Genomics:
What are the advantages?

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Genomics is the study of small differences (called SNPs), in the DNA of animals, and the variation in SNPs that exists between individual animals. It is therefore possible to determine which SNP combinations can relate to specific genes and traits. SNPs influence observable traits on a biochemical level, such as the production of proteins and enzymes or the control of genes. Genomics is therefore a complex new field with many new possibilities.

PARENTAGE

Genomics is currently used very successfully to improve existing technologies, such as very accurate parentage determination, simply because thousands of more markers are available to solve parentage than with previous DNA technology (micro-satellites).

SINGLE GENES

Genomics is also used to detect the carriers of single genes, such as horned / polled, colour genes or genetic defects such as double muscling. Adverse genes have also been discovered, such as the infertility haplotypes identified in dairy cattle.

POLLED AND HORNED

The most common allele that affects the presence or absence of horns in cattle is the dominant Celtic Polled gene. This is reported as follows for animals genomically tested through SA Stud Book:

- PcPc: The animal breeds pure for polled. This means that the animal received a polled gene from both its parents and can only transmit the polled gene to its offspring.
- PcH: The animal is polled, but carries the horn gene, because the polled gene (Pc) is dominant over the horn gene (H). It can transmit either a polled or horned gene to its offspring.
- HH: The animal breeds pure for horns. It can only transmit horn genes to its offspring.
- The exact inheritance of 'Scurs' is still unknown.

COAT COLOUR

Coat colour has fascinated breeders for many years, but the underlying genes have only been discovered fairly recently, and many are yet unknown. The gene causing red and black is the *Melanocortin 1 Receptor* gene (MC1R). This gene has three alleles: ED (dominant black), e (recessive red) and E+ (wild type; also known as the extension or neutral gene). The wild type is thought to represent the ancestral Aurochs colouration, from which modern *Bos taurus* breeds have descended. Animals with E+ can show any colour between red-brown and brown-black or may even be any colour (neutral), or animals may be darker on extremities such as the head, back, neck, ears, feet and tail (extension).

Breeders that genomically test their animals through SA Stud Book will receive results from the *MC1R* colour gene as well as some other colour genes. It is important to note that coat colour may also be influenced by other colour genes that are not included in this genomic test.

DOUBLE MUSCLING

Double Muscling is a single gene trait found in many beef cattle breeds all over the world. Three of the 9 variants have been identified in Stud Book breeds that were genomically tested. These are the two detrimental variants nt821 and Q204X, which causes severe double muscling and affects fertility and growth as well, and the less detrimental F94L which causes less severe double muscling.

MEAT TENDERNESS

Several genomic markers (SNPs) have recently been successfully identified as markers for meat tenderness traits. The inheritance of the Calpain, Calpastatin and DGAT1 variants is additive, indicating that the combined effect is equal to the sum of the effects of individual variants. These markers will be available when genotyping animals through SA Stud Book's Genomic Selection Service.

GENOMIC BREEDING VALUES (GEBVS)

SNPs is also used very effectively for estimating more accurate breeding values. Traditional breeding values are based on pedigree information and measurements, while genomic information is included for GEBVs (genomic breeding values) as an additional source of information. GEBVs are already available for some South African beef cattle breeds. This has the added benefit of improving BLUP technology because breeding values are estimated more accurately at an earlier age, especially for so-called 'difficult' traits that are expensive to measure, such as carcass traits, or measured only late in an animal's life, such as fertility or milk production.

CONCLUSION

The terminology used in genomic research includes terms such as GWAS, 'gene ontology', 'signatures of selection', and 'runs of homozygosity'. Genomics is therefore also the beginning of a new science. With genomics, it is now possible to identify specific genes through SNP markers. For example, an animal that has a certain SNP marker may have the ability to produce a protein that increases the efficiency of a biological pathway. This may have a ripple effect on other biological pathways and result in a cow, for example, that is better adapted to a hot environment. Genomics is thus used to identify large networks of gene interactions. Animals with beneficial combinations will then be able to be identified genomically.

Current BLUP technology works on specific economic traits that can be measured, for example weaning weight, and the heritability and genetic correlations with other traits. However, other traits like for example adaptation and disease resistance, are also important, but relatively difficult to define and measure. Fertility, one of the most important traits for successful beef farming, is also a good example of such a trait. Genomic selection will not only focus on the trait 'fertility', but on the complete gene network, which also considers all biological, metabolic, and biochemical traits that affect fertility.