

GENOMICS

WHAT IS ON OFFER FOR NGUNI BREEDERS AND THEIR CLIENTS?

It is (well) known that the **variation or differences** among the recorded performance of individual animals are caused by two distinct influences, namely their inherent genetic differences and their individual responses to environmental effects.

Good managers of livestock know and manage the physical and production environments to such an extent to ensure a profitable and sustainable livestock business. Although the physical environment varies from year to year, good management practices include fodder flow when animals' needs are at their peak, optimal reproduction and outputs with minimum inputs, including health and labour, and producing a market-needed product.

This is all good and well for successful livestock producers. What if the product of such a producer is not the animal sold but the inherent (genetic) ability of an animal to produce offspring that must excel in a different (or even similar) set of environmental

conditions? Even if the animal is not sold, but considered as a parent of offspring that must outperform the progeny of a different potential parent under the owner's own production conditions, certain criteria need to be adhered to.

Many articles, papers, info packs, talks at information days, workshops and personal advisors have enlighten breeders and other livestock producers on ways to select the right animal suited for optimal production. Even when concepts are not well understood or confused, opinions are sometimes formed and expressed or even spread as gospel, irrespective of the consequences.

Many a time, the use of a tool such as BLUP breeding values are confused with sound breeding criteria to achieve breeding objectives. BLUP is a means to a goal, not a goal in itself.

A breeder will take a step towards higher precision in making an informed

selection decision by using additional information, such as the inclusion of the results of a DNA laboratory test that gives a glimpse into the genome of individual animals, and thereby enhancing the prediction accuracy of the genetic merit of an animal worthy to be a selection candidate. **Adding genomic information to the way the genetic merit is predicted is simply a "step-up" on the current BLUP breeding values.**

QUANTIFYING TRAITS, ALWAYS THE FIRST STEP

The best way to rank animals according to their performance for a specific property or trait is to first properly define or quantify such a property or trait. The more precise the definition and the measurement, the better the chance is of repeating the feat of ranking animals accordingly on successive occasions. A vague description will cause reranking, very much like a sport match where the

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PERSPECTIVE

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referee has no idea of the rules of the game, but nonetheless awards penalties or advantages to the teams or players, at will.

Irrespective of the means of ranking production animals according to their desirability as breeding animals, well defined traits or descriptions are needed. Descriptions such as “a thick bull”, “typical”, “quality” or “muscular” might be appropriate in visualising an animal in the mind of the beholder but cannot be used for rating such an animal in concrete breeding terms.

The obvious next step is to record the defined traits as accurately as possible. No person can assess the weight of an animal as well as a scale or the shoulder (or hip) height as a yardstick.

Even with the best prediction for genetic merit, selection without a goal will lead to a wilderness.

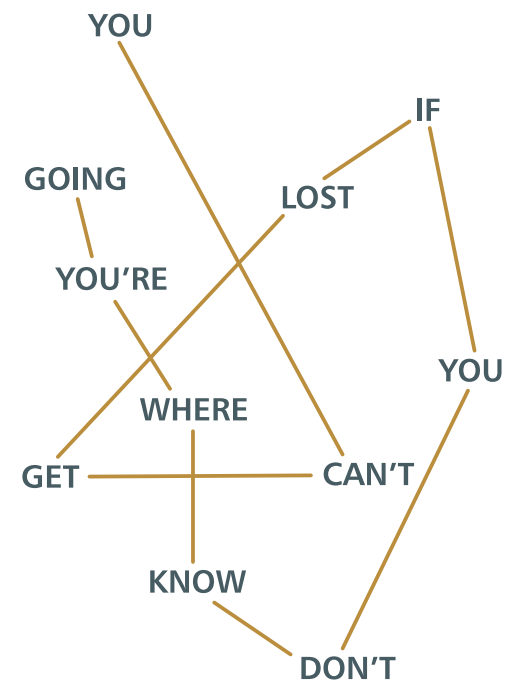
The saying goes something like this: *“if you aim at nothing, you will hit it all the time”*. Having the best and latest means of predicting an animal's genetic merit for a series of traits is of little value if they do not form part of selection criteria and, more importantly, an overall goal. Such a goal will ensure longer term and sustainable profit.

Discussing goals and how they need to be constructed do not form part of this article. The importance of such goals is however paramount to the selection of livestock, irrespective of the accuracy of predicting the genetic merit for traits used in the construction of a breeding goal.

PREDICTION OF GENETIC MERIT

The true genetic merit of an animal for any trait is never truly known. Genetic merit is also, in effect, a description of the inherent genotype of an animal relative to the genotypes of others he or she is compared with. This is conceptually extremely important as it is impossible to compare the genetic merit of animals among unconnected or “unrelated” populations or, especially for populations where such an animal is not likely to bear progeny.

As mentioned at the onset, performance differences among animals are products of genetic differences as well as environmental influences on the expression of such traits. As environmental effects cannot be transferred to the next generation, the challenge is to “isolate” the genetic merit making use of a best possible method. The brilliance underpinning the calculation of a BLUP breeding value is just that.



The measurement (performance, recording, etc.) of each animal is precisely described by means of a linear equation taking all possible relationships with all other animals into consideration as well as its measurement's deviation from that of its contemporaries that were subjected to exactly the same environmental and management conditions. This deviation in performance of measurement is then also adjusted for the fact that this deviation is caused by genetic as well as environmental differences. Put differently, the heritability of the particular trait is also taken into account. As each and every animal's deviation from its group mates are precisely described, and all the mentioned factors taken into account, the biased or unjust favouring due to preferential matings are also accounted for.

So, the Best method is employed through the use of precise Linear equations that lead to Unbiased Predictions of each animal's true genetic merit.

True versus assumed relationships among animals; influencing the accuracy of genetic merit predictions.

If BLUP is the “best” prediction of the genetic merit of animals for traits of interest, why then add an extra source of information? Since BLUP breeding values already rely on pedigree information (being the best indicator of the partial “sharing” of the same genotypes, running in families), performance (as a deviation from the mean of the contemporary group mean that the animal had to perform in), the performance of all other relatives (as deviations from their contemporary group means) and the portion of such performance deviations due to genetic differences (the heritability) one could hardly imagine a need for an extra source of information to increase the accuracy of genetic merit prediction.

Two of the sources of information used in BLUP breeding values can be improved on. BLUP rely on the relationships among animals as constructed by a, so called, average relationship matrix or grid where each and every animal's relationship with each other animal in the population (breed) is recorded. If judged on the whole population (breed), there is nothing wrong with such an assumption. In comparing individual animals, it might be a different story. It is known that looking down the line in a lineage, **each animal receives half of the (nuclear) genetic material from each parent.** This is important, especially in terms of the parts of the genome carrying genes influencing the genetic merit for the economically important traits. **These “additive genes” come in pairs and randomly end up in sperm and egg cells. So, although each of the progeny ends up with half that of the parents, it is unknown if the good or bad additive genes ended up in each of the progeny.** The “additive relationship” among collateral sibs, such as full or half brothers and sisters, cousins, etc. is also averaged out. For example, **half sibs will, on average be 25% related, but some will be more and others less related, based on the randomness in the formation of sex cells.** BLUP breeding value predictions assume relatedness, based on the average probability.



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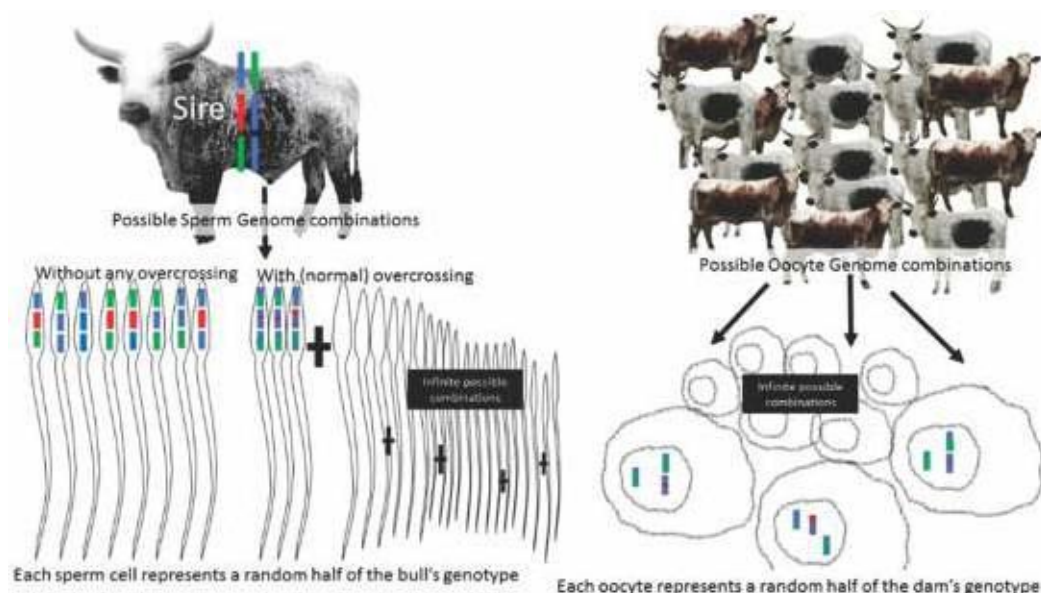


Figure 1: Illustration of the randomness when sperm and oocytes are produced

Furthermore, once an animal is recorded for a trait (and therefore compared with the performance of its contemporaries), a fairly accurate assessment can be made of its breeding value, especially where the additive genes play a bigger role in expressing the measurement (a higher heritability).

More is therefore known about what (type of) genes ended up in the fertilised egg cell (zygote) that resulted in the animal being what it is. There are, however instances where it is not possible to record an economically important trait on an animal. With BLUP breeding values, it has to be assumed that each of the progeny of a sire-dam combination inherited a “combined parent average” value. This prediction will remain through an animal's life until such time when it is measured for the particular trait or produced recorded progeny. In these cases, there is a real need to increase the accuracy of predicting the genetic merit beyond what BLUP has to offer.

Figure 1 depicts the theoretical possibilities of the genomic information that can end up in a single sperm or

oocyte from a bull and cow. As the principle is being illustrated, it was assumed in this example that the complete genetic code (genome) for cattle are on only two sets of three chromosomes ($2N=6$). We know that the real number for cattle is 30 ($2N=60$). In this example, the possible different random sperm genetic (gene) combinations will be eight (2^3) in the absence of any crossing over during cell multiplication in the formation of the sperm. With 30 chromosome pairs, as is the case in cattle the combination jumps up to (2^{30}) or 1 073 741 824 (1.07×10^9).

It is however known that crossing over takes place, where parts of chromosomes are exchanged during the process of spermatogenesis (and when oocytes are formed). In the case where, on average four such exchanges take place per chromosome; the possible combination of genes in the sperm (from one ejaculate) shoots up to 1.33×10^{36} . In all cases, each of the sperm will still carry exactly 50% of the chromosome parts (haplotype) of the sire. The same is true for the randomly formed oocyte from the dam.

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A randomly formed sperm cell will fertilise a randomly formed oocyte. This means that, although each of these cells represents an exact half from the parents, the likelihood of an exact repeat of the genes it carries is basically none existent. Two full sibs will therefore not be exactly 50% related (given the parents are not related at all), but very close to 50%. Given, furthermore that these two animals are from the same breed where the average relationships among animals in such a breed are already higher than their relationships with animals from another breed, the likelihood will be that the relationship among full sibs will, on average, exceed 50%.

GENOMIC TESTING, THE SOLUTION TO DETERMINING THE TRUE RELATIONSHIPS FOR BLUP

Initial thinking to apply Genomic Selection in livestock breeding focussed on determining the relationship between BLUP breeding values and parts of the genome (carrying the additive genes).

This led to the establishment of, so called “reference populations” consisting of large numbers of animals with measurements, or even better with BLUP breeding values predicted with high accuracy to find the “key equation”.

The latest techniques focus on establishing the true relationships among animals in a breed (even over breeds) and replacing the assumed “average” relationships, as mentioned earlier, with it. This is where these true relationships among animals can also become very interesting.

Animals within a breed are obviously more related to each other compared to their relationships with animals of other breeds. In other words, it is now possible to determine the genetic “distance” or “closeness” of breeds. Knowing the real relationships that young animals have with other animals in the breed, with a genetic merit determined with a high degree of certainty, assist in enhancing the accuracy of genetic merit prediction for these younger animals. In other words, how related is this young animal to others in the breed with “good” or “bad” breeding values for the trait interested in.

APPLICATION OF GENOMIC INFORMATION IN BLUP BREEDING VALUE PREDICTION SPEEDS UP GENETIC CHANGE THROUGH SELECTION.

By including genomic information in genetic merit prediction, genetic change will be accelerated, especially for certain traits. These traits are the ones that must rely on using average relationship information in BLUP breeding value prediction. **The most important ones include sex limited traits, such as female fertility (age at first calving and calving interval) and maternal ability (milk). At the age where a bull is usually sold or considered as a selection candidate, none of his female progeny were recorded for these traits.** Irrespective of the performance or even the BLUP breeding values of its parents, the randomness associated with sexual reproduction, as discussed earlier can be associated with the “luck of the draw”. Did he get the bad or good parts of the chromosomes from his parents at the fertilisation combination of the sperm and oocyte?

“At the age where a bull is usually sold or considered as a selection candidate, none of his female progeny were recorded for these traits”

The genomic test can sort that out.

Other economically important traits also include those where the animal was still too young to be measured, such as longevity and traits that can only be recorded on some animals, due to cost or otherwise, such as efficiency of feed utilisation. In certain cases, animals must be killed to record traits, such as carcass and meat quality characteristics. For all these, the inclusion of genomic information will be of benefit.

BENEFIT

The proper inclusion and use of genomic information in the prediction of genetic merit essentially increases the accuracy and therefore lowers the risk associated with making a selection decision. The reliability of predicting the genetic merit of a young animal equals, or even surpasses that of older animals, where the performance of progeny is already known. It is therefore cost effective and serves as assurance, also for commercial buyers.

With true relationships known, inbreeding depression can be avoided, even where the pedigree information is not known. This is one of the big benefits, namely knowing the real parents, not simply by means of eliminating the non-likely parents but confirming the real ones. This is currently not possible when using existing technologies, such as micro-satellite DNA testing.

PERSPECTIVE

Genomic selection is a tool to increase the accuracy of decision making. It is not decision making. Breeders and buyers of herd sires still have to make the right choices, based on their objectives. Recording of economically important traits and other properties have always been important. It has now become even more important. **Breeders understanding the real value of using this technology and applying it in a proper manner will be at the helm of cattle breeding in future. ■**



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