



Sheep CRC Practical Wisdom Notes

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Benefits of genomic selection in Merino, Terminal and Maternal indexes

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Key points

- Genomic testing is available for Merino, Poll Dorset, White Suffolk and Border Leicesters
- Genomic testing provides most benefit where trait measurement occurs after selection and/or is hard to measure
- Testing male selection candidates returns the best value for money
- Not all males need to be tested to realise most of the potential benefit of genomic selection

Introduction

Genomic selection works by DNA testing an animal and comparing its DNA profile with thousands of other animals that have been DNA tested and measured for important traits. Based on this DNA comparison the genomic breeding value of an animal can be predicted.

In Australia, this is based on information from the Sheep CRC Information Nucleus Flock, MLA Resource Flock and sheep in the Sheep Genetics database that have been genotyped and performance recorded. Across all of these research and industry flocks there are close to 54,000 animals. The MLA Resource Flocks continue to measure and genotype animals every year to maintain an ongoing data resource that can be used to predict genomic breeding values.

To predict an animal's breeding values, the DNA information is used in conjunction with other information in the Sheep Genetics database, such as pedigree, the breeding value of its parents and its own performance information. Ram breeders and ram buyers can use Australian Sheep Breeding Values (ASBVs) to select animals based on genetic merit as they are the best prediction of breeding value, combining all the available information.

Genomic-enhanced ASBVs increase accuracy of traits that have not or cannot be measured on an individual. Genomic testing is an important tool to use when selecting for later-in-life or hard-to-measure traits. This lends itself to being used as a tool to more accurately select younger sheep (e.g. using ram and/or ewe lambs to lower the generation interval). This can be an effective way to accelerate rates of genetic gain as per the breeder's equation (Figure 1).

$$\text{Genetic gain} = \frac{i_m r_{IA_m} + i_f r_{IA_f}}{L_m + L_f} \sigma_A$$

Selection intensity/efficiency (points to i_m and i_f)
 Accuracy (points to r_{IA_m} and r_{IA_f})
 Generation interval (points to $L_m + L_f$)
 Genetic variation (points to σ_A)

Figure 1: Breeder's equation and description

Genomic testing also increases variation in ASBVs within a cohort (Figure 2), which gives breeders the potential to increase rates of genetic gain particularly where there are traits in the breeding objective that are hard to measure (Figure 1). Genomic testing currently costs \$27 per animal and requires a 16-digit identification number as supplied from Sheep Genetics.

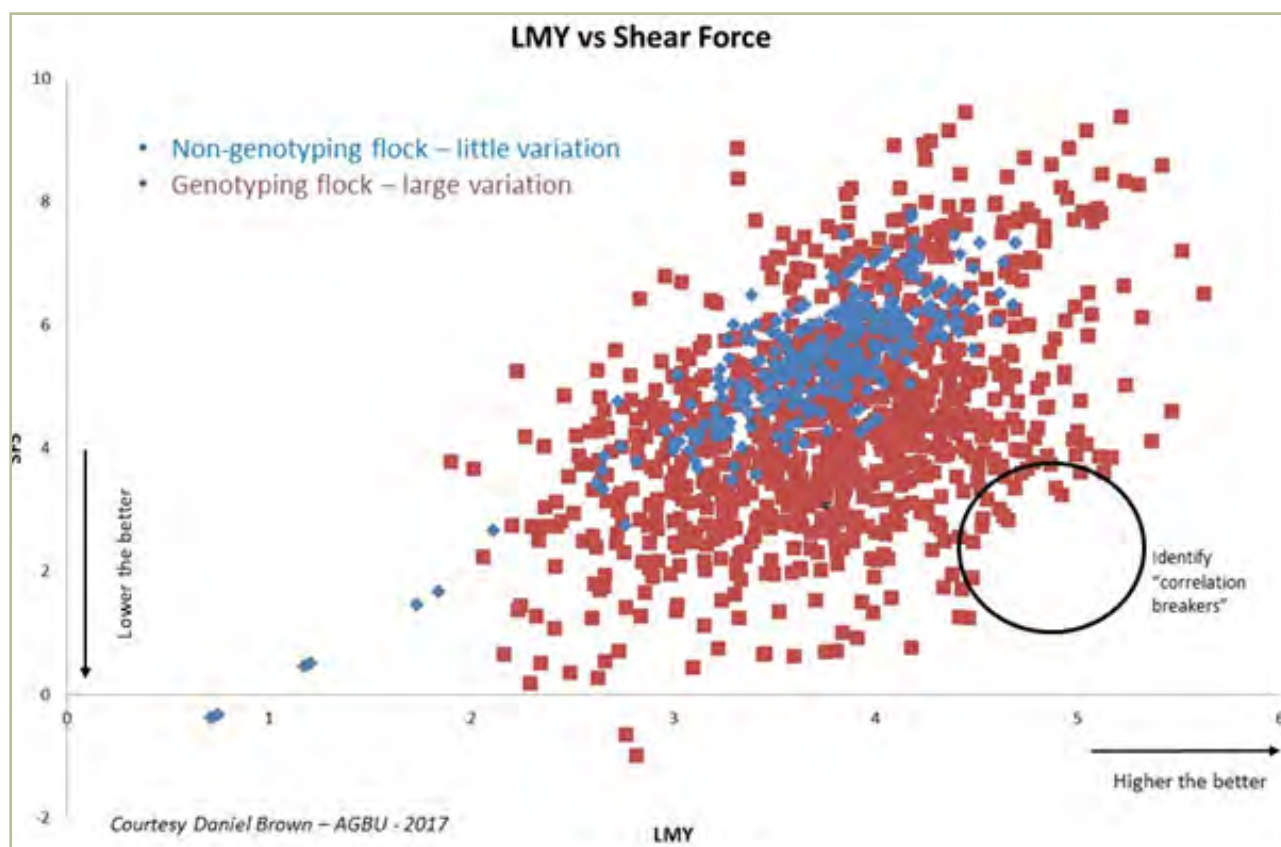


Figure 2: Plot of ASBVs for shearforce (SF5) and lean meat yield (LMY) for a flock that does not genotype (blue) and a flock that does genotype (maroon).

Genomic selection

Genomic selection can be defined as selecting some or all animals that have had a genomic test. When assessing the benefits of genomic selection we often look at index response rather than individual trait response. This is because we select on indexes that have been calculated for the sheep industry where genetic relationships, heritabilities and economics are factored together to achieve balanced genetic gain. When using genomic selection, breeders can either use single-stage genomic selection or two-stage genomic selection.

Single-stage genomic selection

Single-stage genomic selection refers to all selection candidates being genomically tested and using the genomically enhanced breeding values for selection (Column 2 of Figure 3). This option is becoming attractive to breeders who currently parentage test (\$21) all their drop and can now do a genomic test for a small increase in price. For sheep to receive genomically enhanced ASBVs, the animal must have at least one performance record (e.g. birthweight, weaning weight, post-weaning weight etc.).

Where a breeder has previously parentage tested all progeny, new pricing for the genomic test now makes it possible to genomically test all rams. Due to the relatively small benefit of genomically testing females, it is recommended to still parentage test ewes. However, it is important to consider the pros and cons of different pedigree methods. DNA parentage is a viable method however fixed effect data cannot be captured (e.g. date of birth, birth type, maternal behaviour score) as it can with the alternative pedigree determination method of mothering up. If breeders are mothering up their sheep, then two-stage genomic selection is a more economical way to genomic test selection candidates.

Two-stage genomic selection

If parentage is assigned by not using a DNA-parentage, the most economical way to use genomics would be for breeders to rank sheep based on index breeding values and then strategically genomic test a proportion of top ranking sheep (Columns 3-4 Figure 3). This is referred as two-stage genomic selection. After testing and re-ranking, candidates are then selected using updated breeding value rankings.

Should I test only rams and/or ewes?

Genomically testing rams is an economical way of implementing genomics. This is due to the high selection intensity of rams compared to ewes (i.e. few rams have many progeny vs many ewes have few progeny). Some breeding objectives and breeding systems may require genomic testing to occur prior to most performance recording due to the use of ram lambs (e.g. terminal and maternal breeds). Other systems allow genomic testing to occur after performance recording (e.g. Merinos). Once genomic testing has occurred, additional spread or variation can be observed in the updated ASBVs. This gives the potential for increased the rates of genetic gain (Figure 1).

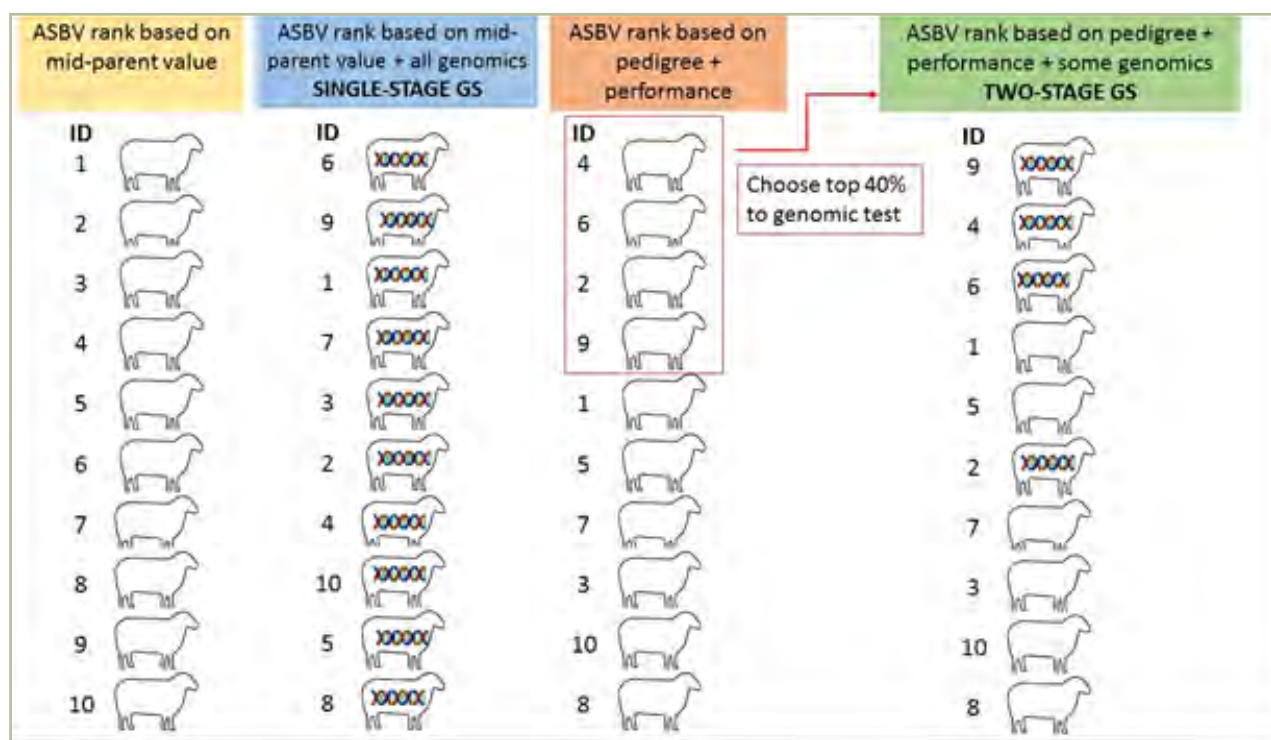


Figure 3: Simple example of the differences between single and two-stage genomic selection

Two-stage genomic selection is more affordable in mature rams

Figure 4 demonstrates that if ram selection candidates are ranked prior to genomic testing, a smaller proportion (x-axis) of selection candidates can be genomically tested and still receive a significant portion of the benefit (y-axis). These models assume full pedigree is known for all selection indexes and basic measurements for each selection index have been recorded.

Test more ram lamb selection candidates to achieve the maximum benefit

Figure 4 shows that fewer 18-month-old ram candidates need to be tested to achieve the maximum benefit (Yellow line) compared to seven-month-old ram lamb candidates (Orange, Green and Light Blue lines). This is the result of more accurate pre-ranking of 18-month-old than seven-month-old rams, with more performance and pedigree information.

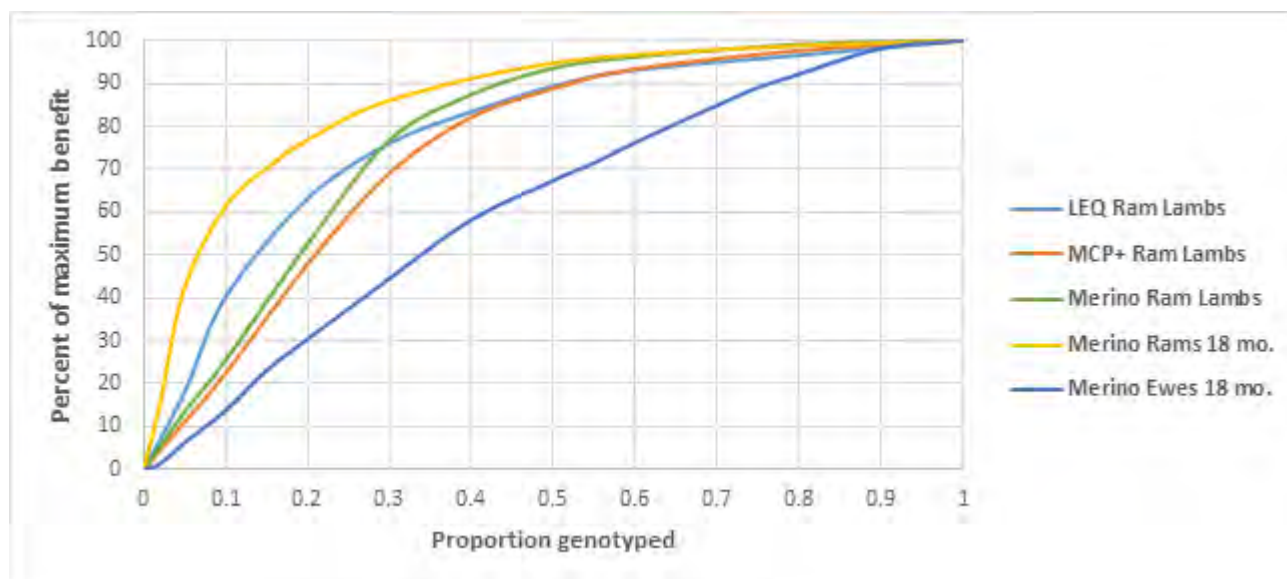


Figure 4: Percent of maximum benefit for proportion of selection candidates genotyped. Note that zero candidates results in zero benefit and 100% genotyped results in 100% of potential benefit. Key: LEQ – Lamb Eating Quality index, MCP+ – Maternal Carcase Production Plus index, Merino Production Plus index.

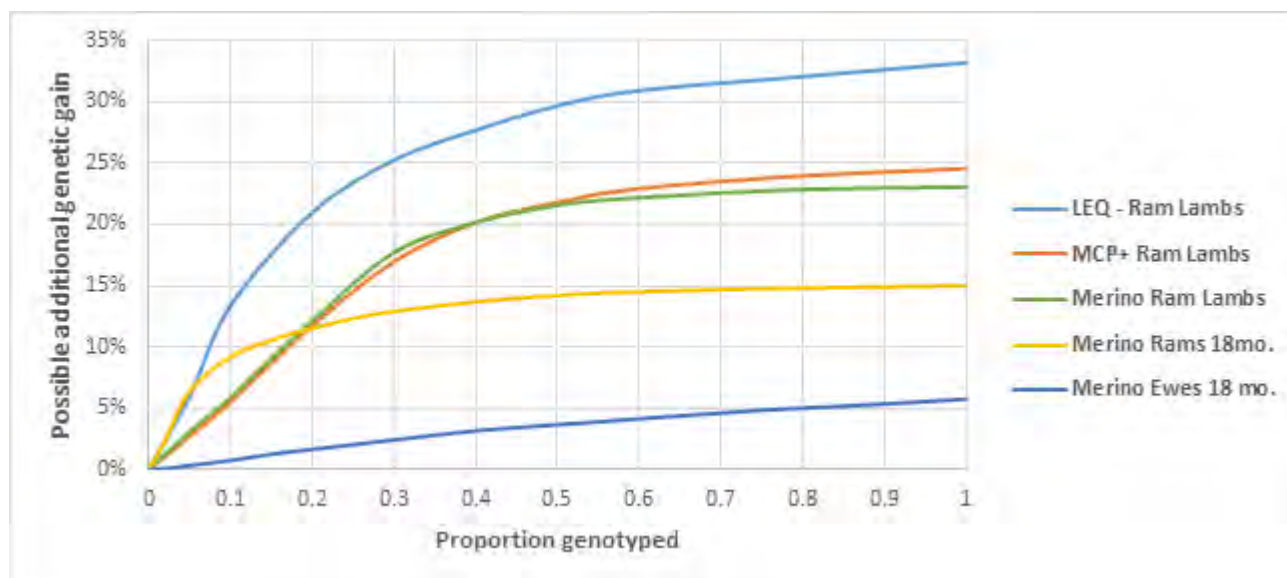


Figure 5: Possible extra benefit for proportion of selection candidates genotyped. Note that zero candidates results in zero benefit. Key: LEQ – Lamb Eating Quality index, MCP+ – Maternal Carcase Production Plus index, Merino Production Plus index.

Genomics has a larger impact when using ram lambs

Figure 5 demonstrates that genomically testing Merino ram lambs has a larger proportionate increase in genetic gain than testing 18-month-old rams. This is the result of shorter generation interval and increased accuracy. As breeders strive to achieve high rates of genetic gain, a balancing act between accurate breeding values and lowering generation interval needs to be found as demonstrated in the breeder's equation (Figure 1).

Genomic selection has different impacts on different selection indexes

Genomic selection has different impacts on rates of genetic gain depending on the breeding objective (Figure 5). This is due to each breeding objective having different traits, some of which are hard-to-measure, measured later-in-life or sex-limited. Each of the traits in the indexes will have differing genetic correlations, heritability and economic weightings.

Figure 5 shows that the terminal LEQ index has the highest potential response to genomic selection. This is due to the strong economic weightings on hard-to-measure traits such as intramuscular fat and shear-force of meat in the index.

Genomic testing rams has a much larger effect on rates on genetic gain

Genomic testing rams is a better investment due to rams having a much higher selection intensity than ewes. Figure 5 shows the possible genetic gain genomic selection can have in a breeding program where Merino rams OR ewes are genomic tested and first mated at 18 months of age. The maximum potential benefit for testing rams is an extra 15% whereas genomic testing ewes only yields an extra 6%.

Furthermore, breeders only need to genomic test the top 23% of ram selection candidates to obtain 80% of the maximum benefit (i.e. 12% potential more gain) whereas testing the same amount of ewes would obtain only 30% of the maximum benefit (i.e. 2% potential more gain).

Is genomic testing the next step for you?

Genomic testing should be viewed as the "cream on the cake". Breeder need to ask themselves whether they have got their breeding sponge cake recipe right before worrying about genomics as genomic testing will not automatically increase the rate of genetic gain. Breeders still need to use breeding values to select sheep to increase rates of genetic gain.

Increasing selection intensity is a very effective method of increasing genetic gain without costing anything extra. Table 1 is a simple checklist for a sound breeding program to drive rate of genetic gain:

Table 1: Checklist for sound breeding program design to generate rate of genetic gain

Task	Influences	Check
Pedigree (sire & dam all progeny)	Accuracy of ASBVs	<input type="radio"/>
Measure traits in breeding objective (entire cohorts)	Accuracy of ASBVs Variation of ASBVs	<input type="radio"/>
Recording fixed effects (birth type, rear type, date of birth)	Removes bias in ASBVs	<input type="radio"/>
Linkage (year-to-year & to Sheep Genetics population)	Accuracy of ASBVs	<input type="radio"/>
Management groups (not too many with linkage between)	Removes bias in ASBVs	<input type="radio"/>
Cull on visual/subjective (after objective measurement)	Visual structure	<input type="radio"/>
Genomic testing (2-stage)	Accuracy of ASBVs Variation of ASBVs	<input type="radio"/>
Using ASBVs to select (Selection intensity/efficiency)	Rate of genetic gain	<input type="radio"/>

Conclusions

Genomics provides most benefit to traits and indexes where trait measurement occurs after selection and/or are hard to measure. Testing male selection candidates returns best value for money compared to testing females, with a proportion of males needed to be tested (2-stage genomic selection) to realise most of the potential benefit.