

Genomic selection: Establishing a reference population for Bonsmara cattle

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Everyone in livestock breeding knows that prediction accuracy took a big step forward with the introduction of best linear unbiased prediction (BLUP) breeding values. BLUP methodology combined the following very important sources of information into a single figure:

- Pedigree information.
- Performance differences among animals.
- What part of the differences among the performance of animals can be attributed to the part that can be transferred to their progeny.
- What the effect of the genetic differences among animals for one trait will be on other traits of economic importance.

The major strength of BLUP breeding values is that it reflects a complete system of genetic merit prediction where all possible information of all animals are taken into account while, at the same time, solutions for environmental effects are also considered. It is therefore a combination of a pedigree selection index, performance testing system and a progeny test, all in one.

Molecular genetic information

BLUP breeding value predictions primarily rely on quantitative aspects of genetics based on average assumptions, as one will expect in family selection. Prediction accuracy is further enhanced by each individual family member's performance as a deviation from the average of their contemporaries.

By including genomic information, if based on the correct assumptions, the specific sample of genetic material an animal has "inherited" from its parents will be known at a younger age (even before an own measurement or progeny is recorded).

The objective of including genomic

information is therefore to identify what unique genetic merit (within the family) each animal received. This is especially useful when:

- The measurement of a trait was not possible.
- The trait is limited to one of the sexes.
- A trait can only be measured very late in life.
- Traits cannot be recorded on the live animal.
- A decision is made on picking an animal early in life that will have a big impact on a breed.

Combining two sources of information

Knowledge about the molecular genetic difference among animals is of no use until the exact link between what is known of each animal's chromosome and its genetic merit for the traits of importance, is not yet established. This is done by comparing the molecular genetic values of high impact animals (with many measured progeny) with their breeding values (genetic merit) as determined with mixed model methodology (BLUP). This relationship is the key to genomic selection.

Genomic selection for the Bonsmara

SA Stud Book, Bonsmara SA and the University of Pretoria, in cooperation with other national and international partners, are currently establishing a comprehensive reference population and a trustworthy system for the Bonsmara cattle breed that will lead to the incorporation of genomic information in breeding value predictions.

These steps entail:

- Identification and collection of biological material (hair, blood or semen) of high impact animals (mainly bulls) with BLUP estimated breeding values (EBVs) predicted with high accuracy for all the economically important

traits. This process is well underway as all these animals have been identified, many samples collected and DNA extractions have been carried out.

- Obtaining genome information from these high impact animals and testing the assumed genetic variability of the breed as evaluated from the specific single nucleotide polymorphisms (SNPs) as used by the specific SNP chip. Genomic information from the first 150 high impact Bonsmara bulls, on the 80k GGP HD chip (based on the Illumina 50K chip enhanced with additional SNPs), have been obtained. Currently the first of a series of genome-wide association studies (GWAS) have already started to establish the genetic variability of this first sample of bulls as detected by the 80k GGP HD chip, trying to establish associations with the genetic merit for the economically important traits and investigating the sample size needed to establish a system where genome information will be added to genetic merit (breeding value) predictions.
- Calculating the SNP key (per trait), based on the genetic variability from the genome information, the relationship with the BLUP and genome information from the high impact animals (the so-called "key") and the reliability of genome information as an early predictor of "true" genetic merit. This last step will be conducted using a (fairly random) group of high impact animals where the established "key" is being tested for prediction accuracy.
- The final step is to include this information in the regular breeding value predictions for Bonsmara cattle using less dense (and cheaper) SNP chips, such as the GGP LD chip (also based on Illumina technology and chips). ⁵⁸