

TALKING GENOMICS



with **Charlotte Broadbridge**, Technical Product Specialist, Neogen Australasia

An Unexpected Shift in Breeding Values? What Role does Genomics Play?

There are several different analytical approaches for incorporating genomic information in the calculation of breeding values within a single-step genetic evaluation. Two commonly adopted approaches include the 'relationship' approach, and the 'marker effects' approach.

While the analytical method behind both analytical approaches differs, research conducted by the scientific community would indicate that when the amount of information included in the genetic evaluation grows (i.e. the number of animals, genomic profiles and phenotypes), the breeding values that are predicted using either approach **are very similar**.

The Relationship Approach

In the relationship approach, such as the TBLUP model that is used by Sheep Genetics & BREEDPLAN, or the APY model that is used in the World Angus Evaluation, 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. In a genetic evaluation that incorporates genomics using the 'relationship' approach, the relationships between animals are determined by combining pedigree and genomic information, which improves the estimation of the relationship between animals.

The 'Marker Effects' Approach

While the 'relationship approach is about 'animal relationships', in a marker effects approach, such as the approach that is used by International Genetic Solutions (IGS), the incorporation of genomics is about the relationship between chromosome segments and the trait of interest.

In a marker effect approach, the influence, or size of effect that an individual Single Nucleotide

Polymorphism (SNP) has on a particular trait is estimated from the genotypes and phenotypes of animals.

For example, a particular SNP may be associated with decreasing birth weight by 10g, while another SNP may be associated with increasing birth weight by 15g. This is commonly referred to as the 'marker' or 'SNP' effect. The genotype of the animal is assessed to determine the number of 'doses' of the SNP effect the animal receives. An animal might have either 0, 1 or 2 copies of a particular SNP, which equates to the animal receiving either 0, 1 or 2 copies of the SNP effect. When the breeding value is calculated by simultaneously analysing pedigree, performance and genomic information, the 'dosage' of marker effects across all SNPs contributes to the breeding value.

If an animal has a higher-than average dosage of SNPs associated with increasing birth weight, the inclusion of genomic information will increase its birth weight breeding value. Conversely, if the animal has a higher-than-average dosage of SNPs that are associated with decreasing birth weight, its birth weight EBV will decrease with the inclusion of genomic information.

The inclusion of genomic information within breeding values is important to ensure you are getting the most accurate breeding values to base your decisions from.

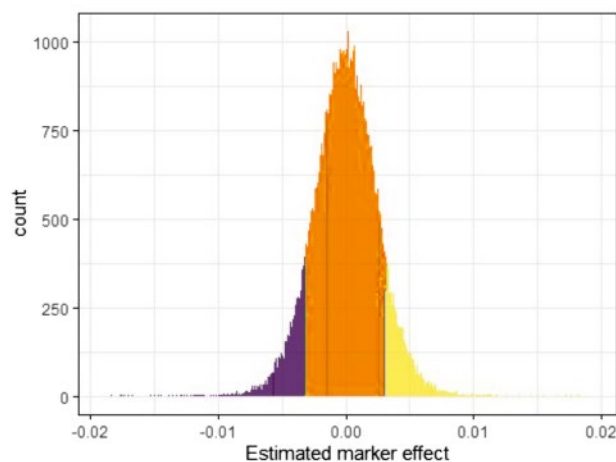


Figure 1 : A plot illustrating the marker effect of different SNPs on birth weight in an Australian cattle breed (Source:AGBU)

For more information please contact your local Neogen Genomics Specialist.

TALKING
GENOMICS

