

Genetic evaluations and the calculation of breeding values are in their simplest form a large system of comparisons.

For Example



If A beats B and B beats C then they rank A...B...C. We know A is better than C, even though they were never compared directly. B is the 'link' to compare A with C. This system of comparison is the same principal that underlies the calculation of breeding values, but there are many more comparisons to make.

In its simplest form the genetic evaluation calculates breeding values for each animal using

- the animals own pedigree and performance information,
- the performance of all known relatives,
- the performance of any progeny that the animal may have,
- the known relationship between traits, and any genomic information that may be available.

The premise of breeding values is that we can compare animals despite their environment, whereas an animal's performance record does not allow this. As everyone knows you can feed animals to be bigger or we can breed them to be bigger. Breeding values allow us to know if the animal is bigger due to feed or genetics.



Phenotypes

Measurements collected which allows BREEDPLAN and Sheep Genetics analyses to estimate breeding values.

- Our genetic evaluations started by calculating estimated breeding values for weight and evolved to capture many measures of productivity.
- As BREEDPLAN and Sheep Genetics continue to evolve, the range of traits evaluated will continue to grow to reflect the diversity of breeding objectives.
- BREEDPLAN and Sheep Genetics promote higher quality recording. With high precision measuring leading to increased genetic gains.



Fixed Effects

Factors impacting the performance of an animal that are highly repeatable.

- Differences in the phenotypes of a flock or herd are a reflection of both genetic and environmental factors.
- We want to select animals based on genetic superiority.
- Some of the environmental factors that impact the performance of an animal are known and highly repeatable, these are known as fixed effects in the analysis. Birth type is a good example of a fixed effect.
- By accounting for known fixed effects within the analysis we are able to compare the genetic merit of individuals more fairly.





Pedigree

The pedigree allows us to model the relationship between the individuals in the analysis.

- Half of the genetic information in a individual will come from the sire and the other half from the dam. The combination of the inherited genes determine the characteristics of the progeny.
- Related animals have genes in common and are likely to have a similar phenotype.
- Breeding values are robust as they use information not just from the individual but also it's relatives, who share genes, when estimating the individuals genetic merit for the phenotypes of value.





Genomics

Including genomic information in the analysis improves our ability to understand and in turn model the relationships between individuals.

- The average animal will have half it's genes in common with it's parents. However, which genes they are is random. The DNA markers, or SNPs as we call them, captured in the genotype allow us to better understand what is inherited from an animals relatives.
- The more we know about the relationship between individuals the more accurate our ability to estimate the breeding values.
- The benefits of genomics are greatest for traits that are difficult or expensive to measure, are expressed late in life, expressed in only one sex or low heritability.
- Genotypes can also assist with parent verification of animals, and commercial benchmarking tools to allow commercial producers to benchmark their animals across the industry.



Heritability

The proportion of differences between individuals due to their inherited genetic factors.

- Difference in the phenotype of an animal is a reflection of both genetic and environmental factors
- Heritability, is the proportion of the phenotypic differences between individuals due to their genetics





Correlations

Refer to the strength of the relationship between different traits or characteristics of your animals. Relationships can be strong or weak, favourable or unfavourable

- Much like using information from relatives to describe the genetic merit of the individuals we can use the performance of an individual for one trait to understand their performance in another trait.
- Breeding values calculated via a multi-trait analysis account for relationships between traits, so you don't need to think about trait relationships when selecting on key traits.





Linkage

Is where genes are represented across multiple environments. In the evaluations this primarily occurs when a sire has progeny in multiple herds or flocks.

- Having the same genes represented across multiple groups of animals, enables the analysis to separate environmental and genetic effects. This gives us the ability to properly benchmark individuals across the whole analysis.
- It is also important to note that linkage is trait dependant. Different breeders record different sets of traits so this means that linkage is not always to same for all traits. When buying bulls or rams you need to make sure your seedstock supplier is recording the traits important to you and linked to the analysis as a whole for those traits.



Accuracy

With more information, the accuracy of breeding values increase.

- The breeding values calculated in genetic evaluations are estimates of the true breeding value of an animal, and the accuracy of these estimates varies depending on how much information we have available.
- With more information, the accuracy of the breeding value increases, and we can make better selection decisions, leading to faster rates of genetic gain.
- The accuracy of young animals can be substantially lifted through genomic testing supported by effective reference populations.



Multibreed

The Repronomics and Southern Multi-breed projects are providing direct comparisons in beef to develop multi-breed analysis, which is already happening in sheep.

- Multi-breed genetic evaluation is not new and is done within the Sheep Genetics evaluation now.
- To generate comparable breeding values, those genetics need to be compared somewhere in the same environment, or the same contemporary group. This is true for sire lines within a breed and it is also true for breeds in a multibreed comparison.
- The hold up in multi-breed beef evaluations has historically been the lack of direct comparisons between breeds. Project such as Repronomics and Southern Multi-breed are providing these head to head comparisons required to develop a multi-breed analysis.



The Evaluations

For Australian beef cattle and sheep producers, the BREEDPLAN and Sheep Genetics evaluation systems have been developed over more than 30 years.

- Importantly, the evaluations have been backed by the efforts of breeders to collect the data and make the selection decisions which have driven genetic progress, increasing livestock productivity and agriculture's contribution to the Australian economy.
- Today the scale of these systems is quite remarkable, and across the major sheep and cattle breeds, we have more than 18 million animals in the extended pedigree, with 1.2 million DNA tests, 64 million trait records on up to 90 traits in the largest evaluation for Merino sheep, in data pipelines updating breeding values and indexes on a fortnightly basis
- High rates of genetic gain in sheep have been sustained over a long period of time, but since genomic information was introduced to the evaluation in 2017, the rate of progress has increased up to 1.7 times more than the rate between 2000 and 2010.







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