

GENOMIC SELECTION: an additional tool for *enhancing genetic progress*

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INTRODUCTION

Since the mapping of the cattle genome was completed in 2009, followed by the discovery of Single Nucleotide Polymorphisms, better known as SNP markers, livestock breeders worldwide have been adding “genomics” to their daily conversations. Genomics as a research field use a whole genome approach and requires an interdisciplinary team of molecular geneticists, quantitative animal breeders and bio-informaticians to provide a better understanding of the function of genes, proteins, and their functions. As livestock breeders, the aim is to use the genomic information for an improved understanding of the phenotypes we include in our selection programs.

Genomic information has the potential to improve the accuracy of pedigrees, effective selection against genetic defects and the application of genomic selection. Genomic selection is an additional tool to assist animal breeders in making more accurate decisions when selecting animals as parents for the next generation. The majority of breeders are using tools such as visual assessment, performance recording, comparisons within contemporary groups, selection indices and/or BLUP breeding values. It is important to note that genomic information is not a replacement for routine and accurate phenotyping or evaluation of functional efficiency.

In this article, I aim to provide some background on the potential of genomic selection for Nguni cattle breeders and highlight the different applications of genomic information.

GENERATION OF GENOMIC INFORMATION

Genomic information originates from the DNA of the animal. To generate a genotype or genotypic profile for an animal, a biological sample must be submitted to a laboratory of which there are several worldwide and in South Africa, where high throughput technology is used for genotyping. Biological samples may include semen, blood, ear tissue, or hair, of which hair is the most convenient to collect by the breeder. Hair collection is non-invasive, can be stored in an envelope, and is easy to send to the service provider.

The discovery of SNP markers resulted in the development of commercial SNP chips containing the genomic information needed to genotype cattle. Different commercial SNP chips are available and these arrays are continuously updated as more genes are discovered associated with, for example, a genetic defect, or genes with positive outcomes, such as for identifying homozygous polled cattle.

GENOMIC SELECTION

Genomic selection in simple terms is based on adding

genomic information (originating from genotypes of the animals) to the phenotypes (performance traits recorded) in the genetic evaluations performed for the estimation of breeding values. The genotypic information is generated using a SNP array containing thousands of SNP markers that are used to estimate the direct genomic value (DGV) for the animal. The DGV can then be incorporated into the routine genetic evaluations to provide a genomic breeding value (GEBV) for the animal.

Breeders could argue that we already have several tools for selection and among these estimated breeding values (EBV) are fairly accurate; so why spend more money on a genomic EBV? The EBV estimated with BLUP only considers the (phenotypic) performance of the animal and the relatives, in comparison with their respective contemporaries. Within a breed, all performance and relationship data will be accounted for and with more records available for a trait, the accuracy of the prediction (EBV's) will increase. Adding genomic information with the available performance recording will account for the underlying genetic variation in the trait and the genetic component inherited from the parents and the grandparents.

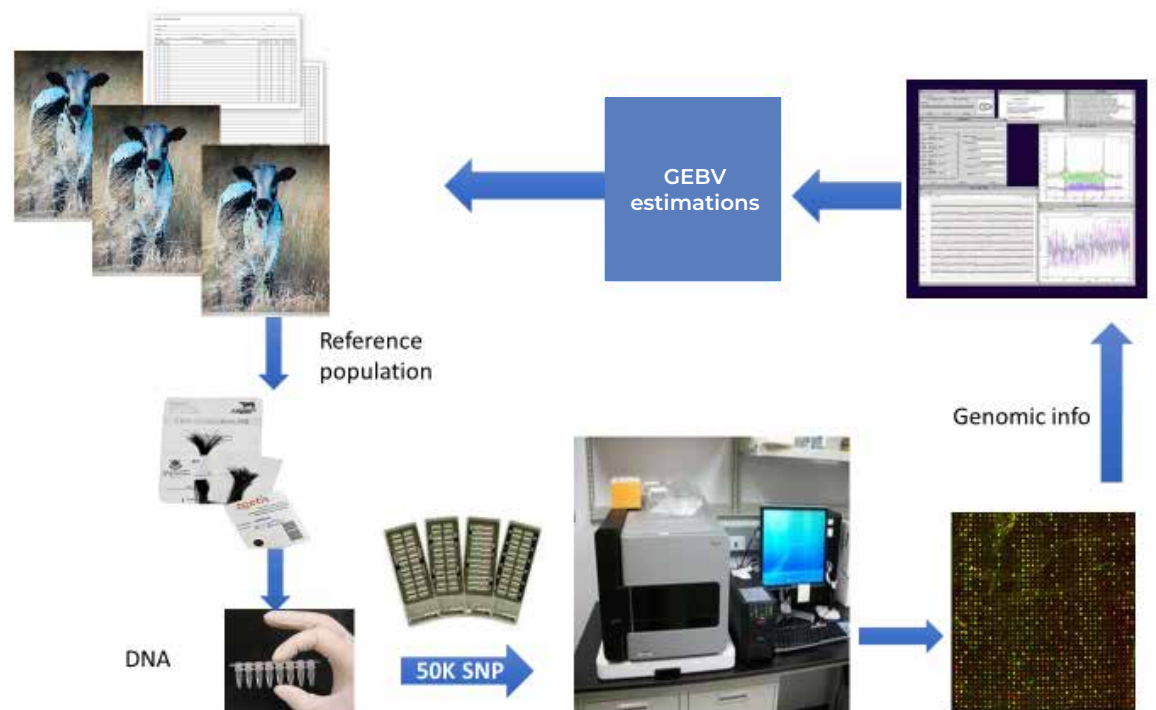
The primary advantage of genomic selection is for selection of the hard-to-measure traits, such as fertility traits, growth efficiency, disease tolerance and sex-limited traits. Genomic information is especially important for the traits we can only measure late in life, such as cow productivity and longevity. The genomic enhanced breeding value will provide the breeder with the possibility to select an animal at a younger age before the trait has been measured.

PREREQUISITES FOR GENOMIC SELECTION

Genomic selection involves a process, similar to animal recording systems, where information must be gathered for a sensible analysis. The most important prerequisite for genomic selection is the availability of a reference population for the breed. It is important to have animals (males and females) in the reference population genotyped with a medium to high-density array such as a 50K SNP. These animals will represent the breed for all the desired traits, having a phenotype and a genotype. In Figure 1 below the process is illustrated.

There is no magic number for a reference population; as a guide, one thousand animals with genotypes and phenotypes will be a good start, although from research we know that the “more the better.” The information of these animals will enable the geneticists performing the genetic evaluation to estimate a correlation between a SNP combination and the level of performance (trait). This correlation is commonly referred to as the “prediction equation.” The genotypic information (Direct Genomic Value) will be included in the Estimated Breeding Value (EBV) of an animal and a genomic estimated breeding

Figure 1: Summary of the activities for genomic selection



value (GEBV) for each individual is estimated. Genomic information is included as an additional source of information together with pedigree and performance records used in routine quantitative analyses.

During Phase I, (2015 to 2018) of the Beef Genomics Programme (BGP), funded by the Technology Innovation Agency, genotypes were generated for all the participating breeds, which served as a basis for building references, also called training populations. This phase of the program highlighted the importance of sufficient phenotypes for the traits of interest and a number of breeds moved forward with routine genotyping and implementing of Estimated breeding values. A second phase of BGP has been launched for South African beef cattle breeders to engage in the generation of genotypes for their breeds.

ADDED BENEFITS OF ROUTINE GENOMIC INFORMATION

Although genomic selection is a useful tool for enhancing genetic progress, we should not forget the added benefits of having genotypic information for a breed. For the first two decades after the discovery of DNA-markers, before we had access to whole genome sequences, livestock farmers relied on microsatellite markers for a DNA-based parentage testing. Microsatellite panels for parentage are affordable and still used by South African livestock breeders. The genomic information generated through routine genotyping has the potential to replace microsatellite markers, as they are more accurate. Whole herd genotyping remains expensive; SNP parentage panels have therefore been developed and approved by the International Society for Animal Genetics (ISAG), which can be applied for parentage testing. Once a breed participates in routine genotyping, parentage can also be solved using the same genotypes.

The use of DNA markers for the identification of genetic defects has been one of the most successful applications in livestock breeding. In 2008, researchers from the University of Illinois and the University of Nebraska respectively, worked on the devastating defect now known as curly calf syndrome. Due to the availability

of DNA-markers, they could trace the recessive gene and identify the carrier bulls. Since 2008, numerous genetic defects have been discovered and added to the commercial SNP arrays, so breeds can decide if they want to test a suspect animal for a variety of genetic defects.

In addition, genomic information has assisted in the identification of major genes such as myostatin and breeders can test animals for unfavourable variants of the gene. In the case of polled and horned animals, breeders can test to confirm if the bull or cow is homozygous polled, or a carrier of the horned gene.

For the majority of breeders, genetic variation may be of limited interest, but where there are recognised ecotypes within a breed, genomic information is used to study the population structure and genetic differentiation. Genomic information can be used to give insight into the ancestry and genetic relationships among these ecotypes and between different breeds. It is a useful tool for conserving unique indigenous genetic resources.

CONCLUSION

Genomic information as an added tool holds the potential for enhancing genetic progress. 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. Genomic selection, in combination with SNP-based parentage testing and other diagnostic tests, are effective in a number of countries worldwide. Genomic information will benefit goal-driven selection where breeders are under pressure to consider the reduction in methane production, animal welfare and consumer traits – all of these are hard to measure. Genomic selection requires consideration and planning to ensure that the breeding goals of the breed are adhered to and that the breed reaps the long-term benefits of this important technology!