by more genotyping per selection candidate, i.e. there are more selection candidates. The proportion of selection candidates that is genotyped may vary, with a lower proportion genotyped giving lower costs but also lower selection intensity. Genotyping a larger proportion is more beneficial. Regarding the other parameters, the attrition rate has a small effect (e.g. for attrition rates of 10% and 5%, the break-even cost of modest accuracy genotyping is $11.59 and $13.76, respectively), whereas the flock size has no effect. Table 14 shows clearly that the accuracy of the genomic test has a large effect on the break-even cost of genotyping.

Figure 13. Break even cost of genotyping (moderate accuracy) for ewe replacement depending on proportion of candidates genotyped (ML Index)



4.5.4 Value of selecting better rams from the multiplier

Multiplier Flock Age structure.

Key Parameters

In Commercial flock:

Nr. of breeding ewes:	8000
Nr of progeny per sire (per year)	50
Nr of years sires are used in commercial flock	3

In multiplier flock:

Nr. of breeding ewes:	400
Weaning rate per breeding ewe	1.2
Attrition rate breeding ewes (per annum)	10%
Cast for age	7
Proportion of selection candidates genotyped	80%

Derived parameters

Age structure	(see Table 15)
replacement rate ewes in multiplier	85/400 = 21%
number of ewes selected as hogget age for mult flock.	95

number of selection candidates suitable (and genotyped)	173
selected proportion repl. Ewes multiplier flock	95/ 173 = 55%

number of rams selected for use in commercial flock	59
selected proportion multiplier rams for commercial flock	59/ 173 = 34%
selection intensity multiplier rams for commercial flock	1.07

Table 15. Example of flock age structure in multiplier flock, assuming 400 breeding ewes with a weaning rate of 1.2 , an attrition rate of 10% p.a. and cast for age after 7 years (6 matings). The males in age classes 2-4 are used as sires in the commercial flock

Multiplier flock age structure

ac	Multiplier Ewes	Males	Females
0	105	240	240
1	95	216	216
2	85	59	85
3	77	53	77
4	69	48	69
5	62	0	62
6	56	0	56
7	50	0	50
8	0	0	0
Total breeding animals (AC 2-8)	400	160	

Selection superiority

Comparing selection on phenotype measured at postweaning age (pWT, pFD and pFW) with selection based on a genomic test, either moderate accuracy (5p) or high accuracy (20p). The selection accuracies are the same as those for female selection (see previous section). The selection superiority will be higher as the selection intensity of males selected for the commercial flock is 1.07. We are now only interested in the genetic selection superiority and will ignore the better phenotype for wool traits by the selected rams themselves.

Table 16. Index selection superiority of selected multiplier males for varying amount of information selected on[1]

Index selection superiority of selected multiplier males	SM Index	ML Index
selection on phenotype	$ 4.24	$ 3.56
selection on genotype (5p)	$ 7.72	$ 7.21
selection on genotype (20p)	$ 11.28	$ 10.37

[1] *Selection on phenotype measured at postweaning age (pWT, pFD and pFW) with selection based on a genomic test, either moderate accuracy (5p) or high accuracy (20p).*

<u>Value of selecting better multiplier males for the commercial flock.</u>

The total value for the commercial flock of selecting multiplier males as sires for the commercial flock is equal to:

$$i.\ S_{g.}CDE_{g}\ .\ EconVal$$

where i is the selection intensity, S_g is the genetic selection differential, CDE_g is the genetic cumulative discounted future expressions of traits in the entire commercial flock and EconVal is the economic value for each trait. The value of CDE_g is equal to 5770.9 for a commercial flock size of 8000 ewes. We will use again 20 traits, reflecting breeding objectives for the Merino Lamb (ML) index and the Sustainable Merino (SM) index. Hence, S_g as well as EconVal are vectors for 20 traits and the value can be accumulated over all traits using EconVal, resulting in an overall dollar value per selected animal

Table 17 shows the benefit of selection, expressed in dollar value per selected ram. The table compares selection on early phenotypes, moderate accurate genomic selection (equivalent to 5 progeny per selected animal) and accurate genomic selection (equivalent to 20 progeny per selected animal). We assume the breeding objective is the SM index. The benefits are detailed for each trait group. In the example we ended up with 59 selected rams expressing the benefit while 173 rams were genotyped (80% of 216 1 year old males). The break-even cost is therefore calculated as the profit per selected animal divided by the number of animals that had to be tested per selected animal (173/59) = 2.92

Table 17. Benefit (per selected male) per trait group and total benefit of three selection strategies for selecting multiplier rams for use in the commercial flock and the break-even cost of collecting the information used for selection, using 20 traits values according to the SM Index.

Selection on phenotype	Genetic benefit	
wool	$ 244.77	59%
repro	$ 91.96	22%
meat	$ 55.81	13%
other	$ 21.48	5%
total	$ 414.02	100%
Break-even measurement cost		$ 141.46
Selection on genotype (5p)	Genetic benefit	
wool	$ 317.64	42%
repro	$ 340.03	45%
meat	$ 56.70	8%
other	$ 39.94	5%
total	$ 754.32	100%
Break-even genotype cost		$ 257.73
Selection on genotype (20p)	Genetic benefit	
wool	$ 393.62	36%
repro	$ 582.12	53%
meat	$ 72.47	7%

other	$ 54.03	5%
total	$ 1,102.25	100%
Break-even genotype cost		$ 376.61

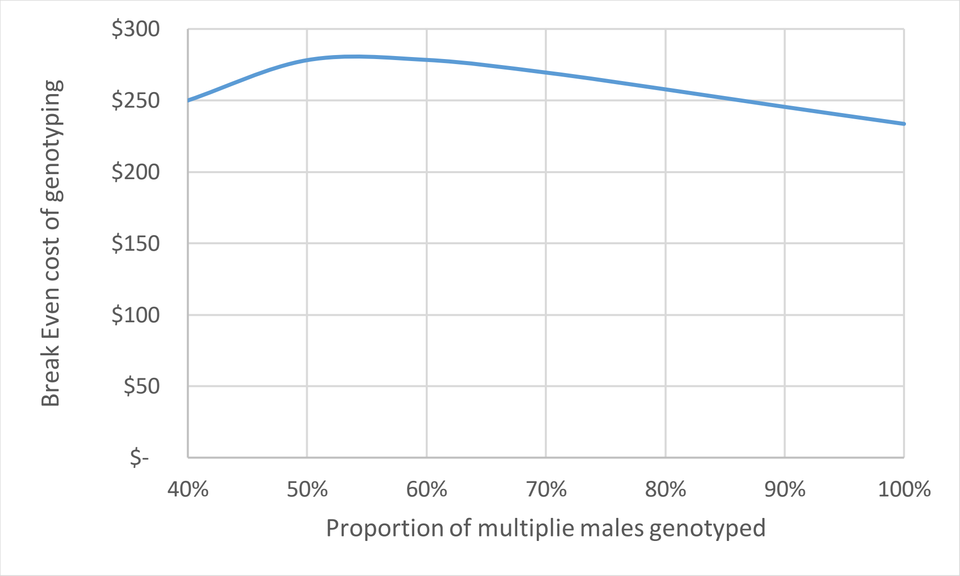
Note again that the difference between phenotypic selection and genomic selection is not only the larger selection differential and benefit that can be obtained with genomic selection. There is also a shift toward more benefit for hard to measure traits, such as reproduction and other traits related to sustainability. In the ML index, there is more emphasis on meat traits with genomic selection.

Table 18 Benefit (per selected male) per trait group and total benefit of three selection strategies for selecting multiplier rams for use in the commercial flock and the break-even cost of collecting the information used for selection, using 20 traits values according to the ML Index

Selection on phenotype	Genetic benefit	
wool	$ 167.26	48%
repro	$ 78.78	23%
meat	$ 101.68	29%
other	$ -	0%
total	$ 347.72	100%
Break-even measurement cost		$ 118.81
Selection on genotype (5p)	Genetic benefit	
wool	$ 233.55	33%
repro	$ 240.82	34%
meat	$ 230.79	33%
other	$ -	0%
total	$ 705.16	100%
Break-even genotype cost		$ 240.93
Selection on genotype (20p)	Genetic benefit	
wool	$ 302.53	30%
repro	$ 433.63	43%
meat	$ 277.78	27%
other	$ -	0%
total	$ 1,013.94	100%
Break-even genotype cost		$ 346.43

Investing in information to select rams from the multiplier males for use in the commercial flock has a positive benefit. The break-even cost is much higher than the typical cost of genotyping. Although selecting on phenotypes measured at postweaning age is already quite profitable, the benefit of investing in a genomic test is still higher due to the higher accuracy of predicting genetic merit. The break-even cost depends on a number of assumed parameters, in particular weaning rate and replacement rate. If ewes are kept longer and have more offspring, the selection intensity will be higher in both males and females selected within the multiplier. However, there are also more selection candidates, so more genotypes would be done per selected animal if the proportion genotyped is the same, making the break-even cost a bit lower. However, it would make sense then to genotype a smaller proportion of the selection candidates. The benefit per selected multiplier male and the breakeven cost of genotyping are shown in Figure 14 for a varying proportion of selection candidates genotyped. The figure shows that the break-even cost of genotyping is highest if about 60% of the multiplier male selection candidates are genotyped. The benefit per selected male is highest when they are all genotyped, because the selection intensity is highest, but the number of genotypes required per selected male relatively increases more.

Figure 14 Break-even cost of genotyping (moderate accuracy) depending on proportion of candidates genotyped (SM Index)



4.5.6 Value of selecting better females in the multiplier

Multiplier Flock Age structure.

Key Parameters

In Commercial flock

Nr. of breeding ewes:	8000
Nr of progeny per sire (per year)	50
Nr of years sires are used in commercial flock	3

In multiplier flock:

Nr. of breeding ewes:	400
Weaning rate per breeding ewe	1.2
Attrition rate breeding ewes (per annum)	10%
Cast for age	7
Proportion of selection candidates genotyped	80%

Derived parameters

Age structure	(see Table 19)
replacement rate ewes in multiplier	85/400 = 21%
number of ewes selected as hogget age for mult. flock.	95
number of selection candidates suitable (and genotyped)	173
selected proportion replacement ewes multiplier flock	95/ 173 = 55%
selection intensity replacement ewes multiplier flock	72%
number of breeding females expressing the benefit	85

Table 19. Example of flock age structure in multiplier flock, assuming 400 breeding ewes with a weaning rate of 1.2, an attrition rate of 10% p.a. and cast for age after 7 years (6 matings). The males in age classes 2-4 are used as sires in the commercial flock.

Multiplier flock age structure			
Age class	Multiplier Ewes	Males	Females
0	105	240	240
1	95	216	216
2	85	59	85
3	77	53	77
4	69	48	69
5	62	0	62
6	56	0	56
7	50	0	50
8	0	0	0
Total breeding animals	400	160	

Selection superiority

We compare again selection on phenotype measured at postweaning age (pWT, pFD and pFW) with selection based on a genomic test. The selection superiority will be equal to the selection intensity time the SD of the index which is equal to 0.72 * the SD of the index (i. S_g). We are now only interested in the genetic selection superiority and will ignore the better phenotype for wool traits by the selected rams themselves.

Table 20. Index selection superiority of selected multiplier females for varying amount of information selected on[1]

	SM Index	ML Index
selection on phenotype	$ 2.84	$ 2.39
selection on genotype (5p)	$ 5.18	$ 4.84
selection on genotype (20p)	$ 7.57	$ 6.96

[1] *Selection on phenotype measured at postweaning age (pWT, pFD and pFW) with selection based on a genomic test, either moderate accuracy (5p) or high accuracy (20p).*

Value of selecting better multiplier females for the commercial flock.

The value of selecting better female replacements in the multiplier is equal to:

$$i.\ S_g.CDE_g\ .\ \text{EconVal}$$

where i is the selection intensity, S_g is the genetic selection differential, CDE_g is the genetic cumulative discounted future expressions of traits in the commercial flock (equal to 3751.9), and EconVal is the economic value for each trait. We will use again 20 traits, reflecting breeding objectives for the Merino Lamb (ML) index and the Sustainable Merino (SM) index. Hence, S_g as well as EconVal are vectors for 20 traits and the value can be accumulated over all traits using EconVal, resulting in an overall dollar value per selected animal.

Table 21 shows the benefit of selection, expressed in dollar value per animal selected. The table compares selection on early phenotypes, moderate accurate genomic selection (equivalent to 5 progeny per selected animal) and accurate genomic selection (equivalent to 20 progeny per selected animal). We assume the breeding objective is the SM index. The benefits are detailed for each trait group. In the example we ended up with 85 selected ewes expressing the benefit while 173 were genotyped. The break-even cost is therefore calculated as the profit per selected animal divided by the number of animals that had to be tested per selected animal (173/95)= 1.83.

Table 21. Benefit (per selected ewe) per trait group and total benefit of three selection strategies for selecting multiplier ewes to improve sires for the commercial flock and the break-even cost of collecting the information used for selection, using 20 traits values according to the SM Index

Selection on phenotype	Genetic benefit	
wool	$ 63.31	59%
repro	$ 23.78	22%
meat	$ 14.43	13%
other	$ 5.56	5%
total	$ 107.08	100%
Break-even measurement cost		$ 58.78
Selection on genotype (5p)	**Genetic benefit**	
wool	$ 82.15	42%
repro	$ 87.95	45%
meat	$ 14.67	8%
other	$ 10.33	5%
total	$ 195.10	100%
Break-even genotype cost		$ 107.09
Selection on genotype (20p)	**Genetic benefit**	
wool	$ 101.81	36%
repro	$ 150.56	53%
meat	$ 18.74	7%
other	$ 13.98	5%
total	$ 285.09	100%
Break-even genotype cost		$ 156.49

Table 22. Benefit per trait group and total benefit of three selection strategies for selecting multiplier rams for use in the commercial flock and the break-even cost of collecting the information used for selection, using 20 traits values according to the ML Index

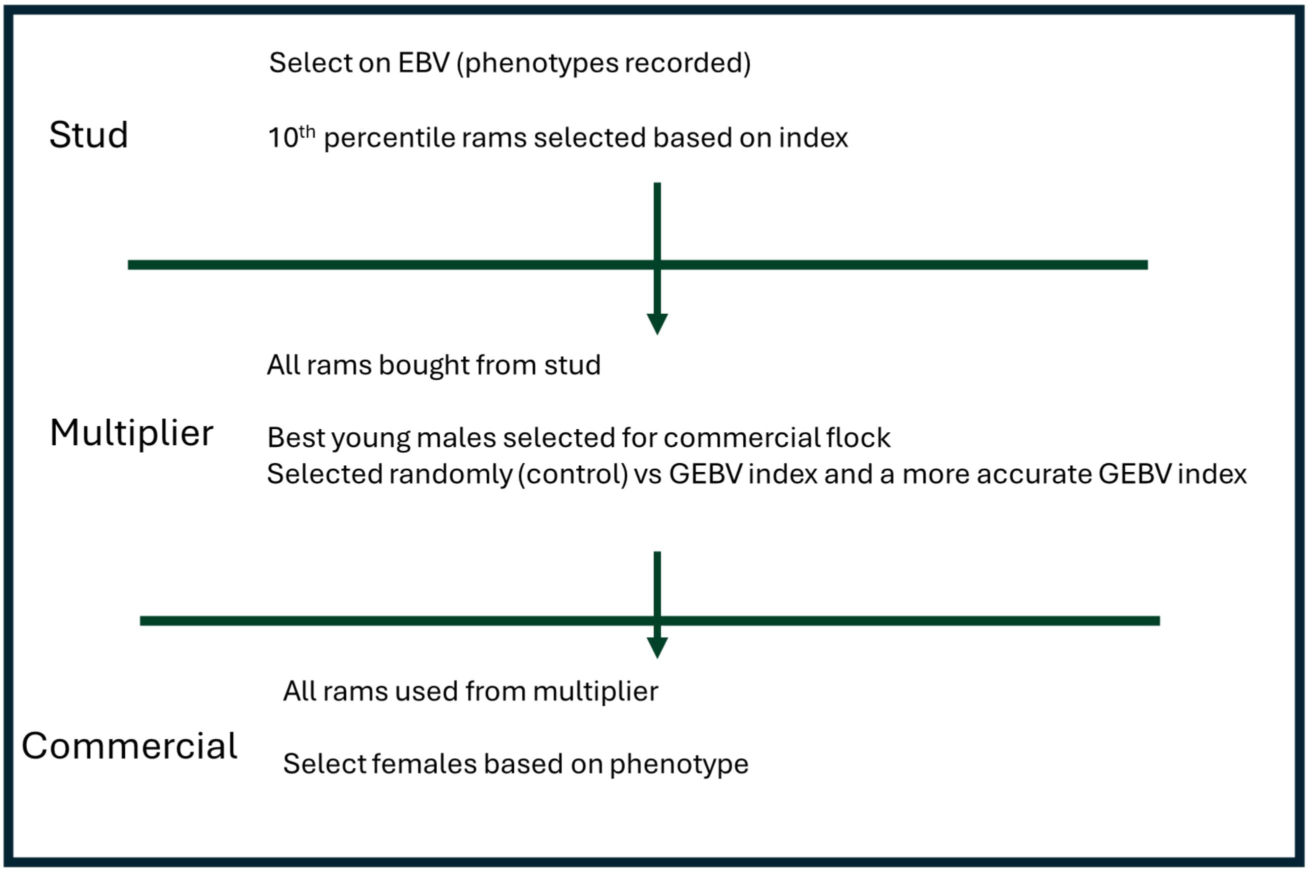
Selection on phenotype	Genetic benefit	
wool	$ 43.26	48%
repro	$ 20.38	23%
meat	$ 26.30	29%
other	$ -	0%
total	$ 89.94	100%
Break-even measurement cost		$ 49.37
selection on genotype (5p)	Genetic benefit	
wool	$ 60.41	33%
repro	$ 62.29	34%
meat	$ 59.69	33%
other	$ -	0%
total	$ 182.39	100%
Break-even genotype cost		$ 100.11
selection on genotype (20p)	Genetic benefit	
wool	$ 78.25	30%
repro	$ 112.16	43%
meat	$ 71.85	27%
other	$ -	0%
total	$ 262.25	100%
Break-even genotype cost		$ 143.95

Investing in information to select ewes for replacement in the multiplier clearly has a positive benefit. The break-even cost is much higher than the typical cost of genotyping. Although selecting on phenotypes measured at postweaning age is already quite profitable, the benefit of investing in a genomic test is significantly higher due to the increased accuracy of predicting genetic merit.

4.5.7. Validation of deterministic predictions with stochastic simulation

To validate the Geneflow method, a stochastic simulation model was used. This model simulates breeding values and phenotypes of individual animals and estimates benefits of selection over a 20 year period within and between multiplier and commercial flocks. From this simulation we can estimate how benefits of different selection strategies are transferred through flocks over time. Figure 15 shows how the simulation tracks gene flow across stud, multiplier and commercial flocks.

Figure 15. Diagram showing how the simulation estimates gene flow between flocks.



Methods

Step 1: Created a virtual flock.

Step 2: Use different selection strategies to select rams from the multiplier to use in the commercial flock.

Step 3: Estimate the benefit of different selection strategies in the multiplier rams on the commercial flock over time.

Creating the flock

The flock was created using MERINOSELECT parameters and economic values. Comparing the Merino Lamb and Sustainable Merino indexes, see the previous section for genetic and economic parameters.

The flock was constructed by simulating breeding values, residual values and phenotypes based on the genetic parameters and phenotypic parameters for animals.

Creating estimated breeding values

Estimated breeding values use phenotypic information from the animal or their relatives. The genomic test information was simulated by allowing animals to have information on 5 progeny for each trait, mimicking the accuracy provided by a genomic test. A more accurate genomic test was simulated with 20 progeny (Table 23).

Table 23. Comparing the accuracy of traits recorded for 2 tests – 1 assuming the equivalent to 5 progeny recorded and the other assuming 20 progeny were recorded.

Trait	Accuracy 5 progeny	Accuracy 20 progeny
acfw	0.61	0.83
afd	0.70	0.89
ass	0.52	0.76
awt	0.64	0.85
bwt	0.46	0.70
ebwr	0.59	0.82
edag	0.42	0.67
hcfw	0.62	0.84
hfd	0.71	0.89
hss	0.51	0.74
hwt	0.64	0.85
imf	0.71	0.89
lmy	0.65	0.85
nlw	0.31	0.52
pcfw	0.56	0.79
pfd	0.70	0.88
pfec	0.50	0.74
pss	0.51	0.75
pwt	0.58	0.80
wwt	0.55	0.77
ywt	0.63	0.83

Simulation structure

The simulation used a 10 year burn in to establish an average population. Following this the project then simulated each selection strategy for 20 years to identify the benefits of gene flow. Figure 16 shows how the flock changes over time in the simulation.

Figure 16. Diagram of how the flock changes over time

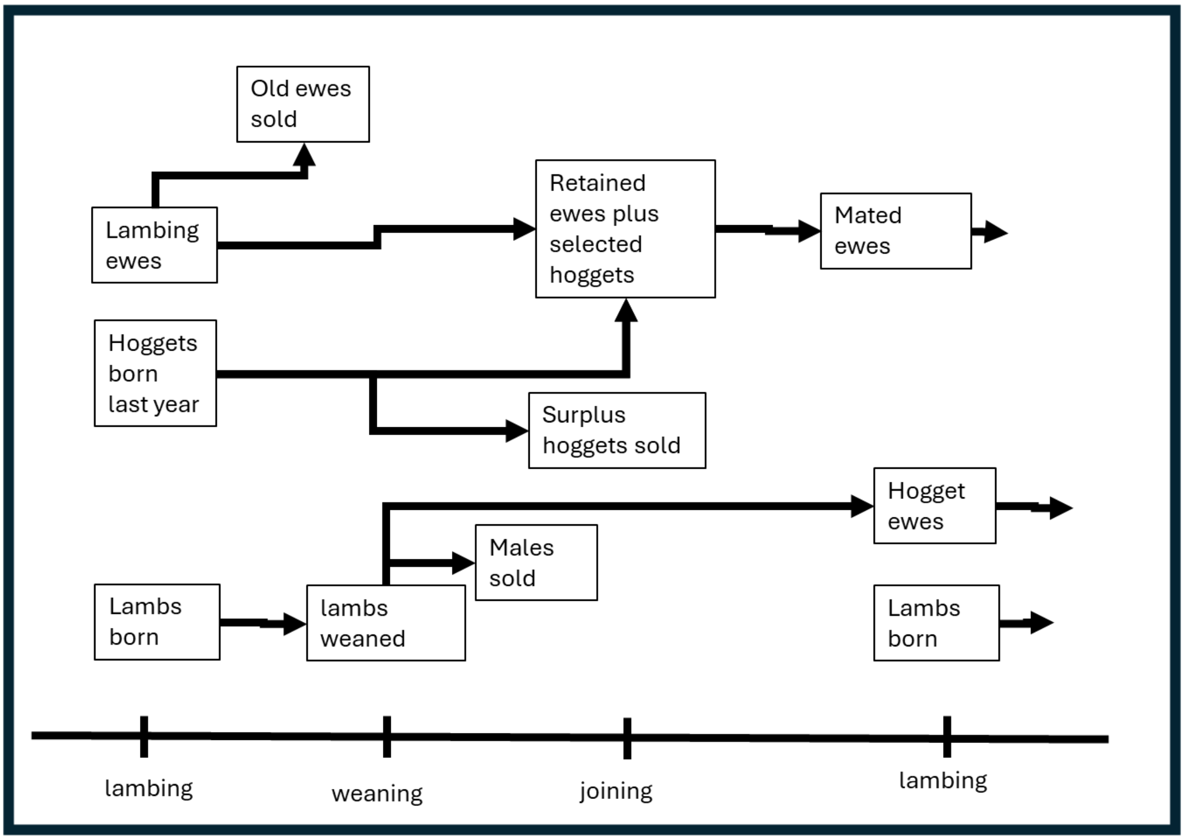
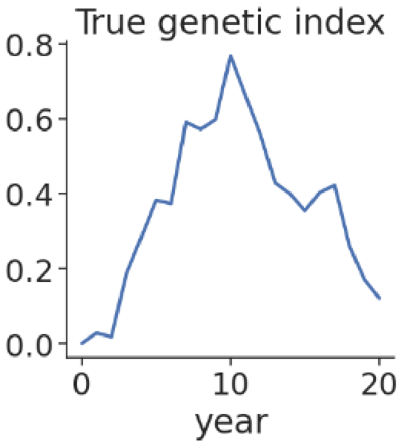


Figure 17 shows the change in the value of the true breeding values of all ewes that are mated for the Sustainable Merino index. These values are the True Breeding values multiplied by the economic values of each trait, like a selection index but substituted with True Breeding values. There is a delay in the response to selecting multiplier rams because lambs born in the first year are not mated until the 3rd year. Therefore, the simulation captures the gene flow from the multiplier flock to the commercial flock.

The y axis in Figure 17 shows how much the ewes mated in each year have a higher genetic superiority. In other words, the extra $ per ewe mated profit the flock will make.

Figure 17. Estimate of true breeding index of mated ewes over 20 years when selecting multiplier rams using a genomic test equivalent to 5 progeny for the SM index. The y axis is the dollar superiority of the ewes mated in each year.



The area below the curve in Figure 17 shows the total benefit per ewe mated in the commercial flock. This is equal to $7.80 and for the whole flock of 8000 ewes the benefit would be equal to $62,400. This gives a profit per selected ram of $1058 and a break even cost of $390, given that 59 rams are selected from 160 genotyped candidates (Table 24). These profit and break-even cost of genotyping were $800 and $295 for a moderately accurate genomic test. These numbers are very similar to the predicted values with the deterministic method.

Table 24. Profit per selected multiplier ram and break even genotype cost for the SM index

Selection on genotype (5p)	Genetic benefit
total	$ 800.00
break even genotype cost	$ 295
Selection on genotype (20p)	Genetic benefit
total	$ 1057.62
break even genotype cost	$ 365.26

5. Conclusion

5.1 Key findings

The project successfully collected DNA samples on more than 10,000 commercial sheep from 19 flocks, and returned genomically estimated breeding values back to 11 producers.

The validation study suggests a reasonable correlation between individual animal performance and its genomic prediction. The estimated genomic prediction accuracies were around 0.5, 0.4 and 0.6 for body weight, fleece weight and fibre diameter, respectively.

Overall participants are excited about the availability of a tool to genomically rank individual animals within flock. Some challenges were encountered on how to use the ranking in the yards to make selection decisions. Two examples of the GBV ranking have shown that it lined up well with the RAMPOWER ranking while others it was not reflective. This posed the question about how accurate or well linked the flock(s) were to the genomic reference population.

The modelling study estimated that for a moderately accurate genomic test, the break-even cost of genotyping males in a multiplier flock for use as sires in a commercial flock was around $250 and the break-even cost of selecting ewes in the multiplier flock is around $100. The break-even cost of selecting replacement ewes in a commercial flock is between $10 and $15. Results indicate there is prospect for cost-effective genotyping in commercial Merino flocks.

The difference between phenotypic selection and genomic selection is not only the larger selection differential and benefit that can be obtained with genomic selection, but there is also a shift toward more benefit for hard to measure traits, such as reproduction and other traits related to sustainability. In the ML index, there is more emphasis on meat traits with genomic selection.

5.2 Benefits to industry

Given the likelihood that genomic predictions of genetic merit will be increasingly accurate, there is opportunity to use genomic testing in commercial Merino flocks, especially for those cases where selected animals have an influence on a lot of offspring, such as selection of rams and ewes in a multiplier flock.

Value propositions can be derived from modelling and simulation, e.g. based on predicted accuracy and selection intensities, as well as based on empirical results. A more detailed list of possible cases that show value is:

1. Ranking animals as a pathway to submitting data to Sheep Genetics
    a. Traditional ram breeder who has been considering submitting data into Sheep Genetics; using the GBV tool to gain confidence; explore the power of full pedigree.
2. Commercial breeder starting a ram breeding nucleus – using multiple foundation ewe sources (3) to set up a foundation ewe base, use GBV ranking within the 3 groups and across the 3 groups to select the final nucleus group to AI.
3. Joining ewe lambs (commercial breeder) – GBV is the early selection tool to identify the ewes to join as ewe lambs + weight thresholds.

4. Breeding own rams – GBV is the ram selection tool (to select rams to be used in the commercial flock); replacement ewe selection for the ram breeding nucleus; AI used in nucleus + GBV selected back up ram(s)
    a. Two tier ram breeding operation
        i. A – submitting data into Sheep Genetics – full pedigree, measurements, ASBVs
        ii. B – GBV ranking (multiplier tier)

6. Future research and recommendations

While prediction maybe accurate for many commercial flocks, there is likely variation in the degree of linkage of such flocks with the genomic reference populations, and therefore accuracy of genomic prediction might vary between flock. It is recommended to invest in some methods that can give some indication of industry linkage and accuracy of specific genomics predictions. Further application of genomic testing and ranking of individual sheep will be explored in a future Producer Demonstration project that will demonstrate and identify clear pathways for sheep producers to utilise a single or combination of genomic tools in their ewe and ram selections to continue to improve on farm productivity via genetic gains.

7. References

DPIRD WA Department of Primary Industries and Regional Development, 2023 Western Australian Sheep Producer Survey 2022, chrome-extension://efaidnbmnnnibpcajpcglclefindmkaj/https://www.agric.wa.gov.au/sites/gateway/files/Western%20Australian%20Sheep%20Producer%20Survey%202022.pdf

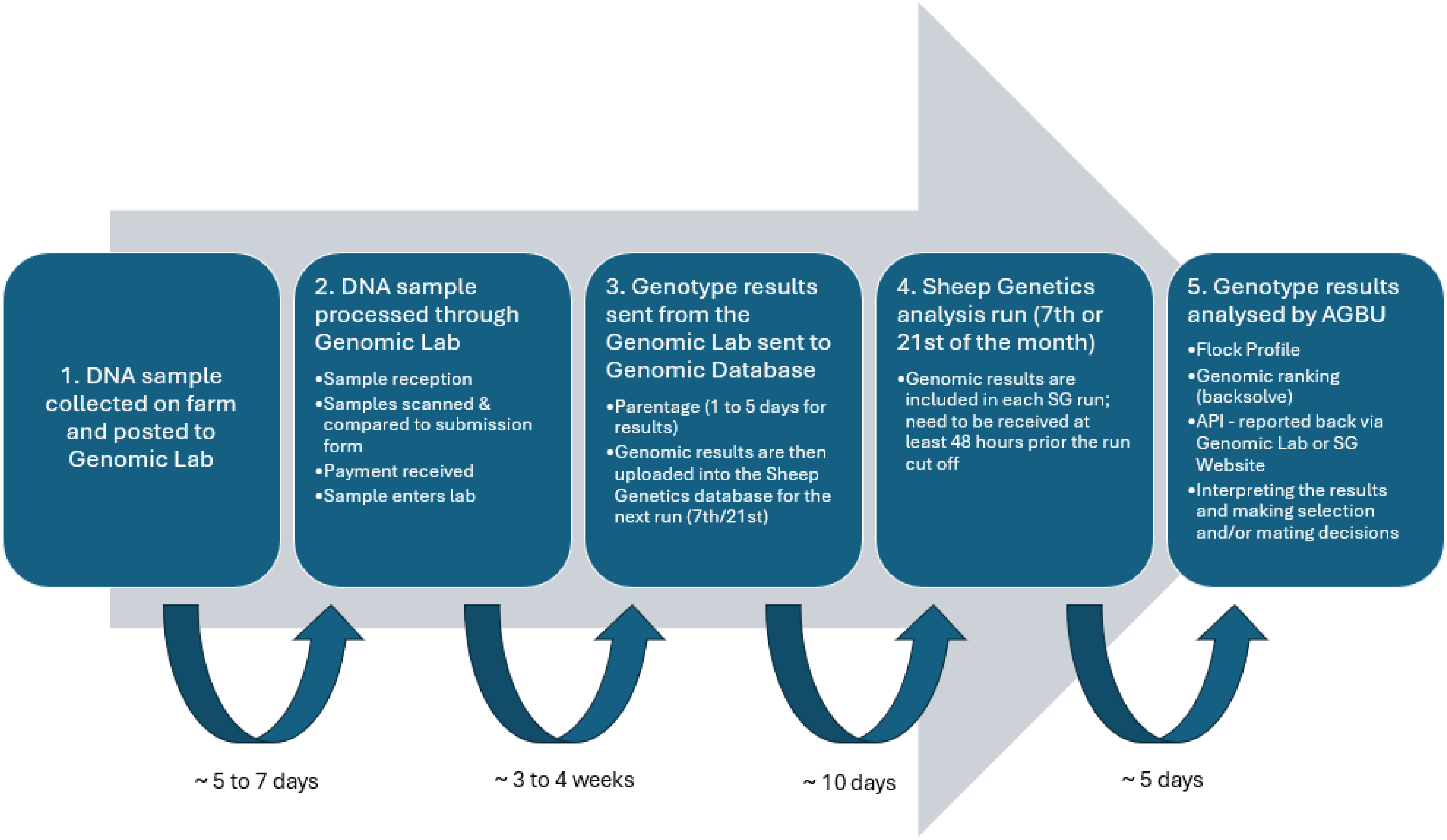
Swan, A.A., Gurman, P.M., Boerner, V., Brown, D.J., Clark, S., Gore, K., Granleese, T. and van der Werf, J.H.J., 2018. Estimating breeding values for animals with genotype only when genetic group effects are important. In Proceedings of the World Congress on Genetics Applied to Livestock Production. Massey University.

8 Appendices

Appendix 8.1. List with participants and sample numbers tested in the project.

Flock	State	GSP	# of samples	Phenotype Supplied	GBVs delivered
1	NSW	Neogen	829	✓	✓
1	NSW	Weatherbys	700	✓	✓
2	VIC	Xytovet	527	✓	✓
3	NSW	Weatherbys	165	NA	✓
4	NSW	Neogen	133	NA	✓
5	NSW	Neogen	120	NA	✓
5	NSW	Weatherbys	149	✓	✓
6	VIC	Weatherbys	196	✓	✓
7	NSW	Neogen	785	✓	✓
8	NSW	Xytovet	501	✓	✓
9	NSW	Neogen	496	✓	✓
10	NSW	Xytovet	984	✓	✓
11	TAS	Neogen	550	✓	✓
12	VIC	Weatherbys	697	✓	✓
13	NSW	Neogen	144	NA	✓
14	NSW	Xytovet	493	✓	✓
15	NSW	Weatherbys	719	✓	✓
15	NSW	Xytovet	656	✓	✓
16	NSW	Neogen	183	✓	✓
17	SA	Weatherbys	1071	✓	✓
18	NSW	Neogen	46	NA	✓
19	NSW	Neogen	94	✓	✓
Total			10,238		

Appendix 8.2. Turnaround time from sampling to obtaining GBV



1. DNA sample collected on farm and posted to Genomic Lab

2. DNA sample processed through Genomic Lab
- Sample reception
- Samples scanned & compared to submission form
- Payment received
- Sample enters lab

3. Genotype results sent from the Genomic Lab sent to Genomic Database
- Parentage (1 to 5 days for results)
- Genomic results are then uploaded into the Sheep Genetics database for the next run (7th/21st)

4. Sheep Genetics analysis run (7th or 21st of the month)
- Genomic results are included in each SG run; need to be received at least 48 hours prior the run cut off

5. Genotype results analysed by AGBU
- Flock Profile
- Genomic ranking (backsolve)
- API - reported back via Genomic Lab or SG Website
- Interpreting the results and making selection and/or mating decisions

~ 5 to 7 days

~ 3 to 4 weeks

~ 10 days

~ 5 days

Appendix 8.3 – Flock Profile Validation

Genomic benchmarking of Merino sheep flocks for traits related to reproduction rate

D.J. Brown[1], P.M. Gurman[1] and A.A. Swan[1]

[1] AGBU, a joint venture of NSW Department of Primary Industries and University of New England, 2351, Armidale, Australia

SUMMARY

This study examined the predictive ability of the “Flock Profile” genomic benchmarking method in Merino sheep flocks, estimated from the MERINOSELECT analysis. The Flock Profile is a product delivered to commercial Merino flocks to provide and estimate of their average ASBV using genomic only breeding values informed from the Sheep Genetics MERINOSELECT analysis. Data from this analysis was used in a validation study to test the accuracy of predicting mean flock genetic 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>0.79) for all traits except ewe rearing ability. However, the Flock Profile results were slightly over-dispersed with an average regression slope across traits of 0.91 and thus had slightly more variation compared to their ASBVs. Genomic predictions for individual animals were also highly correlated (r>0.78) to the full ASBVs. The study also demonstrated that there is variability in genomic connectedness to the reference population across flocks and traits and thus the development of an accuracy metric will be important soon.

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). The Flock Profile is a product delivered to commercial Merino flocks to provide an estimate of their average ASBV using genomic only breeding values informed from the Sheep Genetics MERINOSELECT analysis. While the average Australian Sheep Breeding Value (ASBV) of rams purchased is 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 tests are only commercially available in purebred Merino flocks. 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. To support this aim, another preliminary validation in maternal breeds for reproduction traits demonstrated that genomic flock profiling accurately predicted their true ASBV mean (Brown et al. 2023). In addition to flock benchmarking, the methodology could also be used to perform genomic prediction on individual animals.

Currently, the flock profile test in Merinos excludes reproduction traits. This study aimed to examine the predictive ability of the Flock Profile test for reproductive traits in Merino sheep, estimated from the MERINOSELECT analysis (Brown *et al.* 2007).

MATERIALS AND METHODS

Data from the reproductive component trait analysis for MERINOSELECT (as described by Bunter *et al.* 2019) were utilised for this study. Reproductive data and genotypes were identified for 42 selected seedstock flocks within this analysis, chosen based on volume and quality of data. The data for each trait are illustrated in Table 1. To generate an independent ASBV analysis, all the phenotype data, pedigree and genotypes from these 42 flocks were removed sequentially and 42 special MERINOSELECT analyses were conducted. Using the genotypes only, ASBVs were estimated (BSBV) 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 MERINOSELECT 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. The current MERINOSELECT analysis aligns the genomic relationship matrix (G) to the pedigree matrix using Christensen (2012) and lambda of 0.75, i.e. $G_{mod} = 0.75\mathrm{G} + 0.25A_{22}$. In addition, a "lambda" value of 0.75 was used to mimic what is used in the routine MERINOSELECT analysis.

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, however for MERINOSELECT there is insufficient genetic variation to include yearling ewe rearing ability at this stage. 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 and yearling body weight (PWT, YWT), carcase fat (PFAT, YFAT) and eye muscle depth (PEMD, YEMD), along with post-weaning and yearling (PSC, YSC) scrotal circumferences. An overall breeding value for weaning rate (WR) is also derived by using the component traits (CON, LS and ERA) and index methodology.

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

Trait	Flocks	Animals with records	Recorded and genotyped	Mean	SD
PWT	27	59,876	20,544	48.09	10.53
YWT	32	65,244	20,599	51.50	11.94
AWT	25	73,564	35,348	61.25	11.84
PFAT	27	59,851	20,559	2.85	0.95
YFAT	34	77,237	26,261	2.71	0.97
PEMD	27	59,904	20,578	25.42	4.59
YEMD	34	77,532	26,286	25.34	4.49
CS	14	34,357	23,861	3.22	0.55
PSC	6	12,504	3,445	27.20	4.74
YSC	9	14,459	5,876	30.12	4.70
MBS	7	11,324	4,791	2.13	1.00
YCON	15	13,894	8,485	0.52	0.50
CON	42	179,268	65,021	0.92	0.27
YLS	17	11,406	6,931	1.31	0.48
LS	42	252,585	76,756	1.50	0.55
ERA	42	175,682	59,904	0.83	0.31

The validation analysis was first completed at the flock level by averaging the independent BSBV for all genotyped animals for each flock to create the Flock Profile. This was performed using four different methods to calculate the Flock Profile;

1. Using all genotyped animals within each flock,
2. Selecting the biggest year drop for each flock,

3. Calculating flock-year means for each flock, and
4. Randomly selecting 20 animals with each flock and year.

In each case, the Flock Profile was compared to the average ASBVs from the full analysis for the same subset of animals.

The validation analyses were then investigated at the animal level by estimating the relationship of BSBV with their ASBV across all validation animals with a genotype. This was also repeated with each validation flock with at least 20 genotyped animals.

RESULTS AND DISCUSSION

The data used for validation analysis are summarised in Table 1. Not all flocks recorded every trait and this ranged from 6 flocks recording PSC and 42 recording the key component reproduction traits. The number of animals genotyped ranged from 3,445 for PSC up to 76,756 for LS.

The accuracy of ranking of flocks was high (r>0.79) 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 were significantly less than 1 indicating that the Flock Profile results were slightly over-dispersed compared to their ASBVs.

Table 2. Relationship between Flock Profile (BSBV, n=42) results and ASBV means from the full MERINOSELECT analysis

Trait	BSBV mean (SD)	ASBV mean (SD)	Slope	Corr	RMSE[#]
PWT	3.08 (2.04)	3.66 (1.94)	0.93 (0.03)	0.98	0.41
YWT	4.32 (2.62)	4.84 (2.44)	0.91 (0.03)	0.98	0.51
AWT	4.76 (2.68)	5.29 (2.60)	0.95 (0.03)	0.97	0.58
PFAT	0.22 (0.23)	0.24 (0.22)	0.94 (0.03)	0.98	0.04
YFAT	0.26 (0.27)	0.29 (0.25)	0.92 (0.02)	0.99	0.04
PEMD	1.33 (1.10)	1.48 (1.03)	0.92 (0.03)	0.98	0.18
YEMD	1.46 (1.25)	1.57 (1.16)	0.91 (0.02)	0.99	0.18
CS	0.13 (0.11)	0.13 (0.11)	0.93 (0.03)	0.98	0.02
PSC	0.91 (0.64)	1.09 (0.59)	0.90 (0.03)	0.98	0.12
YSC	0.99 (0.65)	1.14 (0.59)	0.89 (0.03)	0.98	0.13
MBS	-0.10 (0.07)	-0.12 (0.06)	0.87 (0.04)	0.96	0.02
YCON	0.05 (0.05)	0.06 (0.05)	0.94 (0.06)	0.93	0.02
CON	0.03 (0.02)	0.03 (0.02)	0.80 (0.10)	0.79	0.01
YLS	0.01 (0.03)	0.01 (0.03)	0.94 (0.04)	0.96	0.01
LS	0.07 (0.06)	0.07 (0.06)	0.94 (0.04)	0.97	0.02
ERA	0.03 (0.01)	0.03 (0.02)	0.37 (0.16)	0.36	0.01
WR	0.12 (0.07)	0.14 (0.07)	0.87 (0.08)	0.87	0.03

RMSE: Root mean square error

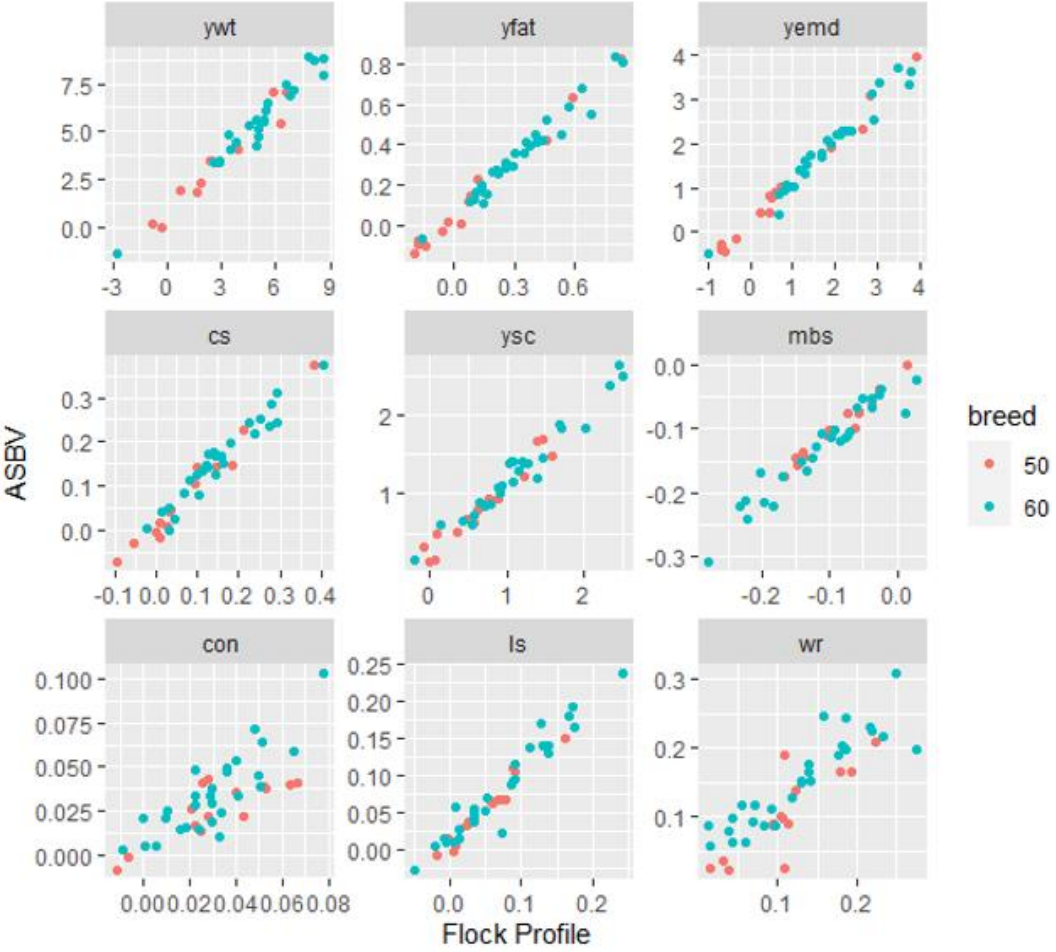


Figure 1. Accuracy of the Flock Profile (BSBV, n=42) results to predict the ASBV means from the full MERINOSELECT analysis

The comparison of the different methods to calculate the Flock Profile for each validation flocks is show in Table 3. All four methods produced very similar results.

Table 3. Comparison of different methods for selecting animals to calculate flock and flock year means. Using all genotyped animals within each flock, selecting the biggest year drop for each flock, using flock-year means and randomly selecting 20 animals with each flock and year.

Trait	All, flock means (n=42)		Biggest year per flock (n=42)		All, flock year means (n=331)		Random 20, flock year means (n=304)	
	Corr	Slope	Corr	Slope	Corr	Slope	Corr	Slope
PWT	0.98	0.93 (0.03)	0.98	0.93 (0.01)	0.97	0.96 (0.03)	0.97	0.93 (0.01)
YWT	0.98	0.91 (0.03)	0.98	0.91 (0.01)	0.97	0.93 (0.03)	0.97	0.91 (0.02)
AWT	0.97	0.95 (0.03)	0.98	0.92 (0.01)	0.97	0.94 (0.03)	0.97	0.93 (0.01)
PFAT	0.98	0.94 (0.03)	0.99	0.91 (0.01)	0.98	0.96 (0.03)	0.97	0.90 (0.01)
YFAT	0.99	0.92 (0.02)	0.99	0.91 (0.01)	0.98	0.94 (0.02)	0.98	0.89 (0.01)
PEMD	0.98	0.92 (0.03)	0.99	0.91 (0.01)	0.98	0.94 (0.02)	0.98	0.91 (0.01)
YEM	0.99	0.91 (0.02)	0.99	0.91 (0.01)	0.98	0.93 (0.02)	0.98	0.90 (0.01)
CS	0.98	0.93 (0.03)	0.98	0.90 (0.01)	0.97	0.95 (0.03)	0.97	0.89 (0.01)
PSC	0.98	0.90 (0.03)	0.98	0.89 (0.01)	0.97	0.93 (0.03)	0.96	0.89 (0.01)
YSC	0.98	0.89 (0.03)	0.98	0.89 (0.01)	0.97	0.92 (0.03)	0.97	0.89 (0.01)
MBS	0.96	0.87 (0.04)	0.97	0.89 (0.02)	0.95	0.96 (0.04)	0.95	0.88 (0.02)
YCON	0.93	0.94 (0.06)	0.94	0.87 (0.02)	0.89	0.98 (0.06)	0.86	0.82 (0.03)
CON	0.79	0.80 (0.10)	0.82	0.85 (0.04)	0.78	0.82 (0.09)	0.77	0.82 (0.04)
YLS	0.96	0.94 (0.04)	0.96	0.95 (0.02)	0.94	0.97 (0.04)	0.94	0.95 (0.02)
LS	0.97	0.94 (0.04)	0.97	0.96 (0.02)	0.95	0.99 (0.04)	0.95	0.94 (0.02)
ERA	0.36	0.37 (0.16)	0.37	0.33 (0.06)	0.31	0.39 (0.15)	0.33	0.34 (0.06)
WR	0.87	0.87 (0.08)	0.91	0.87 (0.03)	0.84	0.95 (0.07)	0.83	0.85 (0.03)

RMSE: Root mean square error

The results of the back-solved breeding values at the level of individual animal are shown in Table 4. These results highlight that the Flock Profile methodology could accurately predict the ranking of ASBVs within the flocks tested, with correlations generally greater than 0.80 for most traits and regression slopes of close to 1.0. The relationships across all animals and flocks were lower with correlations ranging from 0.82 to 0.92.

The Flock Profile and within flock results both demonstrate lower levels of accuracy for the CON and ERA traits. This in part could be due to the lower heritability, reduced across flock effects and smaller reference population sizes. Another complication could be the binomial nature of these traits and potential skewed distribution of breeding values. These issues warrant further investigation.

The variation in correlations with flocks and years (Figure 2) also highlights that there is variability in genomic connectedness to the reference population across flocks and traits. Thus, the development of an accuracy metric will be important soon and further research is required to define a suitable methodology to estimate accuracy metrics for these products.

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 MERINOSELECT 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. This is a further reason for an accuracy metric.

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). 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 4. Accuracy of the genomic only animal level breeding values to predict the ASBV from the full MERINOSELECT analysis both across and within flocks

	Across all flocks					Average of within flock	
Trait	**Flock Profile mean (SD)**	**ASBV mean (SD)**	**Slope**	**Corr**	**RMSE#**	**Corr**	**Slope**
PWT	3.34 (3.01)	3.93 (2.83)	0.89 (0.00)	0.95	0.87	0.94 (0.03)	0.87
YWT	4.58 (3.94)	5.27 (3.64)	0.88 (0.00)	0.95	1.09	0.94 (0.03)	0.87
AWT	5.20 (4.05)	5.83 (3.74)	0.88 (0.00)	0.95	1.14	0.94 (0.03)	0.86
PFAT	0.19 (0.33)	0.22 (0.30)	0.90 (0.00)	0.97	0.08	0.95 (0.03)	0.88
YFAT	0.24 (0.38)	0.28 (0.36)	0.91 (0.00)	0.97	0.08	0.95 (0.03)	0.88
PEMD	1.27 (1.45)	1.45 (1.37)	0.92 (0.00)	0.97	0.34	0.95 (0.04)	0.88
YEMD	1.40 (1.66)	1.57 (1.55)	0.91 (0.00)	0.97	0.37	0.95 (0.04)	0.87
CS	0.12 (0.16)	0.13 (0.15)	0.90 (0.00)	0.97	0.04	0.95 (0.03)	0.88
PSC	0.88 (1.20)	1.11 (1.12)	0.90 (0.00)	0.96	0.31	0.95 (0.02)	0.88
YSC	1.01 (1.26)	1.22 (1.16)	0.89 (0.00)	0.96	0.31	0.95 (0.02)	0.88
MBS	-0.10 (0.17)	-0.12 (0.16)	0.86 (0.00)	0.93	0.06	0.94 (0.04)	0.89
YCON	0.05 (0.12)	0.07 (0.11)	0.81 (0.00)	0.84	0.06	0.88 (0.11)	0.83
CON	0.02 (0.04)	0.03 (0.04)	0.76 (0.00)	0.79	0.02	0.78 (0.12)	0.75
YLS	0.01 (0.05)	0.01 (0.05)	0.90 (0.00)	0.88	0.02	0.88 (0.06)	0.88
LS	0.05 (0.11)	0.07 (0.11)	0.91 (0.00)	0.90	0.05	0.87 (0.06)	0.88
ERA	0.02 (0.03)	0.03 (0.03)	0.72 (0.00)	0.72	0.02	0.80 (0.10)	0.79
WR	0.10 (0.11)	0.12 (0.11)	0.87 (0.00)	0.84	0.06	0.83 (0.08)	0.83

RMSE: Root mean square error

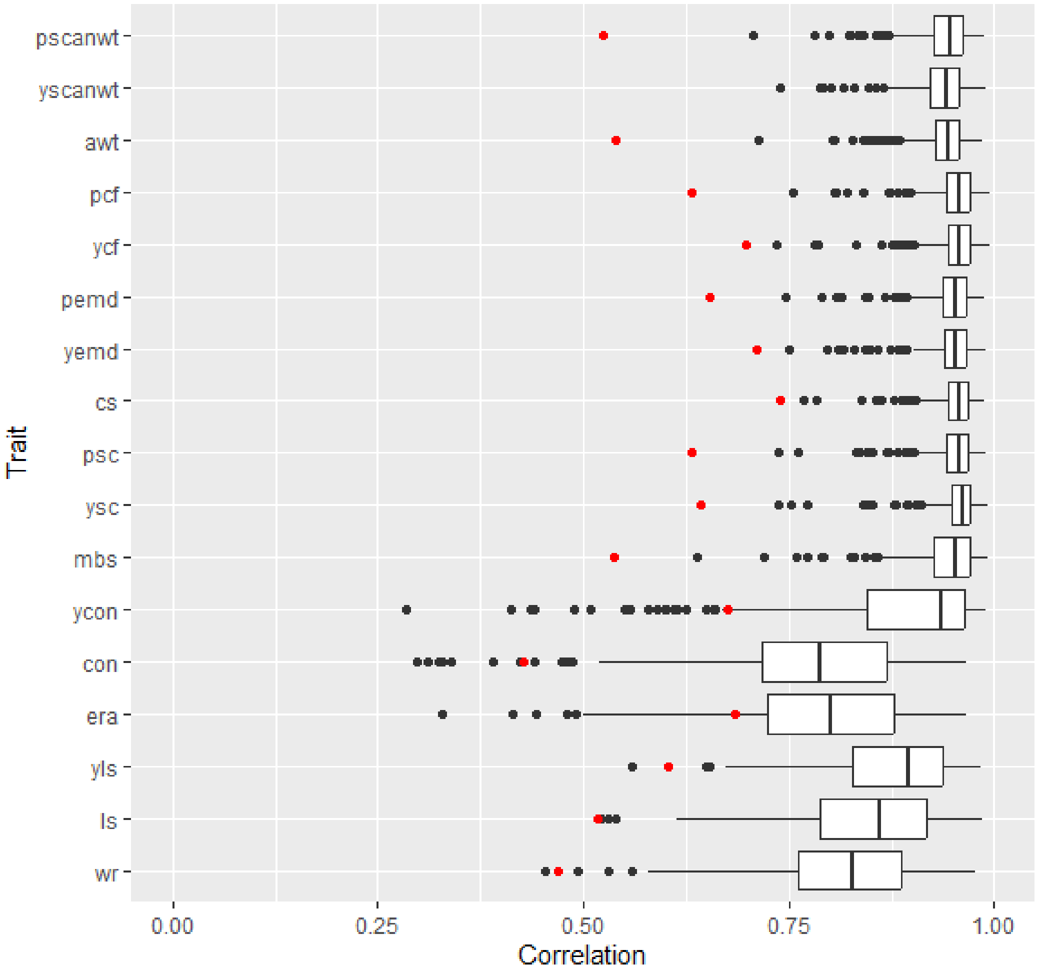


Figure 2. Variation in the correlation between BSBV and ASBV means across all flocks and years. Red dots highlight on outlier flock-year with low correlations across all traits.

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.

ACKNOWLEDGEMENTS

This work was funded by MLA (P.PSH.1483 and L.GEN.2204) and a range of industry partners throughout the supply chain. The authors would also like to thank the industry seedstock producers in MERINOSELECT who contributed to this work.

Appendix 8.4 – Case Studies

Case Study 1: Flock # 9

Genomic Project Objective

- Flock # 9 purchased ewes from 3 external flocks that were identified as having the genetic background and phenotypic traits that are desired to meet their breeding and on farm production objectives. The foundation ewes were made up from the following sources: -
    - Commercial ewes that had been measured for micron and fleece weight as maiden ewes, they were 5 year old when purchased.
    - Cull For Age (CFA) ewes (background was from a commercial breeder using AI to breed own rams.
    - A ram source cull for age stud ewes, (stud ewes from a participant in Sheep Genetics)

The initial joining of the foundation ewes in 2024 was based on a RAMPOWER index (using the original flocks raw data within mob and group to rank) and visual assessment as the GBV results were not available at the time of joining in March 2024.

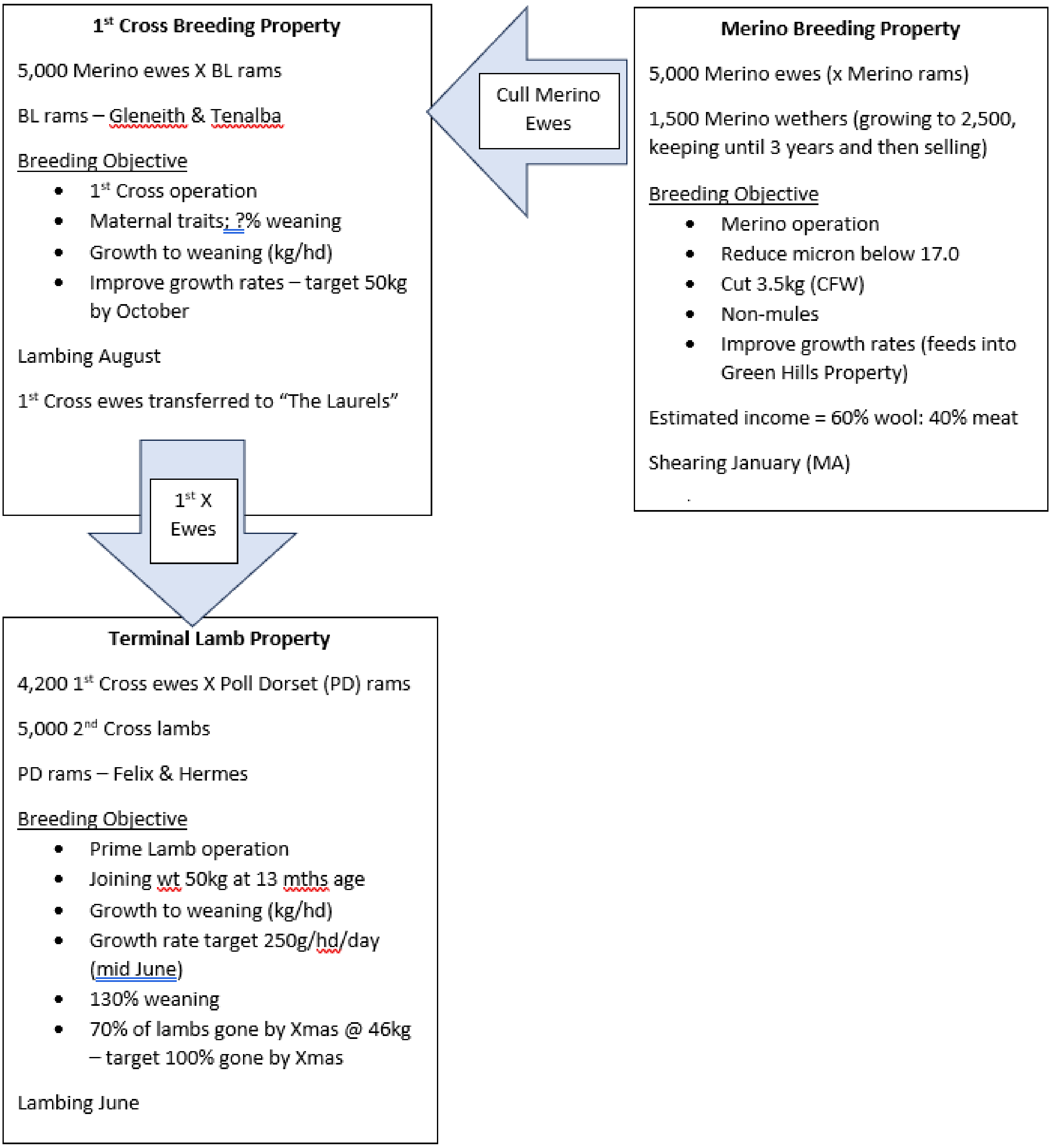
The plan moving forward is to use the GBV to select the foundation ewes to join for 2025 joining. The GBVs are being used as a segway to preparing to start submitting data to Sheep Genetics to generate ASBVs on the 2024 drop to select ram lambs that will be used to join to the commercial ewes in 2025. The aim is to fast track the genetic improvement of the commercial flock.

Foundation Ewe Source	2017 (YOB)	2018 (YOB)	Total
Stud sourced CFA	69		69
Commercial flock using AI CFA		91	91
Commercial flock with raw data on CFA ewes		328	328
Grand Total	**69**	**419**	**488**

Foundation Ewe Source	HH	PH	PP	Failed Sample	Total
Stud sourced CFA	38	26	5		69
Commercial flock using AI CFA	30	41	14	6	91
Commercial flock with raw data on CFA ewes	316	11		1	328
Grand Total	**384**	**78**	**19**	**7**	**488**

Property Structure

Flock # 9 has 3 main property groups and enterprises and are summarised below. The ram breeding operation is focused on the Merinos property.



Merino Breeding Property

5,000 Merino ewes (x Merino rams)

1,500 Merino wethers (growing to 2,500, keeping until 3 years and then selling)

Breeding Objective

- Merino operation
- Reduce micron below 17.0
- Cut 3.5kg (CFW)
- Non-mules
- Improve growth rates (feeds into Green Hills Property)

Estimated income = 60% wool: 40% meat

Shearing January (MA)

1st Cross Breeding Property

5,000 Merino ewes X BL rams

BL rams – Gleneith & Tenalba

Breeding Objective

- 1st Cross operation
- Maternal traits; ?% weaning
- Growth to weaning (kg/hd)
- Improve growth rates – target 50kg by October

Lambing August

1st Cross ewes transferred to "The Laurels"

Terminal Lamb Property

4,200 1st Cross ewes X Poll Dorset (PD) rams

5,000 2nd Cross lambs

PD rams – Felix & Hermes

Breeding Objective

- Prime Lamb operation
- Joining wt 50kg at 13 mths age
- Growth to weaning (kg/hd)
- Growth rate target 250g/hd/day (mid June)
- 130% weaning
- 70% of lambs gone by Xmas @ 46kg – target 100% gone by Xmas

Lambing June

Flock Profiles based on the genomic testing for Flock # 9 – report date 01/10/2024

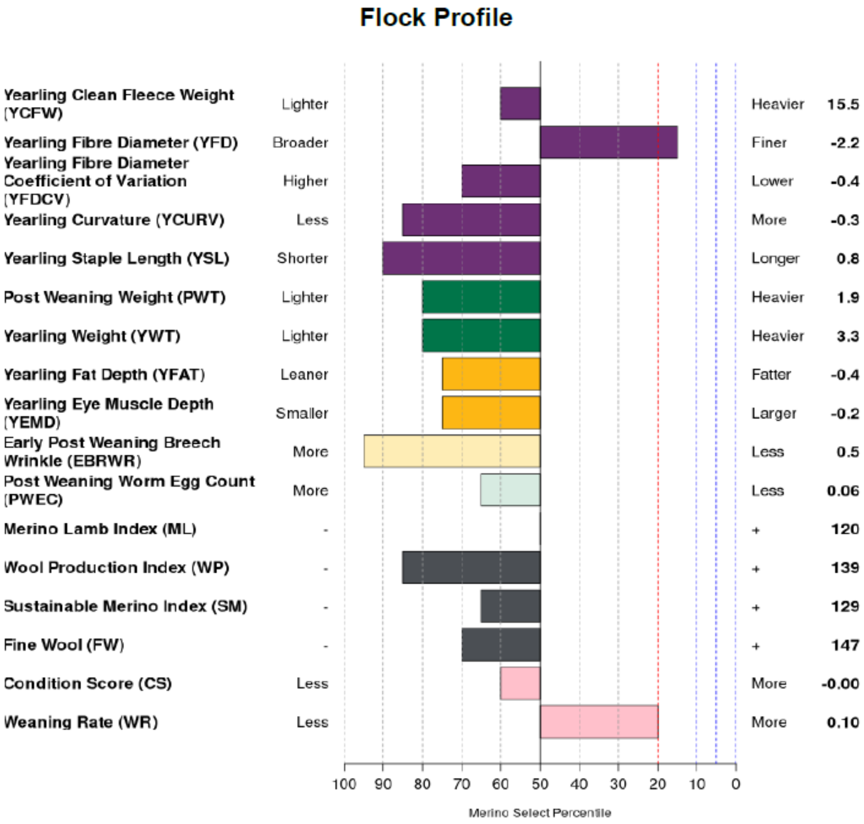


Figure 1 – Flock Profile results – Stud CFA & Commercial flock using AI CFA purchased ewes.

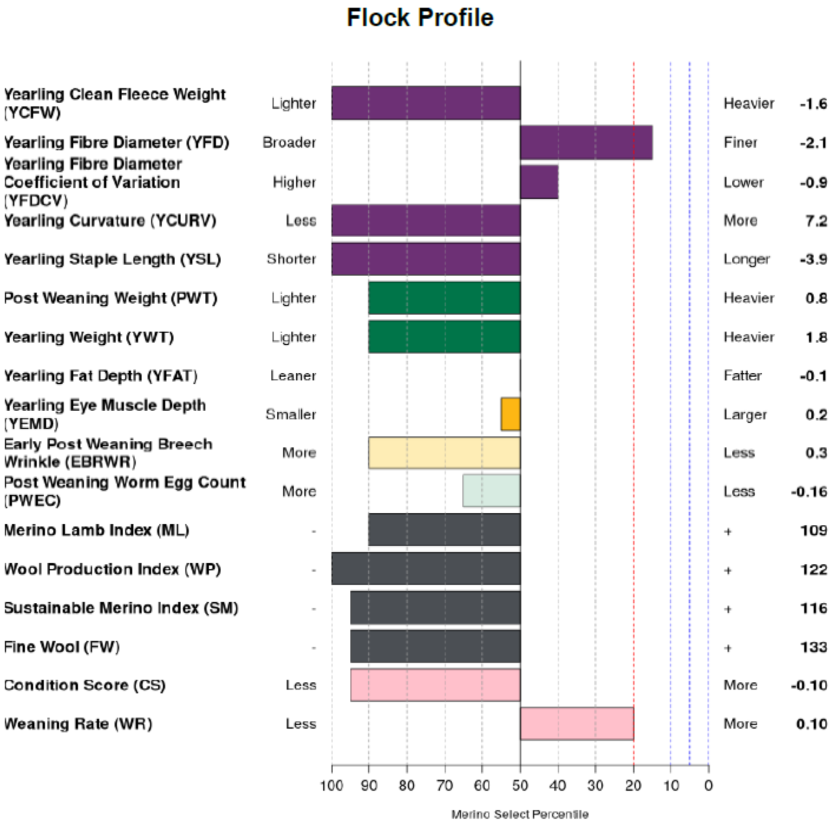
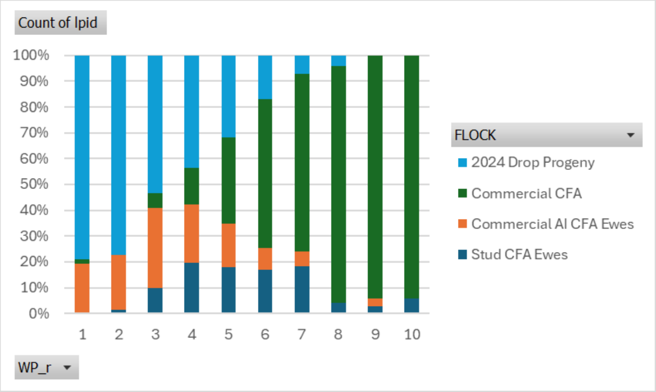


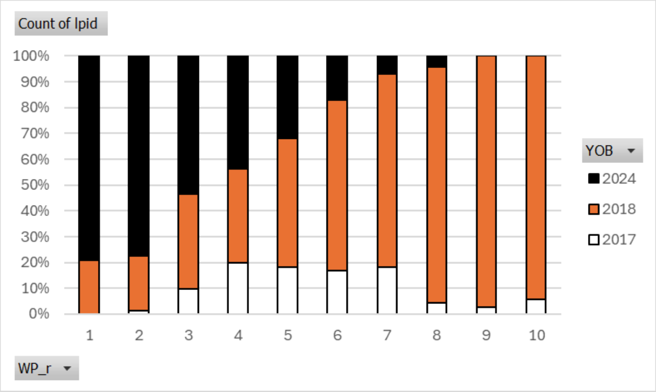
Figure 2 – Flock Profile results – Commercial ewes purchased; previously phenotype measurement collected.

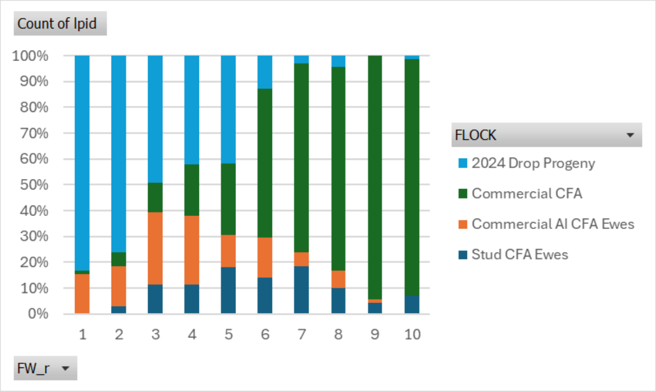
Genomic (GBV) Results – 25-01-2025

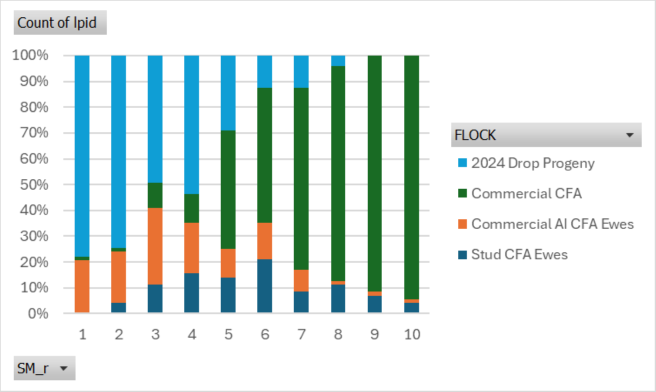
GBV ranking across the 3 flocks used as foundation ewes and the 2024 drop progeny. List of GBVs for flock profile traits [1] – the ranking is based on a percentile where 1 = top 10% and 10 = bottom 90%.

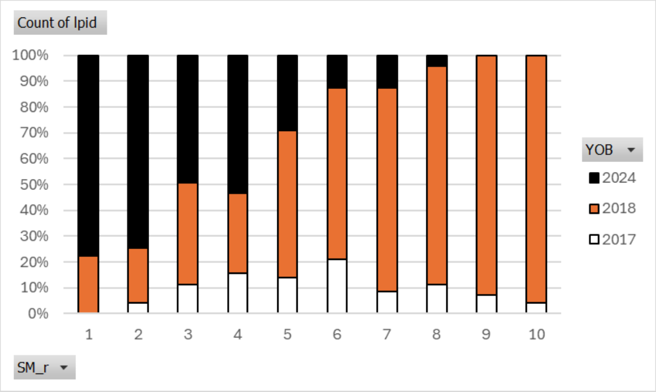
pwt_r ywt_r yfat_r yemd_r ycfw_r yfd_r ydcv_r ycuv_r ysl_r pfec_r ebwr_r cs_r wr_r SM_r WP_r FW_r ML_r

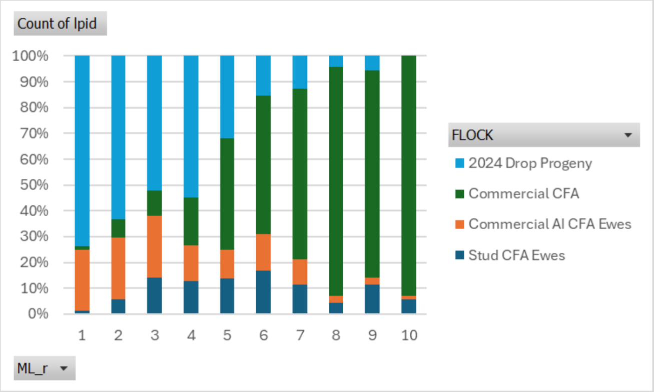


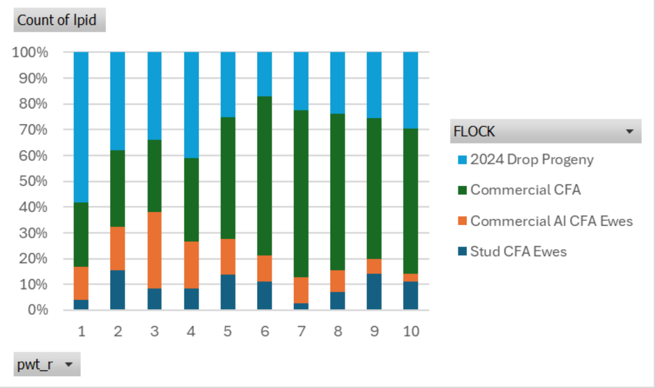








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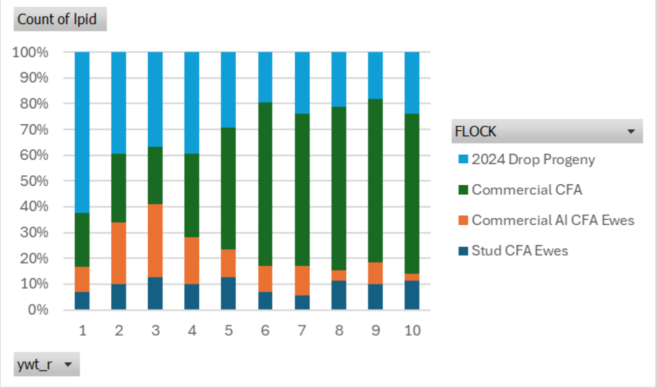
2024 Drop Progeny
Commercial CFA
Commercial AI CFA Ewes
Stud CFA Ewes
pwt_r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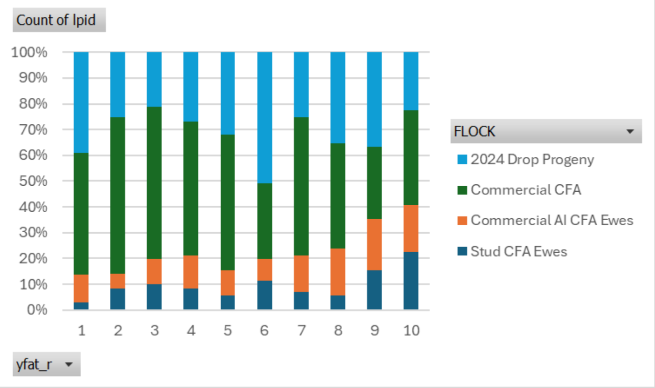
ywt_r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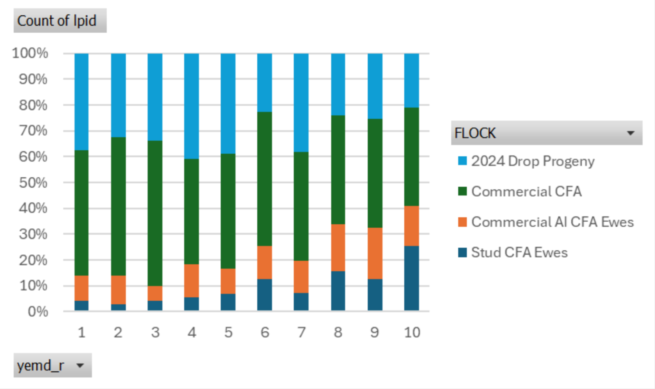
Commercial AI CFA Ewes
Stud CFA Ewes
yfat_r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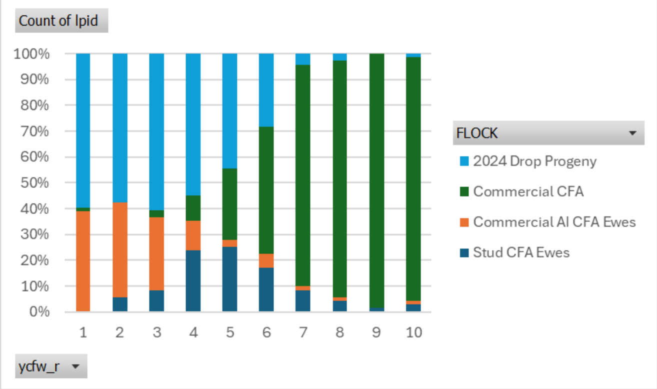
Commercial AI CFA Ewes
Stud CFA Ewes
yemd_r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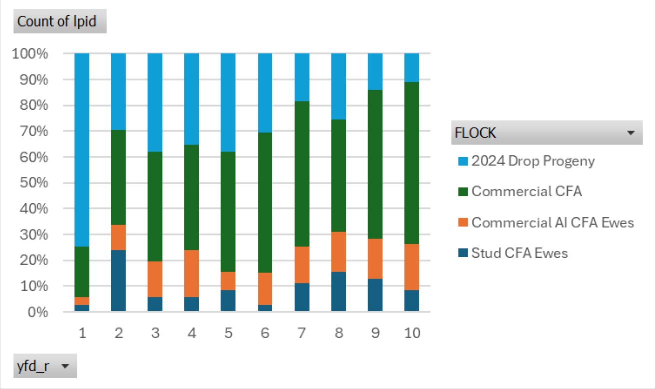
Stud CFA Ewes
ycfw_r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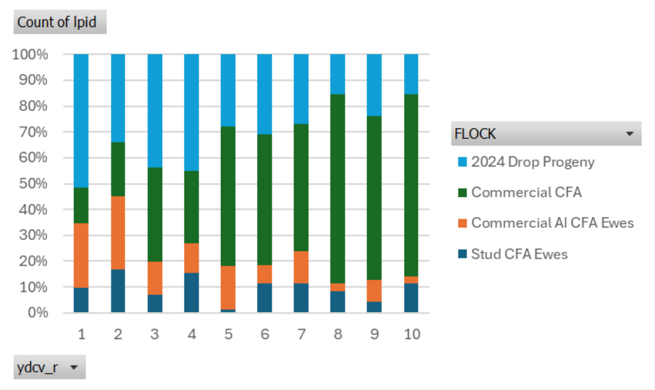
Commercial AI CFA Ewes
Stud CFA Ewes
yfd_r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FLOCK
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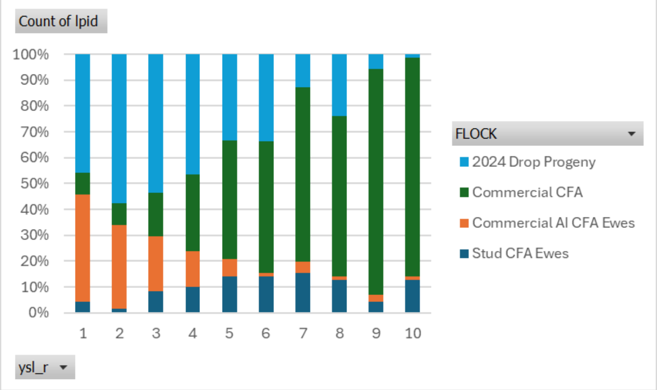
Commercial AI CFA Ewes
Stud CFA Ewes
ydcv_r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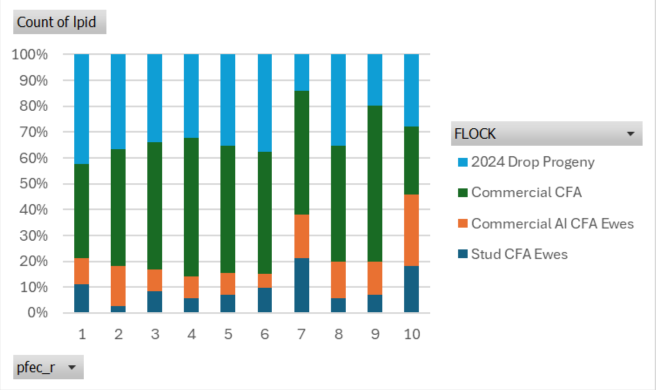
ysl_r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FLOCK
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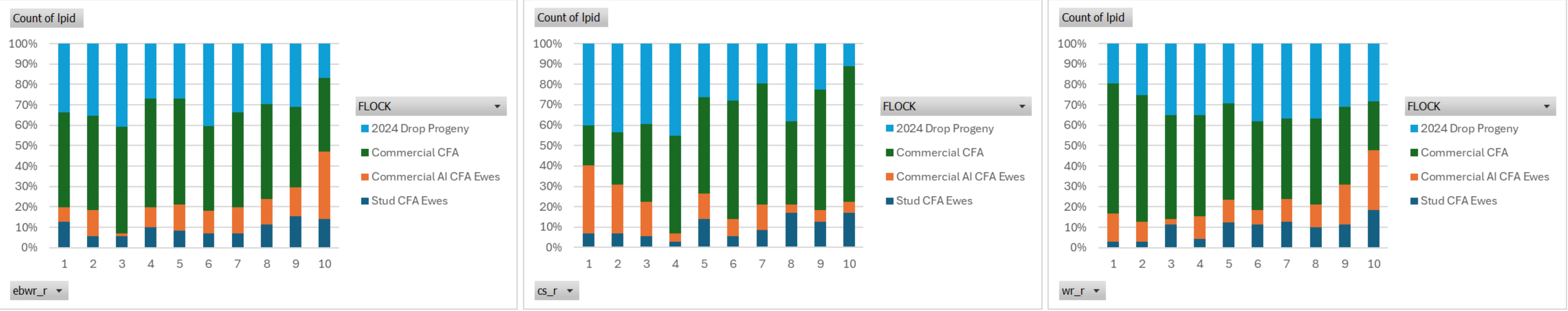
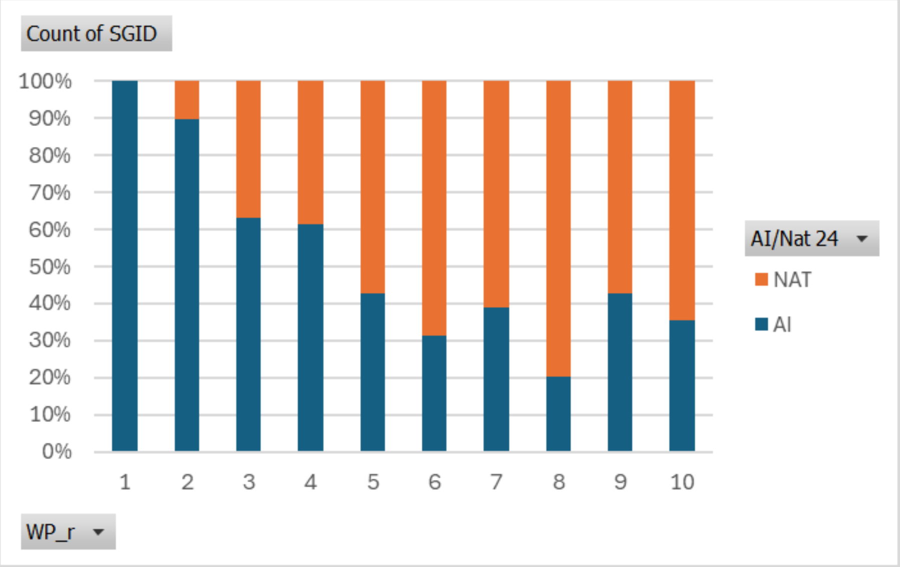
Commercial AI CFA Ewes
Stud CFA Ewes
pfec_r



Selection for the AI program 2024 – WP index ranking

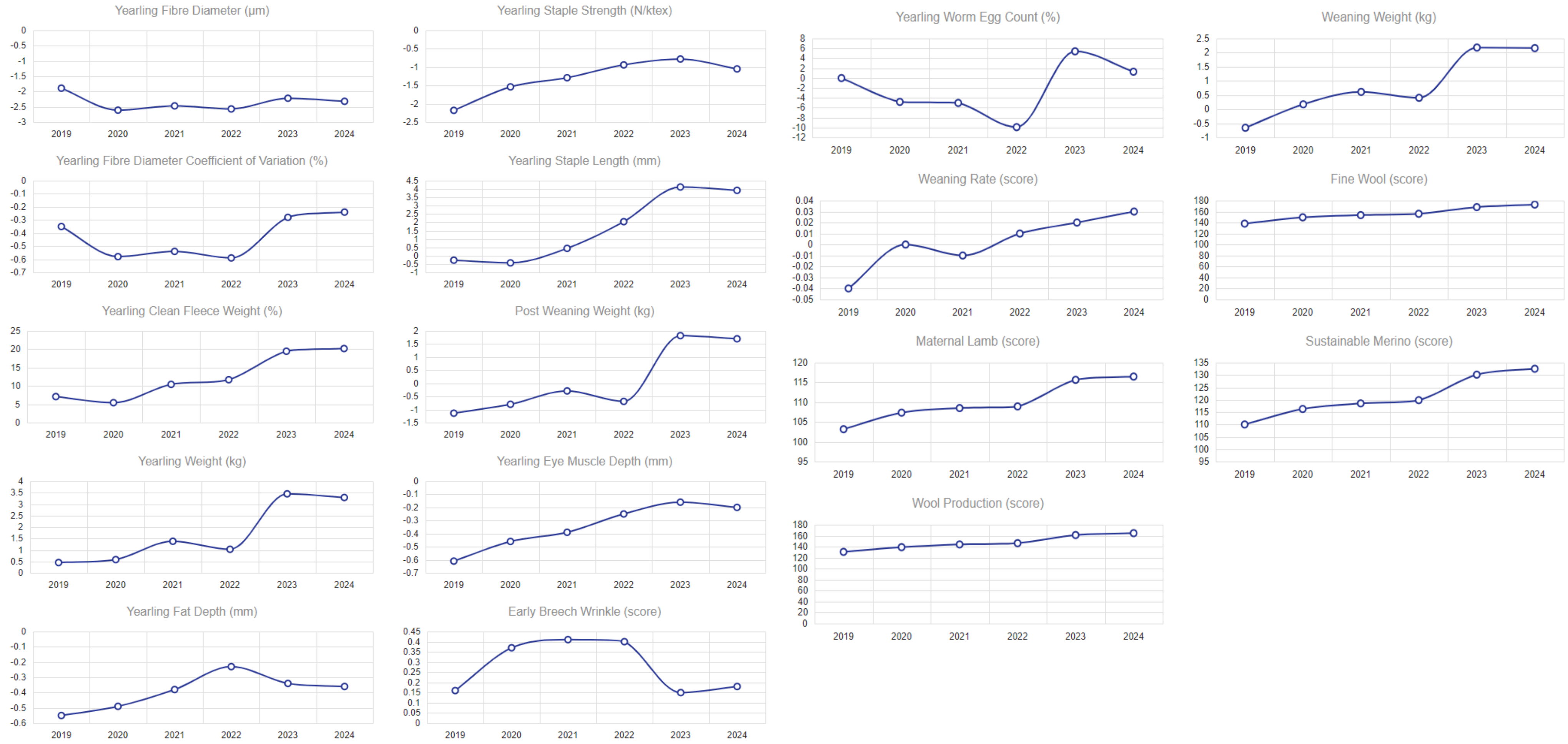


[1] traits are pwt_r = post weaning weight, ywt_r= yearling weight, yfat_r = yearling fat depth, yemd_r= yearling eye muscle depth, ycfw_r = yearling clean fleece weight, yfd_r = yearling fibre diameter, ydcv_r = yearling fibre diameter coeff. of variation, ycuv_r = yearling curvature, ysl_r = yearling staple length, pfec_r = postweaning worm egg count, ebwr_r = early breech wrinkle, cs_r = condition score, wr_r = weaning rate, SM_r = Sustainable Merino Index, WP_r = Wool Production Index, FW_r = Fine Wool Index, ML_r = Merino Lamb Index

Ram Team Manager (10th October 2024) – not related to the foundation ewes, current rams on hand – breeding program is aiming to move the Breeding Objective traits.

ASBV	Description	Breeding Objective	Units	Team Avg.	Team Percentile	Team Min.	Team Max.	Industry Avg.	Industry Min.	Industry Max.
yfd	Yearling Fibre Diameter	Maintain	µm	-2.4	10	-4.12	-0.9	-1.02	5.8	-6.47
yss	Yearling Staple Strength		N/ktex	-1.2	80	-5.82	6.36	0.99	-13.26	14.37
ydcv	Yearling Fibre Diameter Coefficient of Variation		%	-0.2	80	-1.66	1.08	-0.98	3.99	-4.63
ysl	Yearling Staple Length		mm	4.4	85	-3.75	13.64	9.89	-20.5	38.28
ycfw	Yearling Clean Fleece Weight	Increase	%	18.7	55	-0.44	39.6	18.83	-37	57.27
pwt	Post Weaning Weight	Increase	kg	1.1	95	-4.33	7.01	5.76	-10.67	19.3
ywt	Yearling Weight	Increase	kg	2.7	95	-3.01	8.69	7.52	-11.04	22.64
yemd	Yearling Eye Muscle Depth	Increase	mm	-0.3	85	-2.11	1.36	0.93	-3.57	5.72
yfat	Yearling Fat Depth	Increase	mm	-0.4	80	-1.48	0.74	0.26	-2.92	4.29
ebwr	Early Breech Wrinkle	Reduce	score	0.2	85	-0.5	1.28	-0.4	2.13	-2
ywec	Yearling Worm Egg Count		%	-6.0	65	-57.65	70.73	-19.42	196.74	-98.24
wwt	Weaning Weight		kg	1.7	90	-2.39	6.14	4.01	-7.34	13.44
wr	Weaning Rate		score	0.04	85	-0.07	0.21	0.15	-0.34	0.56
fw	Fine Wool		score	170	35	121.41	222.2	162.13	12.2	238.37
ml	Maternal Lamb		score	114	90	97.93	129.97	127.16	77.04	164.73
sm	Sustainable Merino		score	129	80	104.08	154.46	139.52	77.33	180.27
wp	Wool Production		score	160	55	116.25	204.43	160.54	33.33	231.13

Ram Team Manager – Genetic Trend 10th October 2024



Case Study 2: Flock # 5

The aim was to select foundation ewes from the home bred flock to generate a ram breeding nucleus to breed their own rams that would supply their 5,000 commercial flock.

Breeding Objective

- The breeding objective had been focused on wool production with surplus sheep sales a moderate priority.
- The new breeding objective is to maintain fleece traits and have a greater focus on improving meat and carcase traits

Foundation ewes

- CFA and surplus stud ewes purchased
  - Some with ASBVs and pedigree
  - Some without ASBVs or pedigree
- Homebred ewes – classed in for type
  - Ewe have been genotyped to generate GBV to finalise selection

Foundation Ewe Group	Count
Home bred ewes	149
Purchased stud ewes – Group 1	80
Purchased stud ewes - Group 2	88
Purchased stud ewes – Group 3	196
Total	**513**

Objectives for using GBV tool

- To select a mob of foundation ewes that will meet the future breeding objective.
- To be able to utilise the best commercial ewes and purchased ewes in the foundation nucleus flock.
- To determine that the GBV will be sufficient for breeding replacement rams or if moving to ASBVs will provide greater benefit.

What was genotyped as part of the Genomic Project?

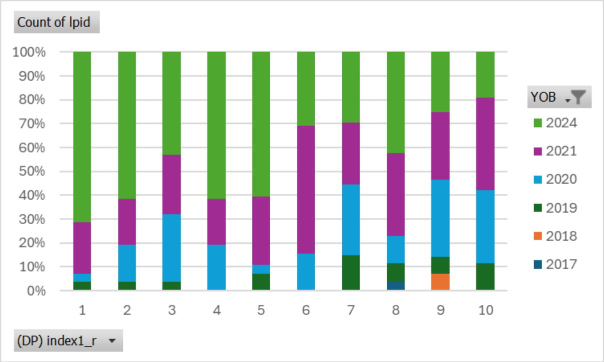
- The current homebred ewes were genotyped as well as their progeny (2024 drop).
- The 2024 drop bred from the homebred ewes that will be used as replacement ewes.
- The 2024 drop bred from the purchased stud ewes (the stud ewes were a mix of genotyped and non genotyped – these were not genotyped as part of the project).

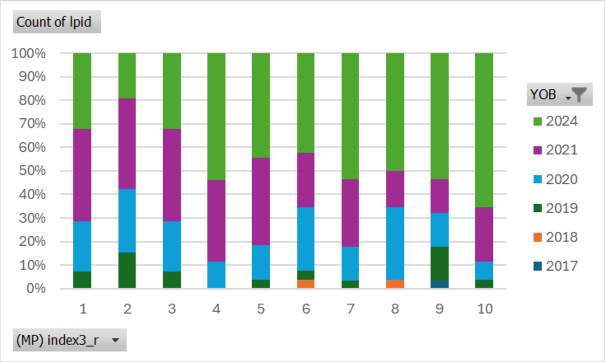
Results presented in August/September 2024

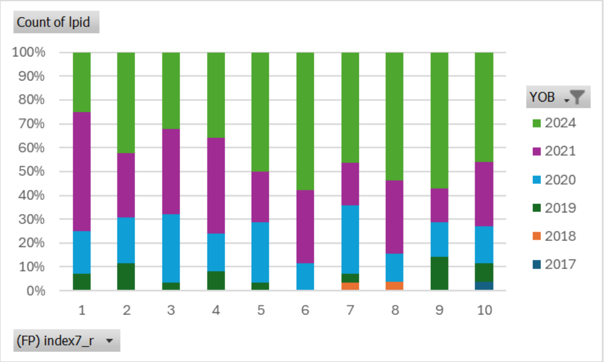
Based on the BO the DP index has been used to rank the animals that have a GBV. Figures 1, 2, and 3 present the GBV ranking on the three main indexes (DP, MP and FP) and the % per age group that were ranked in the respective percentiles.

Percentiles 1 = top 10% and 10 = bottom 0%

From this information the DP index seems to be the best fit to match the breeding objective with great percentage of the 2024 drop being ranked in the top

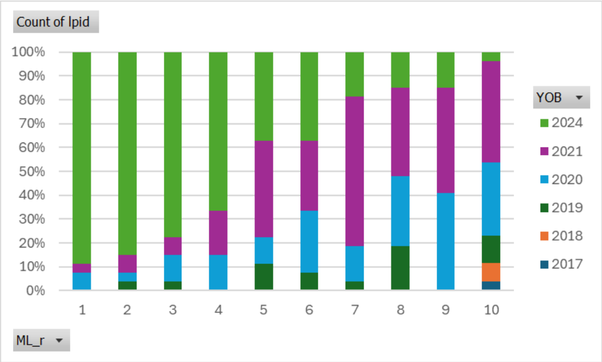


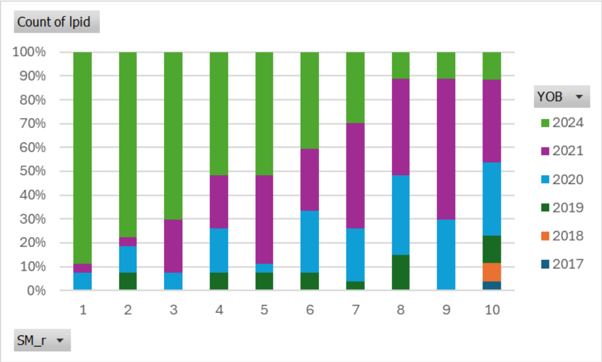


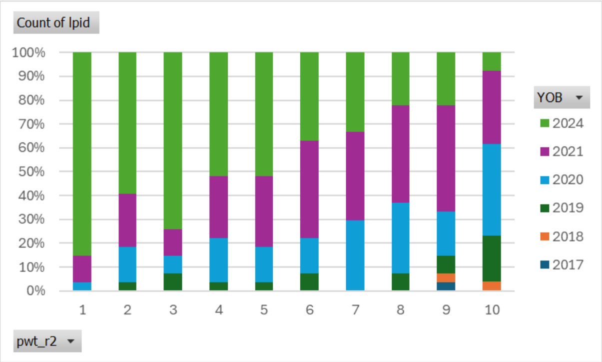


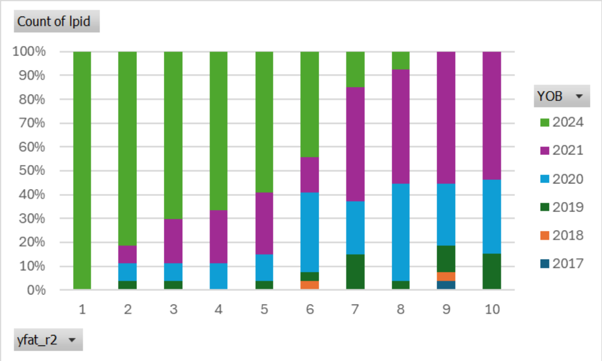
Results presented in October 2024 (post Sheep Genetics update to the new Merino indexes)

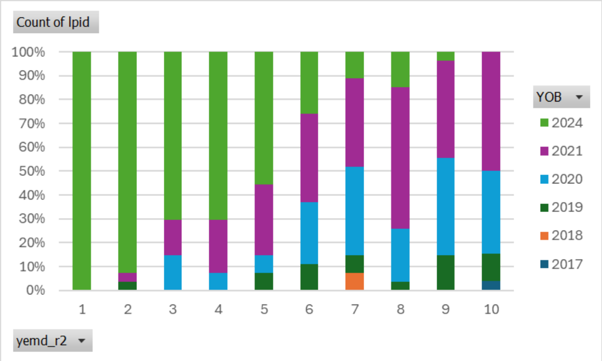
Based on the BO the ML index now seems to be the best fit to match the breeding objective with a greater percentage of the 2024 drop ranked in the top percentile for the key production traits in the index and BO. All sheep that were genotyped within the project have been included in the figures below showing the % per age group that were ranked in the respective percentiles. Percentiles 1 = top 10% and 10 = bottom 90%.

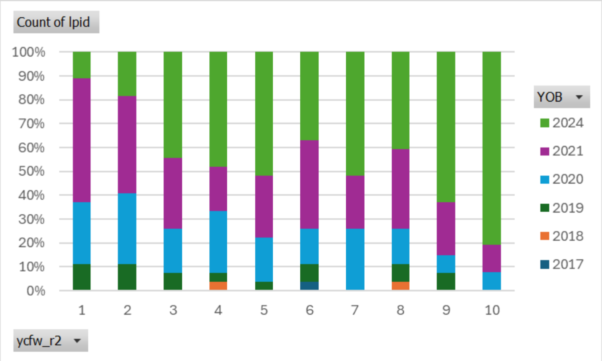


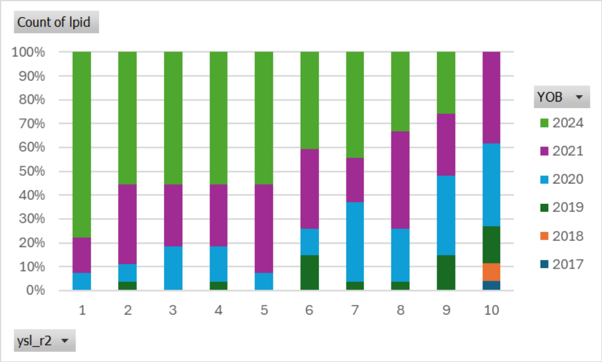


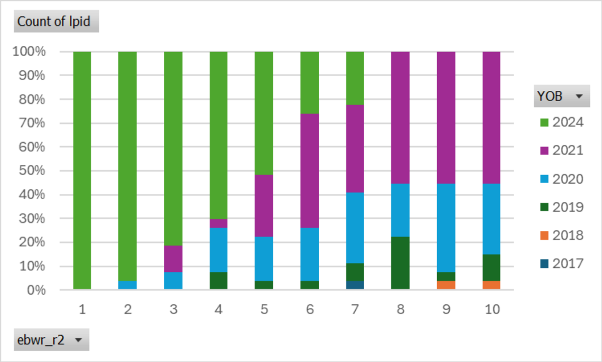


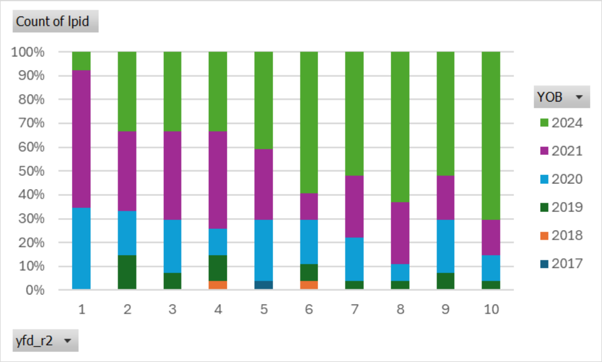






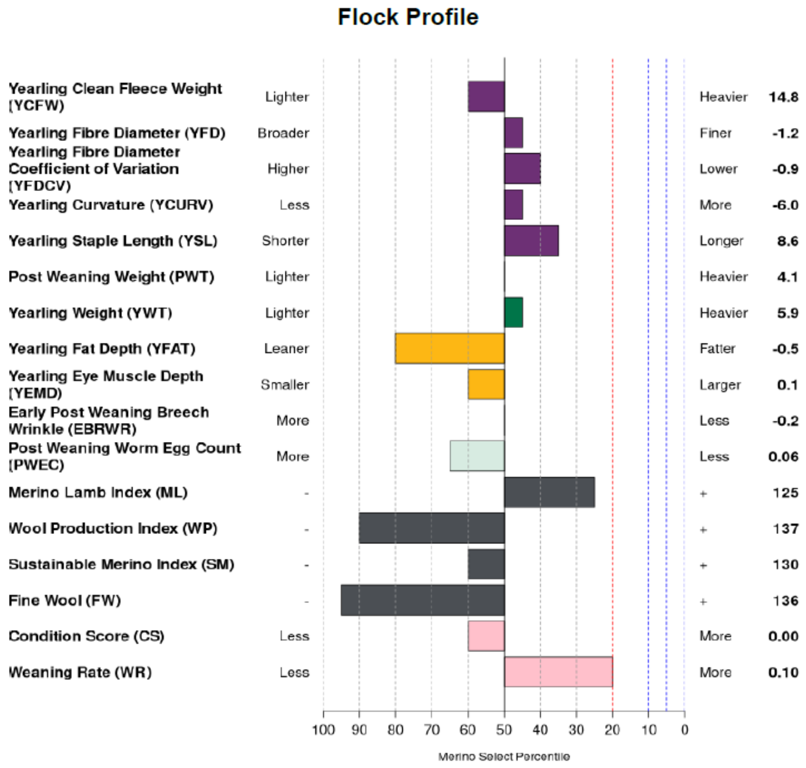




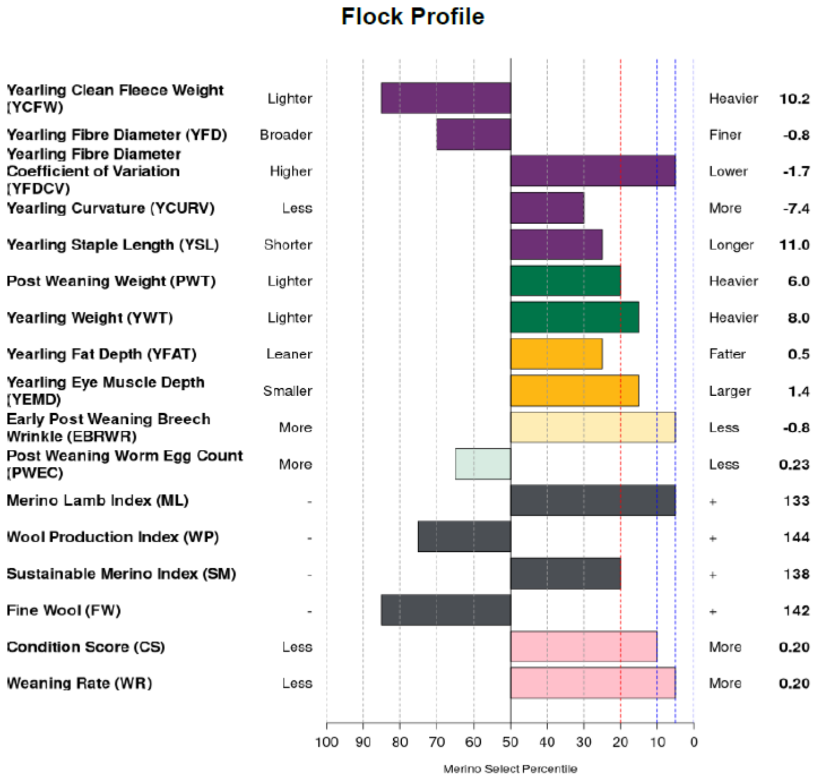


Flock Profile results

Home Bred Ewes – original Breeding Objective



2024 Drop – New Breeding Objective (aggressive ram selection)



Case Study 3: Flock # 7

Note: this case study will flow into the PDS project.

Flock # 7 currently run a ram breeding nucleus that feeds into their commercial ewe operation. They have been measuring phenotype (fleece traits and body weights) and generating within flock breeding values for 20 years (since 2005). This project has provided an opportunity to test the value of GBVs with the option of moving to submitting data into Sheep Genetics to generate ASBVs.

Currently classing and selection is based on both a within flock index ranking and visual assessments. The within flock index is able to be generated across years.

Breeding objective

- Increase fleece weight.
- Reduce micron.
- Improve early growth and lamb survival.
- Production system keeps wethers and runs a high stocking rate.

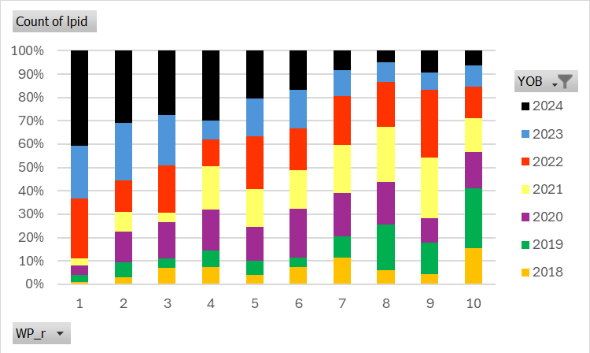
Experience with using GBVs

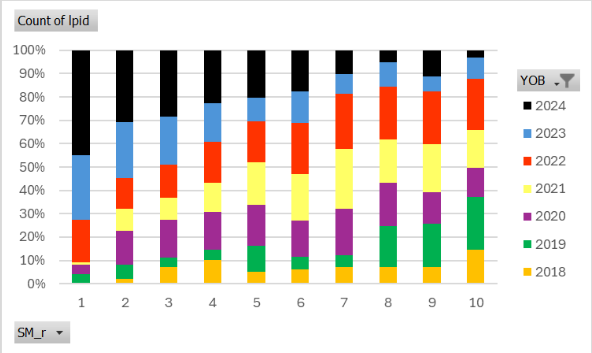
Flock # 7 were one of the first participants within the project to use the GBVs as part of their classing program. The GBV rankings were used in conjunction with the within flock index ranking and visual assessment. Key take home messages included the visual appearance of some rams and ewes did not match the GBV ranking and that the GBV aims to predict what their progeny will do not what they have done themselves (same as an ASBV, it is a predictive tool).

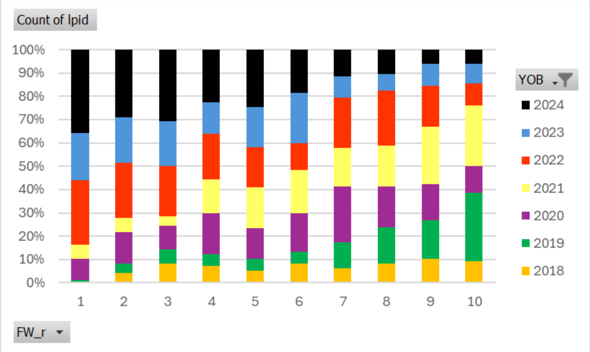
Percentile ranking of progeny genotyped

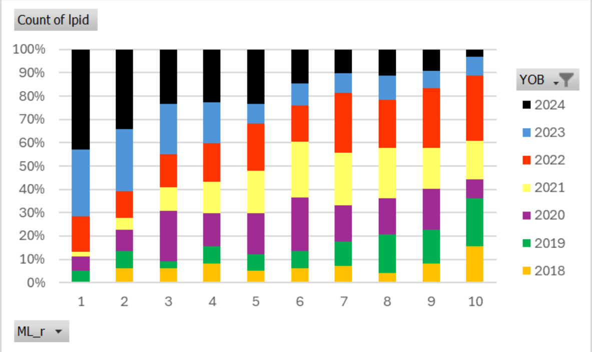
All sheep that were genotyped within the project have been included in the figures below showing the % per age group that were ranked in the respective percentiles. Percentiles 1 = top 10% and 10 = bottom 90%. Year of birth (YOB) colour coding has been adapted to year of birth tag colours that are standard within the Australian Sheep Industry that rotate every 8 years.

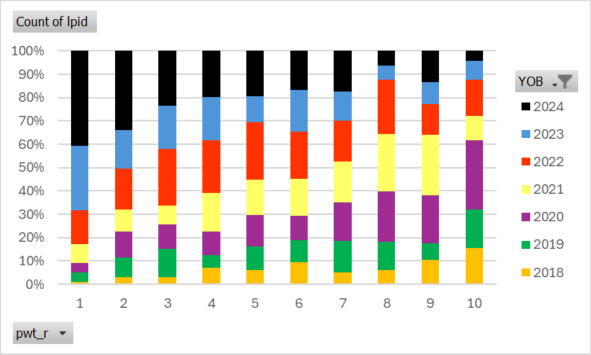
Colour	Red	Blue	Black	White	Orange	Green	Purple	Yellow
Year	2022	2023	2024	2025	2026	2027	2028	2029







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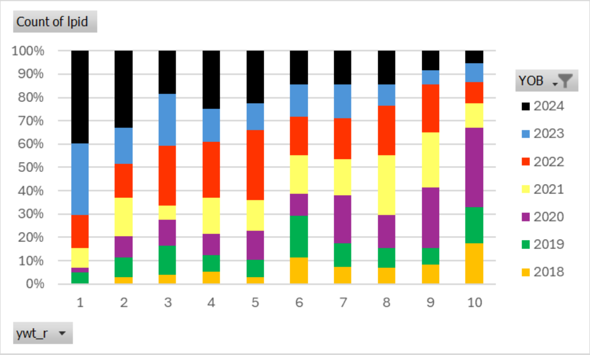
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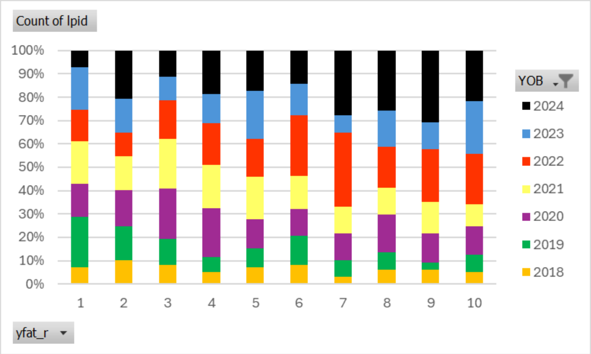
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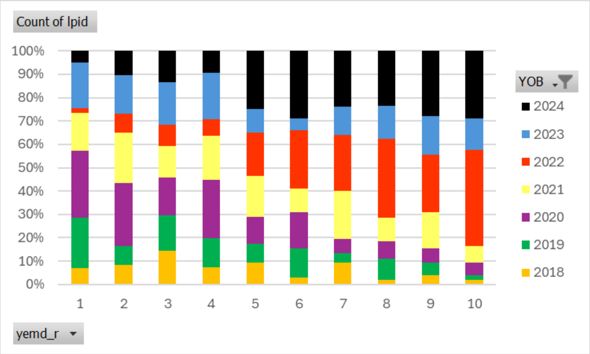
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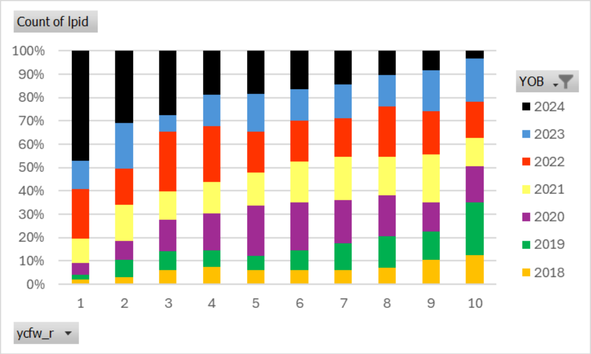
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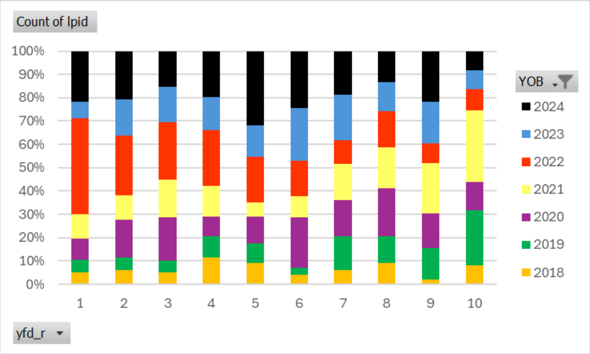
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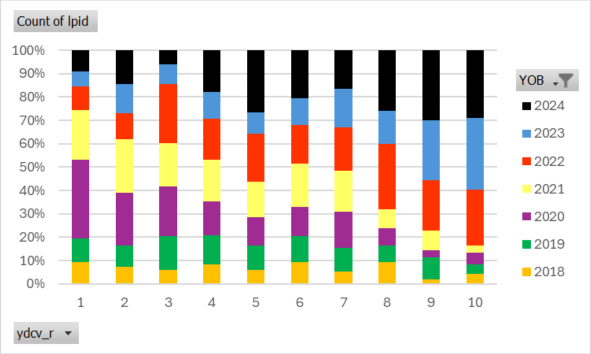
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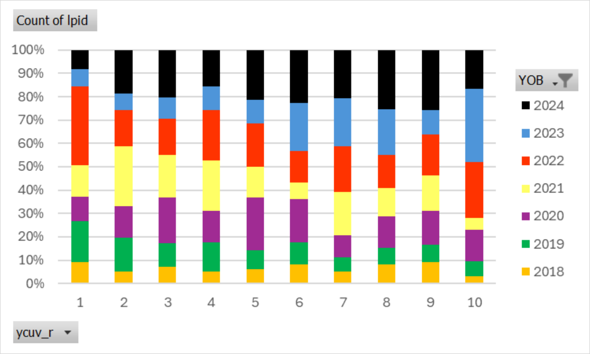
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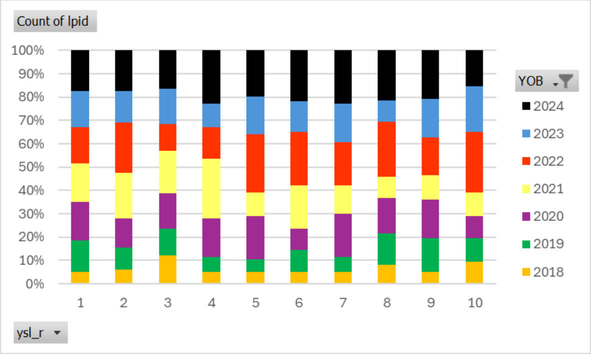
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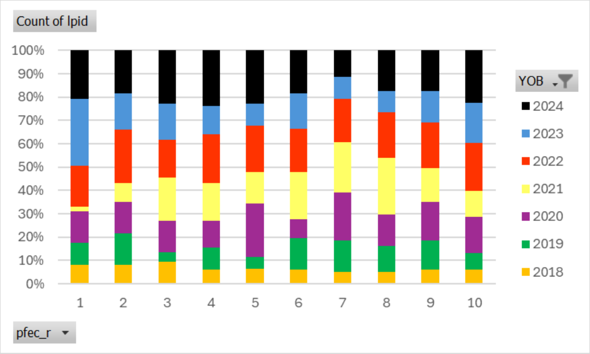
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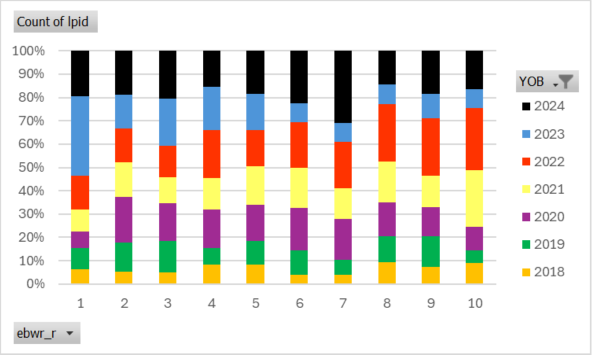
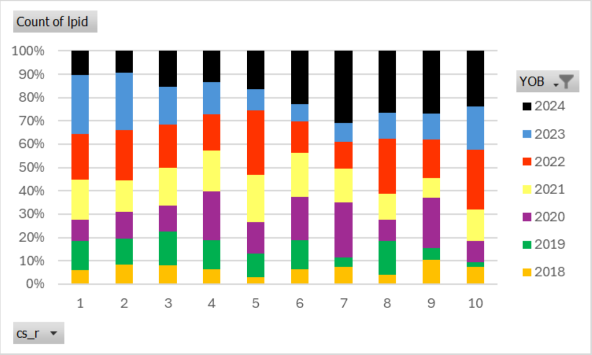
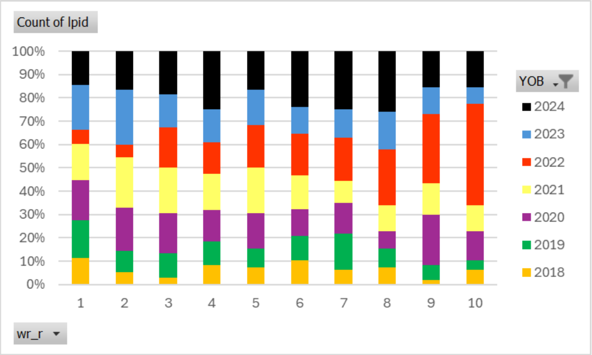


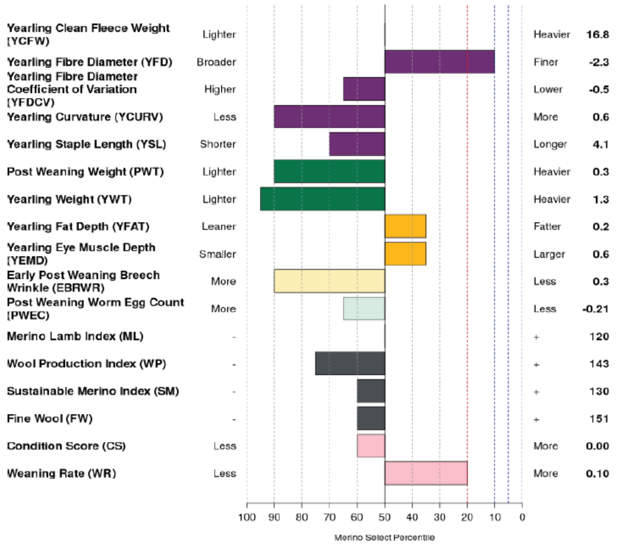




Flock Profile

Mixed age ewes and rams – 2018 to 2022 drop

Flock Profile



2023 Drop ewes and rams

Validation of GBV rankings on farm – Sire Evaluation

Do the GBV rankings work? This was a question posed by Flock # 7, and to test the index ranking two syndicates of rams were joined with one age group of ewes. The table below shows the GBV rankings of the rams selected to be in the two syndicates (high and low) based on the FP index available at the time of joining. The two mobs of ewes were separated at joining and lambing. Lamb marking is scheduled for the end of October 2024 and data collection will continue in the next phase of the Producer Demonstration component of the Genomic Tool Project.

GBVs generated March 2024 - PDS Syndicate Sire Evaluation

Animal ID	YOB	pwt_r	ywt_r	yfat_r	yemd_r	ycfw_r	yfd_r	ydcv_r	ycuv_r	ysl_r	pfec_r	ebwr_r	DP_r	MP_r	FP_r	PDS Option
1	2020	8	8	1	2	**10**	**9**	9	2	2	6	4	10	10	**10**	Low
2	2020	7	9	2	4	**9**	**9**	7	3	4	3	5	10	10	**10**	Low
3	2021	4	4	6	9	8	**9**	2	4	9	2	6	5	9	**10**	Low
4	2021	9	9	1	1	**9**	**9**	7	6	1	5	1	10	10	**10**	Low
5	2022	1	2	8	9	**1**	**1**	9	9	7	2	2	1	1	**1**	High
6	2022	7	6	9	10	**2**	**2**	7	9	7	9	9	3	1	**1**	High
7	2022	9	9	10	10	**2**	**1**	5	6	8	3	8	8	2	**1**	High
8	2022	3	3	10	10	**2**	**1**	3	8	5	3	7	2	1	**1**	High (AI backup)
9	2020	10	8	5	5	**2**	**1**	6	10	1	1	1	5	1	**1**	High

Appendix 8.5 – Flock validations

Summary of data for flock 6

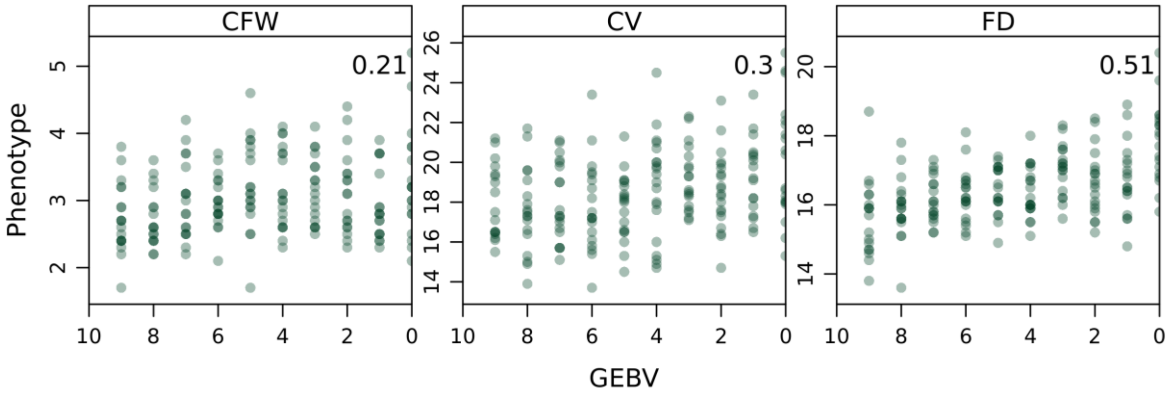


Figure A5_3: Corrected phenotype vs GBV for traits on animals recorded (number is the correlation).

Summary of data for flock 7

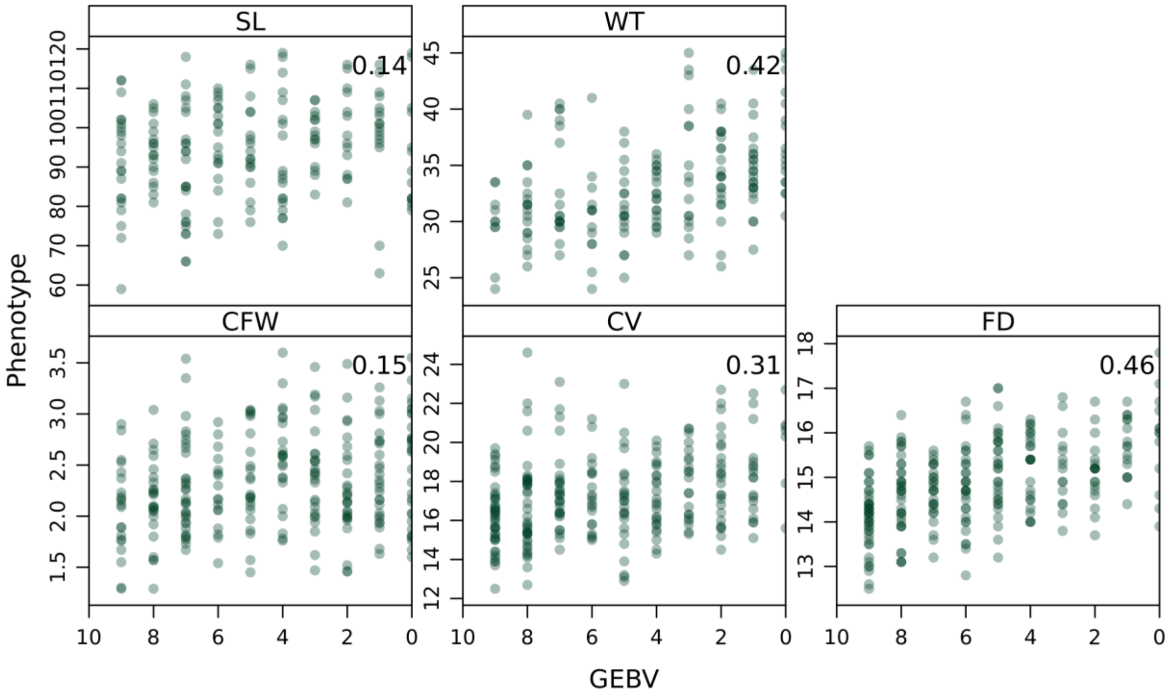


Figure A5_4: Corrected phenotype vs GBV for traits on animals recorded (number is the correlation).

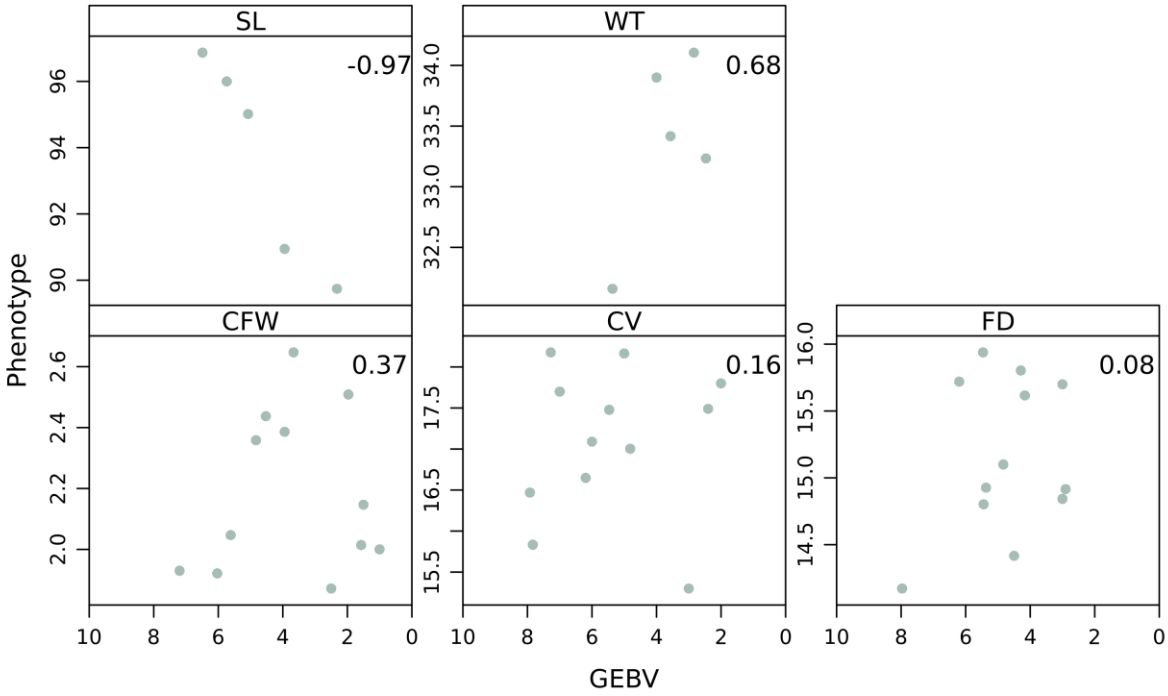


Figure A5_5: Corrected phenotype vs GBV for averaged for each sire (number is the correlation).

Summary of data for flock 11

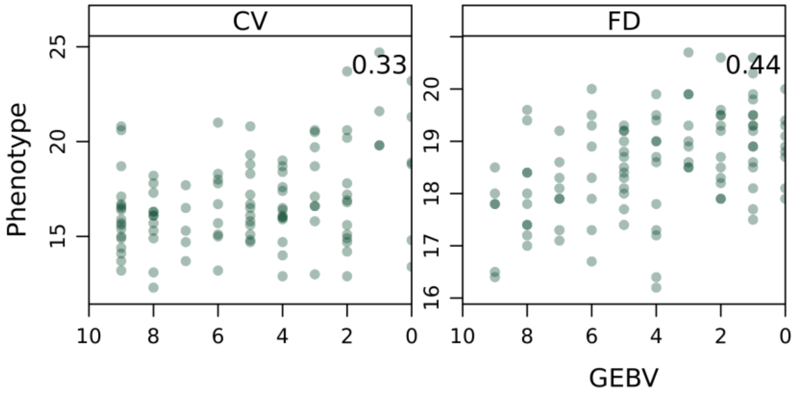


Figure A5_6: Corrected phenotype vs GBV for traits on animals recorded (number is the correlation).

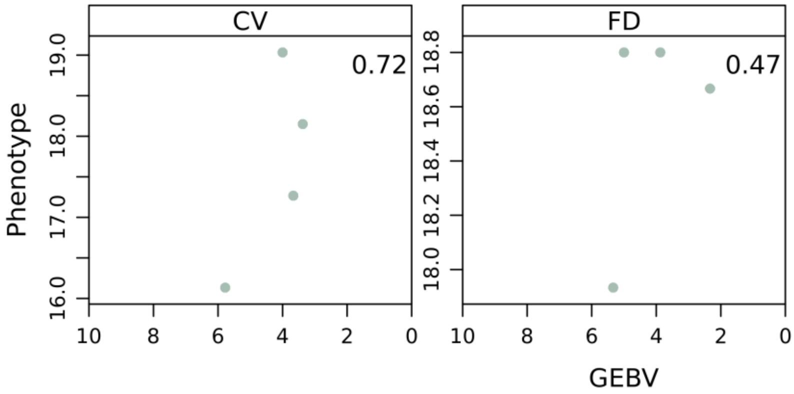


Figure A5_7: Corrected phenotype vs GBV for averaged for each sire (number is the correlation).

Summary of data for flock 8

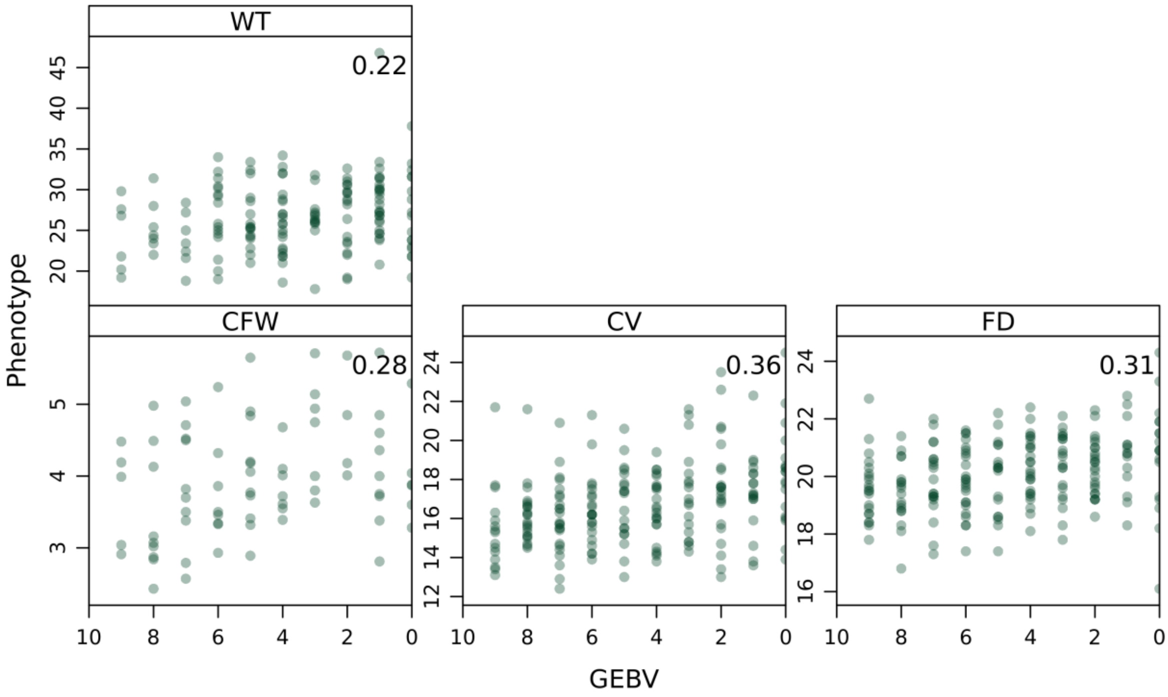
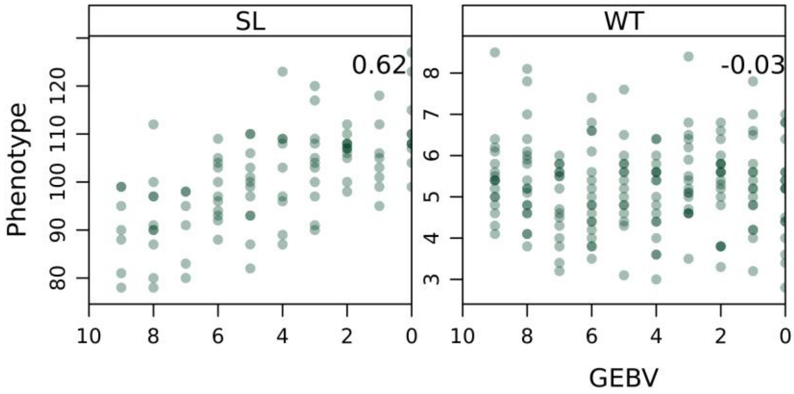


Figure A5_8: Corrected phenotype vs GBV for traits on animals recorded (number is the correlation).

Summary of data for flock 16



FigureA 4_10: Corrected phenotype vs GBV for traits on animals recorded (number is the correlation).

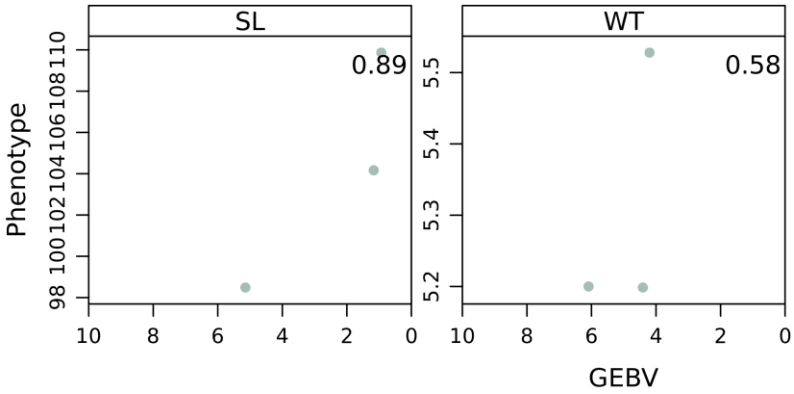


Figure A5_11: Corrected phenotype vs GBV for averaged for each sire (number is the correlation).

Summary of data for flock 10

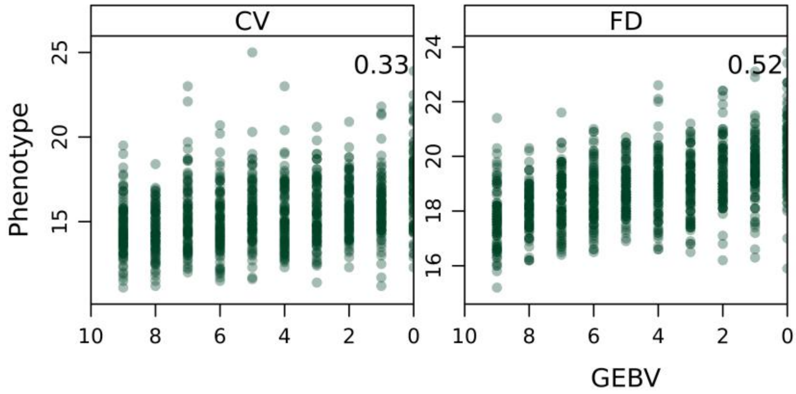


Figure A5_12: Corrected phenotype vs GBV for traits on animals recorded (number is the correlation).

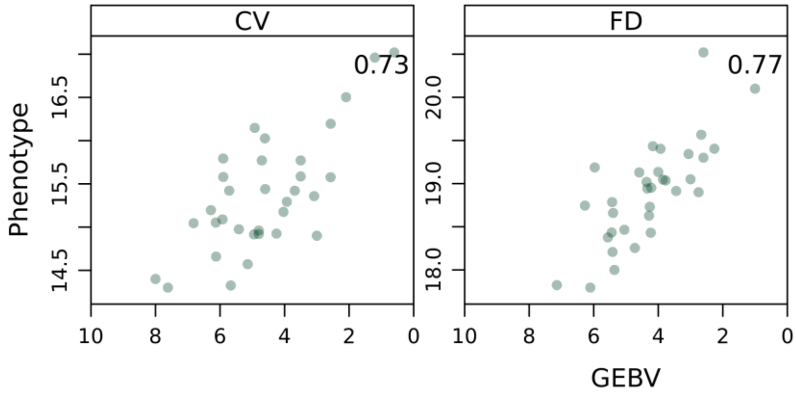


Figure A5_13: Corrected phenotype vs GBV for averaged for each sire (number is the correlation).

Summary of data for flock 19

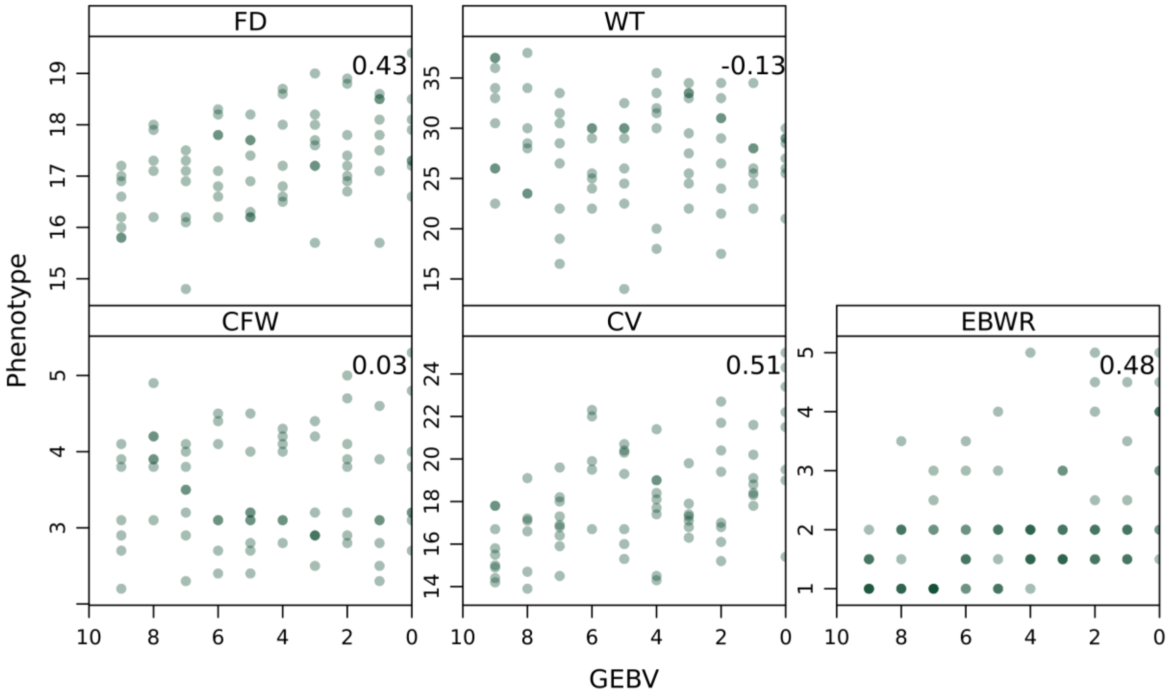


Figure A5_14: Corrected phenotype vs GBV for traits on animals recorded (number is the correlation).

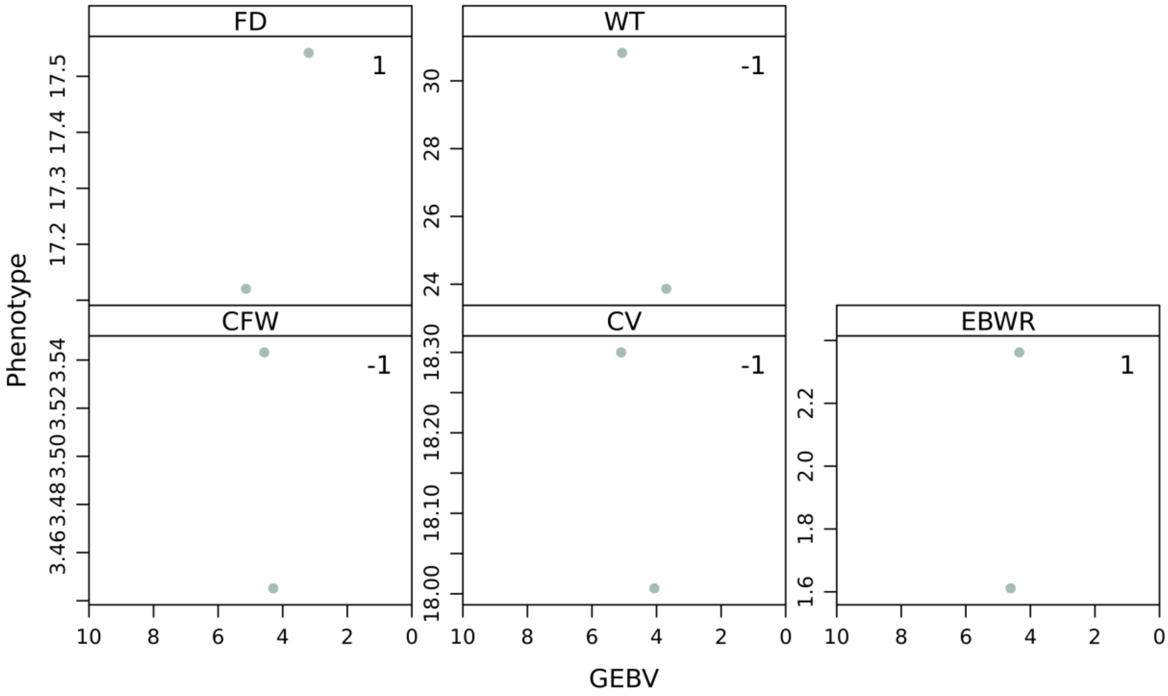


Figure A5_15: Corrected phenotype vs GBV for traits on sire recorded (number is the correlation).

Summary of data for flock 2

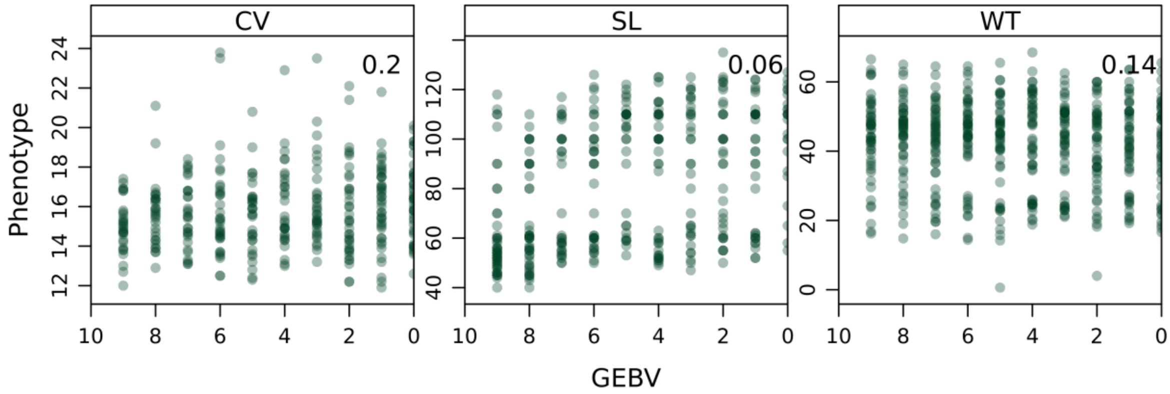


Figure A5_16: Corrected phenotype vs GBV for traits on animals recorded (number is the correlation).

Summary of data for flock 14

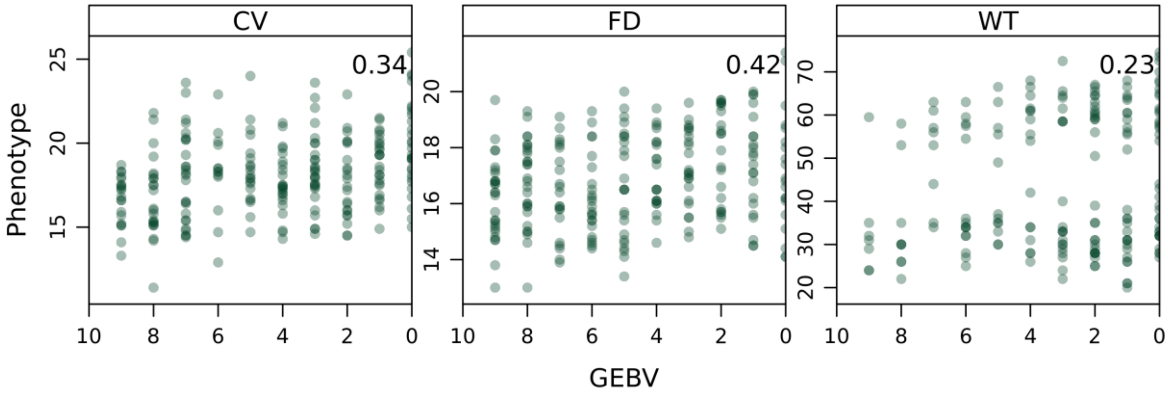


Figure A5_17: Corrected phenotype vs GBV for traits on animals recorded (number is the correlation).

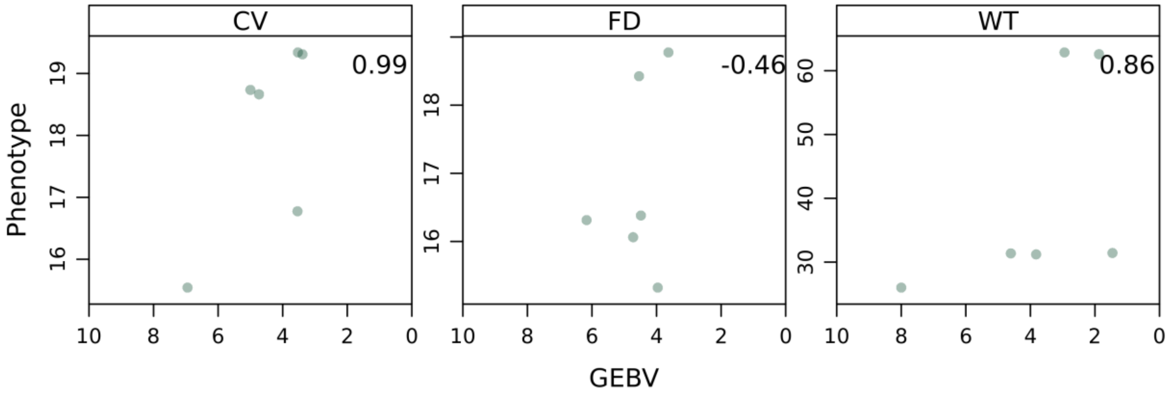


Figure A5_18: Corrected phenotype vs GBV for traits on sire recorded (number is the correlation).

Summary of data for flock 1

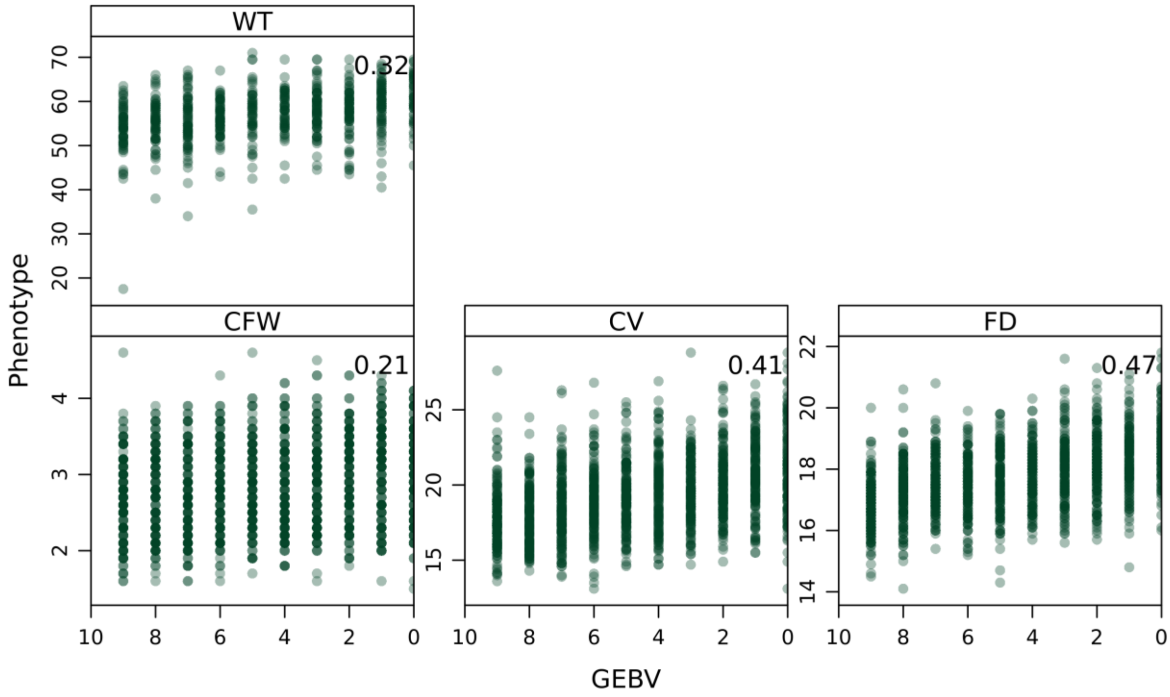


Figure A5_19: Corrected phenotype vs GBV for traits on animals recorded (number is the correlation).

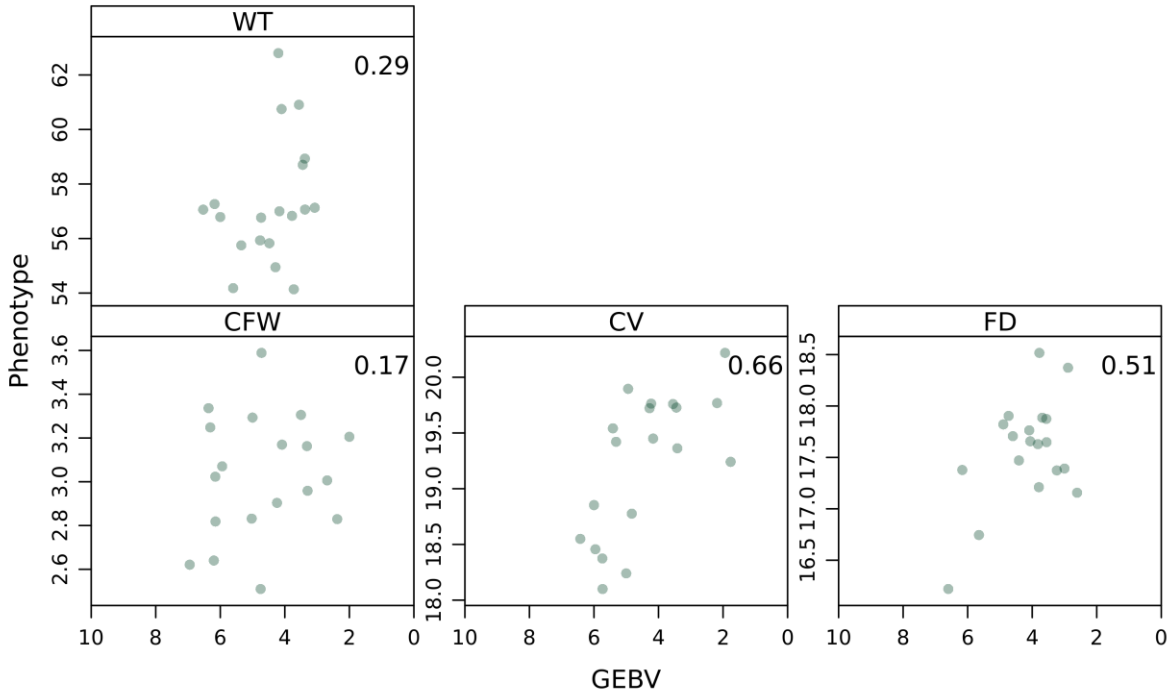


Figure A5_20: Corrected phenotype vs GBV for traits on sire recorded (number is the correlation).

Summary of data for flock 15

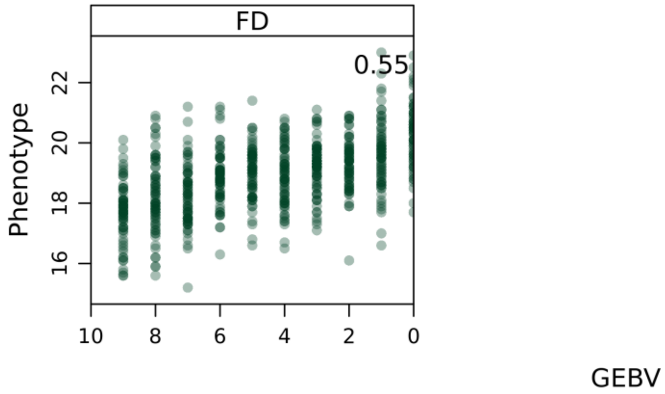


Figure A5_21: Corrected phenotype vs GBV for traits on animals recorded (number is the correlation).