

TALKING GENOMICS



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How Are Genomically Enhanced Breeding Values Calculated?



Genomic selection in seedstock animals most commonly involves the inclusion of genomic profiles in existing industry genetic evaluations, such as those conducted by BREEDPLAN and Sheep Genetics, to calculate genomically enhanced breeding values.

Genomically enhanced breeding values enable more accurate selection decisions, earlier in an animal's life, and for additional traits and animals, and ultimately, greater genetic improvement.

This edition of talking genomics discusses how genomic information is incorporated in the calculation of genomically enhanced breeding values within the BREEDPLAN and Sheep Genetics genetic evaluations.

Single Step Genetic Evaluation

The manner in which genomic information is included in industry genetic evaluations is often referred to as a 'single-step' genetic evaluation, reflecting that genomic profiles are analysed simultaneously with other sources of information (e.g. pedigree, phenotypes), placing appropriate emphasis on all available sources of information, to calculate a single, genomically enhanced breeding value.

A unique feature of single-step genetic evaluation is that breeding values can be calculated for both animals with and animals without genomic profiles. This differs to some earlier approaches that could only handle individuals with genomic profiles.

Likewise, in contrast to some earlier approaches, a 'genomic breeding value' is not calculated in a single step genetic evaluation, only the overall, genomically enhanced breeding value that is published.

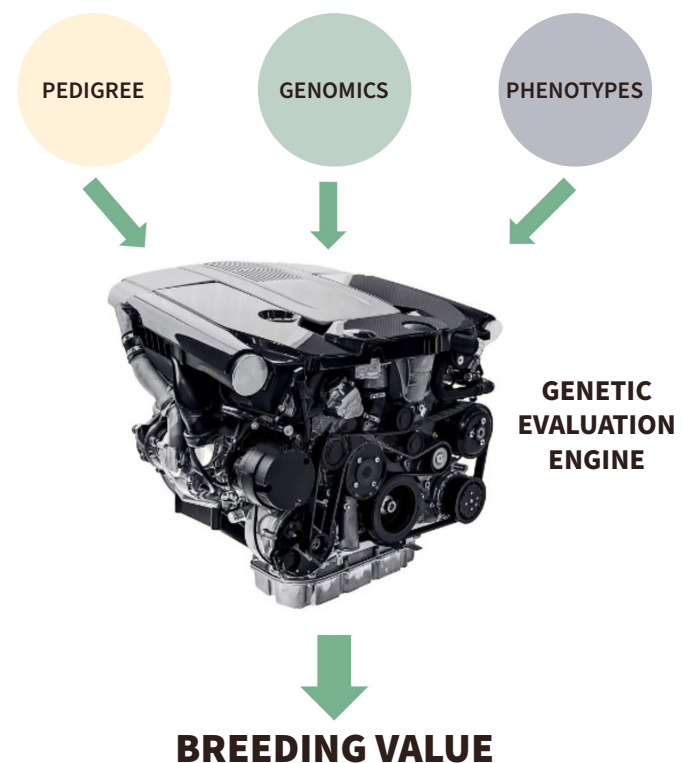


Figure 1. In industry genetic evaluations, such as those conducted by BREEDPLAN, Sheep Genetics and DataGene, genomic profiles are analysed simultaneously with other sources of information (e.g. pedigree, phenotypes) to calculate a single, genomically enhanced breeding value.

Analytical Approaches for Incorporating Genomic Information

There are a number of different analytical approaches for incorporating genomic information in the calculation of breeding values within a single-step genetic evaluation. The BREEDPLAN and Sheep Genetics Evaluation utilise a 'relationship' approach known as GTBLUP.

In the relationship approach, the incorporation of genomics is about 'animal relationships'.

In a simplistic form, a breeding value is calculated by a) estimating the relationship between an animal and the other animals in the genetic evaluation, and b) using the performance information that has been collected for the animal and the animals to which it is related to predict an animal's breeding value.

The more closely an animal with a phenotype is related to the target animal whose breeding value is of interest, the more influence that its performance has on the breeding value being calculated.

In traditional, pedigree based genetic evaluation, the relationships between animals are determined by pedigree alone. (Figure 2)

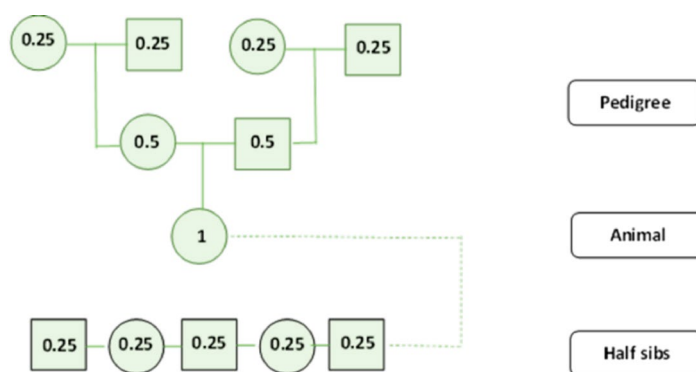


Figure 2. Example of relationships between animals in a traditional genetic evaluation. Based on pedigree relationships, the animal is estimated to have 50% of genes in common with each parent, 25% of genes in common with each grand-parent, and 25% of genes in common with each of its half siblings.

In a genetic evaluation that incorporates genomics using the 'relationship' approach, the relationships between animals are determined by combining pedigree and genomic information.

Utilisation of genomic relationships, being the genetic relatedness between two animals based on their genomic profiles, improves estimation of the relationship between animals in the genetic evaluation, and ultimately results in the calculation of more reliable breeding values.



Genomic relationships enable:

- the relationship between animals to be estimated when no, or incomplete pedigree information is available;
- a more precise estimate to be made of the genetic relationship between two animals who are related by pedigree. i.e. rather than assuming an animal has 25 percent of its genes in common with each grand parent (based on the law of averages), genomics assesses the random shuffle of chromosomes the animal has inherited to provide a more precise indication of the proportion of genes that an animal has in common with each relative;
- the relationship between animals unrelated by pedigree to be determined, and any performance information that is available on these animals to be used in the calculation of the animal's breeding value. e.g. pedigree may indicate that two animals are unrelated, but in reality, genomics indicates that they share a proportion of genes in common. This is particularly advantageous as it allows the performance information of animals in the genomic reference population to be utilised in the calculation of an animal's breeding value.

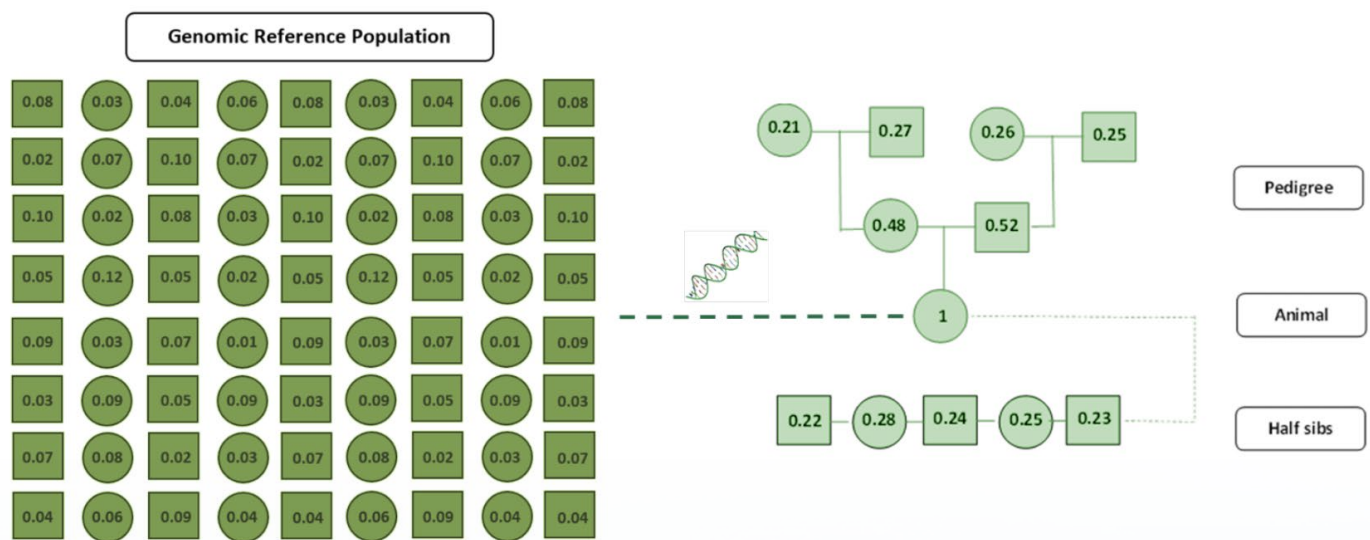


Figure 3. Example of relationships between animals in a single step genetic evaluation. Utilisation of genomic relationships enables a more precise estimate to be made of the relationship to each animal in the pedigree, while also enabling the relationship to be estimated to animals in the genomic reference population.



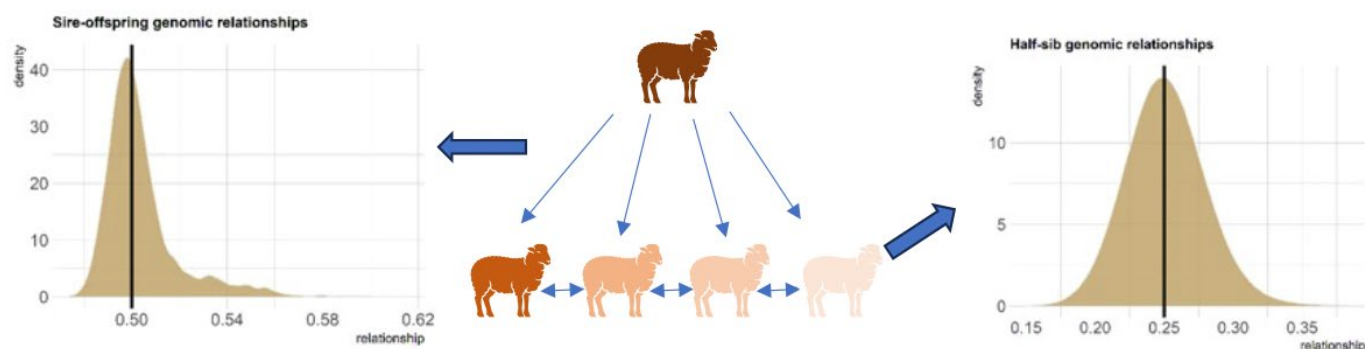
Genomic Relationships in Practice

The real-world examples below demonstrate how utilisation of genomic relationships improves the estimation of the relationship between animals in a single step genetic evaluation.

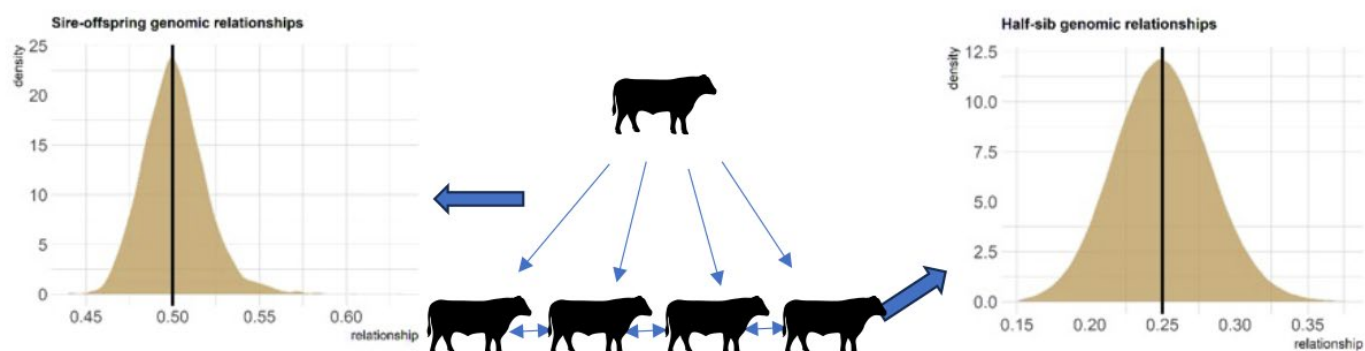
Based on pedigree information, the sires would be estimated to have a relationship of 0.5 with each of

their offspring. Similarly, the sire's offspring would each be expected to have a relationship of 0.25 with one another.

Genomic testing reveals that while, on average, these relationships are correct, the relationship between the sire and each individual offspring differs, and some offspring are more closely related to each other than they are with others.



Genomic relationships between 2,813 progeny of Merino sire, Anderson Poll, 160729 in the MerinoSELECT genetic evaluation conducted by Sheep Genetics. (Source: AGBU).



Genomic relationships between 2,259 progeny of Angus sire, Millah Murrah Paratrooper P15, in the TransTasman Angus Cattle Evaluation. (Source: AGBU).

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