GENOMIC SELECTION AND HOW IT FITS INTO BLUP BREEDING VALUES

(Participation in the BGP: an opportunity looms for Nguni breeders in the future.)

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WHY GENOMIC SELECTION?

Genomic Selection is an 'extra' tool added to the arsenal of animal breeders to assist in making the correct decisions when selecting animals as parents for the next generation. Tools used over time, and that are still being used to a bigger or lesser degree, are: visual assessment, recording and comparisons within contemporary (treatment) groups, indices (or sometimes called 'ratios'), progeny comparisons (in one or other form) and BLUP breeding values.

BLUP breeding values started a new revolution for the accurate prediction of genetic merit in farm animals. The methodology combined some very important sources of information into a single figure.

These sources are:

• *Pedigree information.*

Based on the fact that related animals share common genes, pedigree information serves as the 'perfect' link among all these related animals and enables BLUP to make a comparison over time (animals born and recorded in

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different birth years) and space (animals born and recorded on different localities, e.g. farms or contemporary groups).

- *Performance differences among animals.*

The most important aspect of BLUP breeding values is taking the differences in performance among animals that were subjected to exactly the same (environ-mental) conditions into account. The principle is that any differences would then mainly be due to genetic differences among them. The key equation is: P = G + E (the recorded value for a trait equals the genetic merit of each animal plus the effect of the environment on the expression of the particular trait).

- *The part of the differences among the performance of animals that can be transferred to their progeny.*

In genetic terms, this is defined as the 'heritability' of the particular trait.

- *The effect of the genetic differences among animals for one trait on other traits of economic importance.*

In genetic terms, this is defined as the 'genetic correlation' among traits.

The question can therefore rightfully be asked: 'Why then also add molecular genetic information to the already very accurate BLUP breeding values?'

BLUP is therefore a complete system where all possible information of an animal is taken into consideration. It is a combination of a pedigree selection index, performance test system and a progeny test, all in one.

This can mainly be answered in view of the fact that BLUP primarily relies on the, so called, quantitative aspects of genetics. In short, BLUP uses 'average assumptions' based on what one will expect in family selection. Based on the (phenotypic) performance of an animal and its relatives, in comparison with their respective contemporaries, the probability of having a specific genetic merit is calculated for each animal. Obviously, once an animal is measured for the specific trait (within a contemporary group) and especially if many of its progeny are also measured (as an indication of the breeding ability as reflected in the progeny's performance relative to the progeny of other parents), the accuracy of prediction increases.

The inclusion of genomic information, if based on the correct assumptions, is a move closer to a step where the specific sample of genetic material (in effect a part of the chromosome) an animal has 'inherited' from its parents will be known at a younger age (even before an own measurement or progeny are recorded).

The real value for using Genomic Selection is therefore to identify what unique genetic merit within the family a specific animal (family member) received without having to first test its own and its progeny's performance.

These 'early predictions' are especially useful where:

- *The measurement of a trait was not possible (for any reason, such as non-testing in a growth test or not subjected to certain environmental constraints like a disease or parasite challenge).*
- *The measurements of the trait are limited to one of the sexes (examples are female fertility, mothering ability or semen quality).*
- *A trait can only be measured very late in life (for example, ewe or cow productivity, longevity, retention of progeny and productive herd life).*
- *Traits cannot be recorded on live animals (e.g. carcass or meat quality traits).*
- *A decisive decision is to be made on picking (selecting) an animal early in life that will have a big impact on a breed (e.g. decision on a male to be included in an artificial insemination program, a female as ovum donor or a bull/ram mother).*

Two main sources of information combined

Although the molecular genetic difference among animals are established with a genome test, the exact link between that what is known on each animal's chromosome and its true genetic merit for the traits of importance is not yet established. Knowing the sequence on the chromosomes is only one (important) source of information. The other extremely important source is the relationship between the molecular genetic values of the animals and the value of these animals as breeding animals (breeding values).

This relationship is best established by comparing the molecular genetic values of animals that already have many measured progeny, in other words, animals with very reliable BLUP breeding values.

This relationship holds the key for future use of Genomic Selection. In other words, animals with many measured progeny are used to find the key between the sequence on their chromosomes and their breeding values, as predicted by using mixed models (BLUP). These males and older females are called the reference population. Usually at least one thousand animals per breed is needed in the reference population.

Once this relationship has been established, the calculated relationship needs to be validated for accuracy of prediction. This is usually done by testing the predicted genomic values against a new set of animals (the validation population), also with very accurate BLUP breeding values.

The following should be kept in mind:

- The genomic information is basically useless for selection purposes if the relationship with accurate BLUP breeding values is not yet established. In that regard recording and continued measurements of economically important traits remains essential.

- The genome information is no indication of specific genes of major influence as it is not a real map of genes. It is purely a sequence of, so called, single nucleotide polymorphisms (SNPs). Normally these 'road markers' are listed at regular intervals on the chromosome and is not a complete set of all the information on the nucleotides.

- There are different 'SNP Chips' available on the market that varies in 'denseness' (more or less of the total genome described), usefulness for information exchange (the exact location on the chromosomes described and intervals between these points) and usefulness in combining with other more (or less) dense chips (making use of the 'partial' information from cheaper, less dense chips to 'predict' [impute] the values on the denser [and more expensive] chips).

Combining the different sources and the ultimate use of Genomic Selection is illustrated in Figure 1.
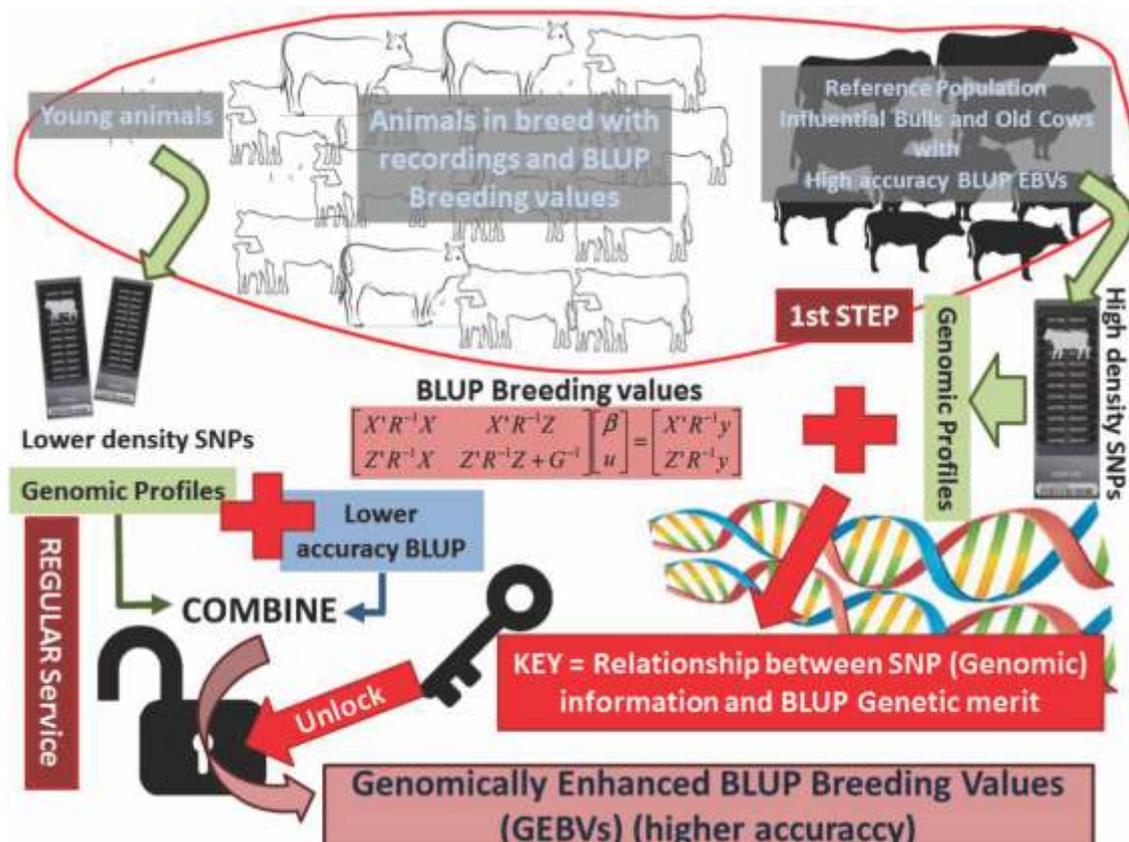

Figure 1. Illustration of how different sources of information are combined for GEBVs

- The top left corner represents a whole population (breed), already dead (parents and other animals in the lineage) and current animals, with and without recordings for the traits of importance and BLUP breeding values predicted for each animal. The accuracy of the BLUP breeding values vary from very accurate (for animals with many measured progeny) to fairly inaccurate (animals without own recordings, no progeny and from families with very few recordings). Among the population is also young animals that were not yet recorded and therefore their BLUP breeding values are based on parent average predictions.

- Among the population, as mentioned, are also animals with high accuracy BLUP breeding values. The figure illustrates the actions taken by genotyping a portion of this group with a fairly dense SNP (150K) chip to build up a reference population. This is illustrated at the top right hand corner of Figure 1. Two very important sources of information are therefore known for this particular group of animals, namely their genetic merit (based on very accuracy BLUP breeding values) and information obtained from genotyping a biological sample (blood, semen or other body tissue) from each animal.

- By combining the information for these animals a relationship ("correlation") is calculated between the information from the genotype techniques and the genetic merit. This is, first of all, verified with a different portion of the population and is then ready to be used in unlocking information to assist in predicting genetic merit for young animals in future.

- The prediction of genetic merit for young animals is illustrated on the bottom left hand corner of Figure 1. Biological material from young, potential breeding animals from the population (breed) are obtained and the genotypic information measured against the now known relationship with their breeding value prediction. This genotyping is usually done on a cheaper, less dense SNP Chip as a service to breeders or other industry role players.

- The last, very important step is to combine the newly predicted genomic values (Direct Genomic Values or DGVs) with the parent average BLUP breeding values to predict the genetic merit (breeding value) for these animals. This prediction is called a Genomically Enhanced Estimated Breeding Value or GEBV.

Future use of genomic information.

Once the initial steps have been completed, genomic information can be incorporated in future genetic (BLUP) evaluations for a breed with an established reference population. In practice, this means that a service can commence where breeders choose to subject young animals to a genomic test to enhance the accuracy of prediction of the BLUP breeding values. Of special value, in the case of Nguni cattle will be maternal ability (milk) and female fertility (daughter fertility) values for young bull calves.

The use of genomic information in breeding value predictions has become commonplace in dairy cattle breeding and a new dawn is about to break for beef cattle. The proviso is still that the frequency and accuracy of production recording will dictate the success of implementation of this exciting technological tool. ■

"Somewhere,
SOMETHING INCREDIBLE
IS WAITING TO BE KNOWN"

Carl Sagan