

GENOMIC SELECTION:

A new tool for **genetic improvement** of SA livestock



Over the past two decades major discoveries and technological developments in the field of molecular genetics have opened up new opportunities for genetic improvement in farm animals that were previously beyond the reach of animal breeders. The bovine genome has been mapped and sequenced and several DNA-marker types have been discovered. The discovery of single nucleotide polymorphism (SNP) markers and the concurrent development of appropriate high through-put technology have given rise to commercial SNP chips available for generating useful genomic information.

SNP markers and genomic selection

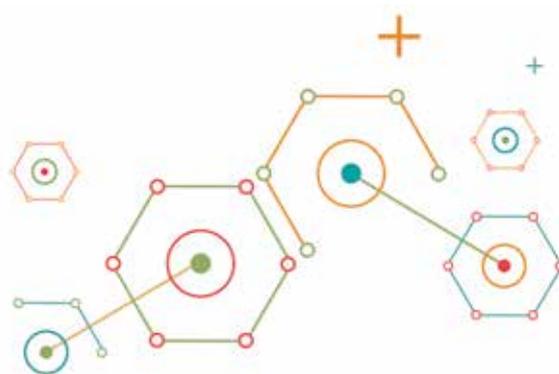
The DNA markers used for generating genomic information for genomic selection are single nucleotide polymorphisms (SNPs) commonly referred to as “SNIPS”. Each of these markers has two alleles and they occur very frequently across the genome. The *Bos Taurus* genome has an estimated total of nearly 4 million SNPs. It is estimated that a trait of economic importance (i.e. weaning weight, carcass weight, feed conversion ratio, etc.) is governed by between 100 and 300 genes. Each of these genes represents only a small aspect of the phenotype that is expressed.

In the past, individual genes and markers associated with genes were identified and only a very small portion of the phenotypic variation could therefore be explained. By using a very dense SNP panel for genotyping animals, it is assumed that each individual SNP will be associated with at least one gene contributing to the trait of interest. When all the SNP effects are added, they should explain the total phenotypic variance that is expressed.

If a number of animals of a specific breed have been genotyped, and their phenotypic records are available, it is possible to draw a correlation between a SNP combination and the level of performance associated with it. This correlation is commonly referred to as the “prediction equation” or “SNP key”. Genomic selection is therefore based upon the basic principle of using the information of many DNA markers, coupled with accurate and

complete phenotypic records. In practical breeding, the genotypic information (direct genomic value) will be included in the estimated breeding value (EBV) of an animal.

In this way, genomic data will be included as an additional source of information, together with pedigree and performance records used in routine quantitative analyses. This process is referred to as blending and will result in providing a genomic estimated breeding value (GEBV) for each individual.



Prerequisites for implementation

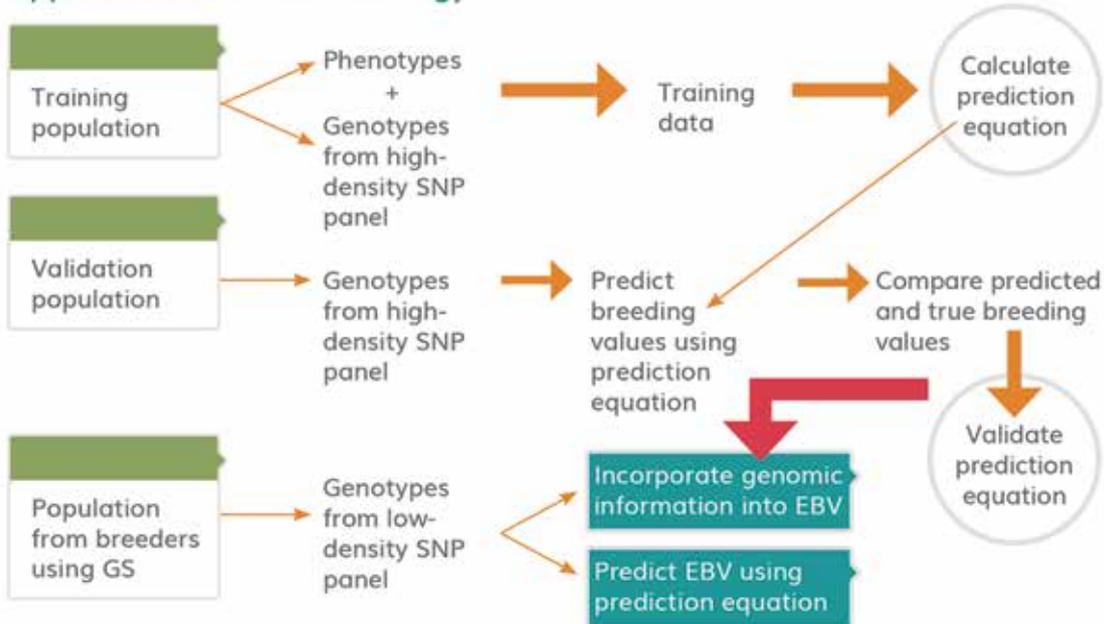
The implementation of genomic selection is not a simple process and each phase requires careful planning to ensure that the end result will be accurate, useful and cost effective.

The first step is the selection of the bulls to form the reference or training population. These bulls should represent the specific breed and include bulls with low, medium and high breeding values with accuracies above 60%. It is important for the traits recorded on these bulls to be the traits that breeders would like to include in selection programmes and that form part of the breeding objectives for the breed. A biological sample of these animals should be available and this could be a hair, blood, semen or tissue sample for extracting DNA.

Once the DNA is available, the samples will be analysed using an appropriate high-density commercial chip. In this step the SNP effects based on high-density chips and their correlation with the animals' known performance (EBV values) are established, in order to calculate the prediction equation.

There is no doubt that genomic selection has significant advantages for improving farm animal

Application of SNP technology



genetics. Dairy cattle have thus far led the way and have experienced some of the advantages of having an added source of information. GEBVs can be obtained in a relatively short period after birth compared to a six to seven-year period of progeny testing before a progeny-based EBV becomes available. GEBVs have distinct advantages for dairy cattle with regard to reducing costs on progeny testing and decreasing the generation interval. Genomic technology has been well received by dairy cattle breeders in the US and Canada and indications are that genomic evaluations will replace traditional evaluations in these countries.

The use of genomic selection in selection programmes holds the most potential for sex-limited traits, traits that are expressed late in life and traits with low heritability.

In South Africa we are fortunate to have a long history of animal recording for a large number of cattle breeds.

This data have routinely been used for EBV calculations and are widely used by South African stud breeders. The current challenge is to ensure the banking of biological samples of animals with the desired traits and phenotypes, in order to obtain both molecular and phenotypic records from individuals. The use of genomic selection (GS) globally in both the dairy and beef industries has become inevitable and smaller countries with fewer resources, like South Africa, will have to collaborate and carefully plan genetic programmes to remain part of the international arena.

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