Genomics for Beef Cattle: WHAT ARE THE BENEFITS?

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Introduction

Genomics in livestock has made tremendous advances in recent years. The ability to capture an animal's unique DNA sequence has become a cornerstone of stud breeding in the local and international community. Over 50 000 DNA markers, called single nucleotide polymorphisms (SNPs), are analysed on a genomic chip (genotype) and is sometimes referred to as an "All in One" DNA test. Genomic services provided to beef breeds associated with SA Stud Book allows breeders to take the next step in boosting the prediction of an animal's true genetic merit, ensuring pedigree integrity and unravelling the status of single genes within your herd. The use of genomic information in beef cattle has a large impact on increasing the prediction accuracy of production and fertility traits that are lowly heritable, sex-limited and are only measured later in life (Berry *et al*., 2014; Van Marle-

Köster & Visser, 2018). Breeders unfamiliar with genomics and genomically enhanced breeding values (GEBVs) must be scratching their heads and wondering what the benefit of genotyping your stud animals truly is. This short article will hopefully illustrate the impact of genotyping an animal, the effect of parentage verification and how genomics is integrated into a genetic evaluation to enhance the accuracy of breeding values. The South African Santa Gertrudis population currently have 699 genotyped animals of which 85% are cows and receives GEBVs monthly.

Parentage Verification

The use of DNA Microsatellite markers for Parentage Verification is widespread across the livestock industry in South Africa but has limitations that can result in the incorrect identification of an animal's parentage. The DNA Microsatellite test is not a true confirmation of parentage, but rather an exclusion of who is not the parent. The low number of markers used (12–20) may result in more than one animal being nominated as the possible sire of the tested progeny, especially if a breeder is using bulls that are highly related to each other due to a common ancestor in the pedigree.

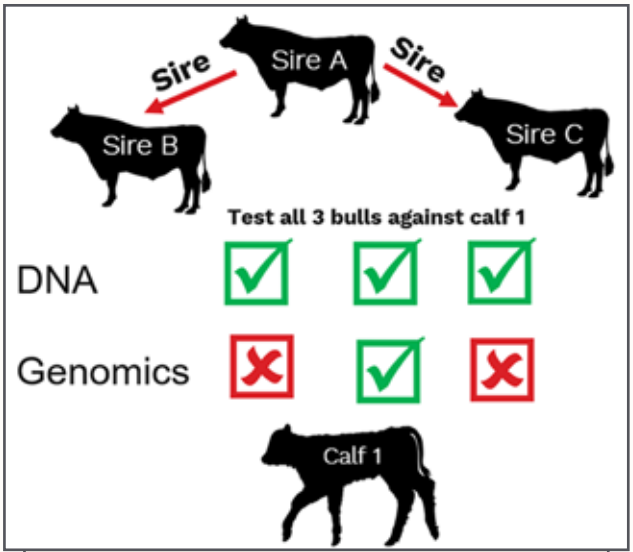

Figure 1: *This picture indicates the how DNA would indicate that all 3 sires could possibly be the sire of Calf 1, while only the genomics can truly confirm that Sire A is the correct sire of Calf 1.*

Genomics, which is currently the most powerful commercially available tool for parentage verification, uses around 15 000 to 25 000 markers (SNPs) to correctly identify the animals that are directly related to each other. A stringent mismatch threshold of 1% is applied, where animals with less than 1% opposing homozygote differences are considered directly related. If the mismatch exceeds 1%, the parentage is flagged as a conflict, necessitating the discovery of the true sire. Accurate identification depends on the availability of genotyped data for all potential sires in the herd. When all sires are genotyped, the system can automatically resolve parentage conflicts and identify the true sire. Genomic testing enables robust parentage verification by identifying true parents when conflicts arise, provided the potential parent is also genotyped. This is particularly effective in cases involving multiple sires or unknown sires, as genotyping both offspring and sires can determine the correct lineage.

SA Stud Book is currently the only Data Interpretation Centre on the African continent accredited for Parentage Verification through the International Committee for Animal Recording (ICAR) using Genomic Information. Unfortunately, the genomic data is not backward compatible with DNA Microsatellite data, meaning that in order for Parentage to be verified with genomics, both the parent and the progeny must be genomically tested.

Genetic Relatedness using Genomics

Apart from accurate parentage verification how does genomics benefit the breeder's ability to more accurately select his top animals? Research on genomics in beef and dairy cattle, as well as small stock breeds, indicates that genomics has the biggest impact on traits that are lowly heritable, sex-limited and are only measured later in life.

The integration of genomic data into a genomic evaluation does occurs in one simple step, it fills in the gaps of the pedigree. The pedigree will at times indicate that animals within the same breed are not related, as breeders may not yet have genetically linked their herds by using other breeders' animals, which is known to be a limitation of using simple mendelian inheritance as the pattern of inheritance across generations. Animals within the same breed will be inherently related to each other, as they are the same species (in this case cattle; *Bos*), subspecies (*taurine* vs *indicine*) and of the same breed (Santa Gertrudis), indicating that they will indeed share a similar genetic makeup. Table 2 showcases how the pedigree matrix uses

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simple mendelian inheritance to estimate genetic relatedness, while Table 3 showcases the genomic matrix using the 50 000 markers in conjunction with the pedigree matrix, to refine and truly estimate the relatedness between the animals.

Table 2: Genetic relatedness between animals using the pedigree and traditional mendelian inheritance.

	SGT_1	SGT_2	SGT_3	SGT_4	SGT_5	SGT_6
SGT_1	1.00					
SGT_2	0.00	1.00				
SGT_3	0.25	0.0625	1.00			
SGT_4	0.00	0.00	0.00	1.00		
SGT_5	0.125	0.0625	0.125	0.00	1.00	
SGT_6	0.50	0.03125	0.50	0.00	0.0625	1.00

Animal 6 is the Sire of both Animal 1 and 3, which is indicated by the 50% relatedness estimated between them. This makes Animal 1 and 3 half-siblings, meaning that it is assumed they share 25% of the same genetic makeup from the sire's side. Animal 5 is a close relative to Animals 1 and 3, with the pedigree estimating they are 12.5% related. Animal 4 has no pedigree links to any of the other animals; thus, it is assumed that they are 0% related to the rest of the animals in Table 2.

Table 3: Genetic relatedness between animals combining the pedigree information and the genomics to estimate the true genetic relationships between these animals.

	SGT_1	SGT_2	SGT_3	SGT_4	SGT_5	SGT_6
SGT_1	1.00					
SGT_2	0.06	1.00				
SGT_3	0.315	0.08	1.00			
SGT_4	0.04	0.03	0.07	1.00		
SGT_5	0.146	0.05	0.095	0.01	1.00	
SGT_6	0.50	0.02	0.50	0.04	0.085	1.00

By comparing Table 2 with Table 3, the genomics has corrected the assumed genetic relationship to a realised genetic relationship. Animals 1 and 3, who are half-siblings, are now indicated to be 31.5% related, meaning they inherited more similar genetics from the sire than was originally assumed. The genomics has revealed that Animal 5 is more related to Animal 1 (14.6%) than to Animal 3 (9.5%). Most importantly Animal 4 is no longer not linked to the other animals but is between 1% - 7% related to the other animals. Genomics allows the BLUP analysis to make connections between genetically related animals that the traditional pedigrees are unable to make and thus aids in accurately predicting an animal's genetic potential not just from animals it is directly related to.

Single Genes

Genes can mutate, resulting in changes that create variations from the original or "wild type" form. While some genes exhibit multiple variants, an animal inherits only two—one from each parent. These can be identical (homozygous) or different (heterozygous). In heterozygous cases, one allele may dominate; for example, an animal with one polled and one horned allele will appear polled due to the dominance of the polled allele. However, traits are rarely determined solely by a single gene, as interactions with other genes and environmental factors often influence the phenotype. Detailed information on the mutations discussed here is available on the Online Mendelian Inheritance of Animals website (Nicholas et al., 1995).

Polledness

The genetics of polledness has been of major interest to cattle breeders and livestock geneticists. With the revolution of genomics, this has allowed for the unravelling of the true genetic mechanism that controls the expression of horns or polledness. Referred to as the POLLED gene, this gene is located on Chromosome 1 of the cow genome. The first mutation was identified in Brahman cattle and is called the Celtic variant. This is the main mutation causing polledness in beef and dairy cattle worldwide and was confirmed in the Bonsmara and Drakensberger breeds by (Grobler *et al.*, 2018). A few researchers noticed that some cattle breeds were still phenotypically polled but were homozygous horned (HH) for the Celtic variant. This indicated that a different mutation on the POLLED gene may be responsible. Further research has revealed three other variants within this POLLED gene such as the Friesian variant discovered in Holsteins which is now present in a few beef cattle breeds, the Mongolian variant in Kazakh breeds and more recently the Guarani variant in Nellore and Gyr breeds (Nicholas *et al.*, 2023). Currently, all four of these POLLED gene

mutations can cause polledness in all cattle breeds. The current genotyped Santa Gertrudis population shows both the Celtic and Friesian variants causing polledness within the breed.

Double muscling

The myostatin protein regulates normal growth and development of muscle in an animal's body. A few mutations can disrupt myostatin's ability to function normally, causing muscles to grow uncontrollably, resulting in an animal being double-muscled. Q204X and nt821 mutations cause a break in the myostatin protein, and affected animals will be double-muscled. The F94L mutation is seen as the "for profit gene" as it doesn't break the myostatin protein, but rather affects its ability to bind to muscles and ensure normal muscling. These mutations behave recessively, meaning it is almost impossible to identify carriers of double-muscling mutations, as they only appear in an affected calf, which is a result of mating two carrier animals (Csürhés *et al*., 2023). Due to the direct effect on heavier birth weights, dams with double-muscled calves may experience calving difficulties. Affected animals will have less fat deposition, which will lead to a lower lifetime production, fertility and longevity. It is recommended to ensure that sire bulls are "Free" from these mutations, in order to minimise and potentially eradicate incidences of double muscling in your herd. The detrimental nt821 mutation is currently the only detrimental mutation present in the Santa Gertrudis population, therefore genotyping your animals before mating is essential to avoid further issues due to double muscling in your herd.

Meat Tenderness

A recent study in South African beef cattle breeds revealed that a few mutations on the Calpastatin and Calpain genes affect meat tenderness, during the conversion of muscle to meat in the post-slaughter process (Basson *et al*., 2022). Certain mutation combinations result in an animal being genetically predisposed to having more tender meat. These mutations can be combined to reveal a tenderness score, which ranges from 1 (Average) to 6 (Most Tender). Figure 2 shows the current distribution of meat tenderness scores in the genotyped population. The majority of animals are sitting at a level of between 3 to 5.

Milk-related mutations

Genes associated with milk traits in dairy cattle also influence these traits in beef cattle. The interplay between single-gene effects and polygenic factors impacts the quantity and quality of milk a dam produces, which in turn affects calf weaning weight. The ABCG2 gene is known to increase milk volume while reducing milk fat content and percentage. DGAT1, a major gene in beef cattle, has a significant additive effect, increasing milk fat, intramuscular fat, and carcass fat. Beta-Casein, commonly associated with A2 milk, enhances both milk volume and protein production. Variants of Kappa-Casein also play a role, with the A-variant boosting milk production and the B-variant reducing milk protein percentages. Similarly, Beta-Lactoglobulin affects milk composition, where Haplotype A increases milk volume and Haplotype B enhances milk fat and protein content.

Detrimental Mutations

Genetic disorders such as Crooked Tail, Osteopetrosis, and Ehlers-Danlos Syndrome (a connective tissue disorder) cause distinctive phenotypic abnormalities, often mistaken for general weakness or poor health in calves. Glycogen Storage Diseases (GSD, including Pompe's disease), results from mutations that impair glycogen storage, and occur in breeds with Brahman ancestry. Mucopolysaccharidosis

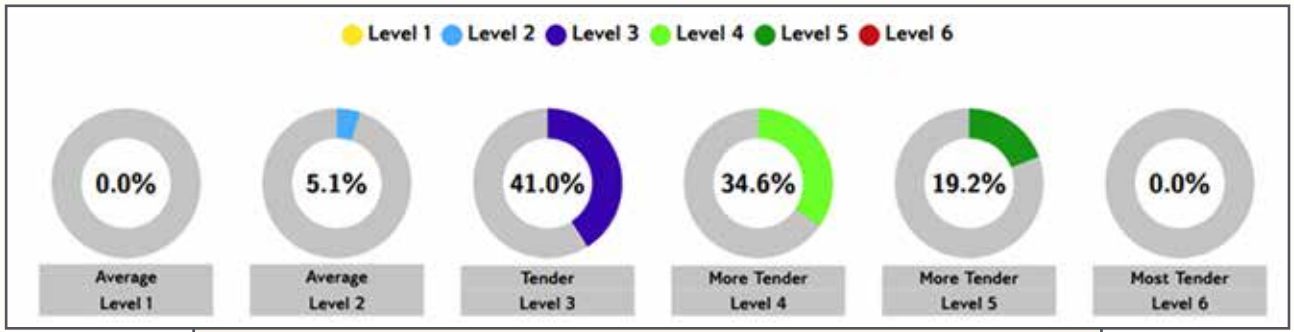

Figure 2: *Distribution of meat tenderness levels in the Santa Gertrudis population*

(NAGLU), a lysosomal storage disorder, manifests as a staggering gait, giving affected animals a "drunken" appearance. Other detrimental mutations observed genomically include Spinal Muscular Atrophy, Pseudomyotonia, Bovine Hereditary Zinc Deficiency, Maple Syrup Urine Disease, and Thrombopathia. To reduce the risk of these disorders, genetic testing of sire bulls is essential to exclude carriers and ensure herd health. In the Santa Gertrudis population, current genotyping has identified two carriers of Crooked Tail Syndrome and three carriers of Ehlers-Danlos Syndrome. The current genotyped population shows no carriers of any of these detrimental mutations but proactive genomic screening and selection are vital for preventing the propagation of genetic disorders in future generations.

Future applications

As research constantly innovates, genomics can assist in revealing the true underlying genetic mechanisms that influence adaptability and fertility traits. Infertility haplotypes, genes which cause embryo or foetal re-absorption, are a widely known problem in the dairy cattle industry, with recent studies revealing similar haplotypes in Limousin and Simmental beef cattle populations. The use of genomics is ushering in a new era of stud breeding, especially for those breeders who may have closed herds or are new members of the Santa Gertrudis Society. The recording of performance and fertility traits will not be replaced by genomics, as genomics only assists in boosting the pedigree side of the BLUP equation. Phenotype will always remain King, while Genomics is the Queen the King has always been looking for. A common misconception widely stated is that "Genomics is the future", when genomics is now available in South Africa with current and relevant applications, so take advantage and advance your herd to the next level!

References

Basson, A., Strydom, P. E., van Marle-Köster, E., Webb, E. C., & Frylinck, L. 2022. Sustained Effects of Muscle Calpain System Genotypes on Tenderness Phenotypes of South African Beef Bulls during Ageing up to 20 Days. Animals 12 https://doi.org/10.3390/ani12060686.

Berry, D. P., Wall, E., & Pryce, J. E. 2014. Genetics and genomics of reproductive performance in dairy and beef cattle. Animal 8, 105–121.

Csürhés, T., Szabó, F., Holló, G., Mikó, E., Török, M., & Bene, S. 2023. Relationship between Some Myostatin Variants and Meat Production Related Calving, Weaning and Muscularity Traits in Charolais Cattle. Animals 13 https://doi.org/10.3390/ani13121895.

Grobler, R., Visser, C., Capitan, A., & van Marle-Köster, E. 2018. Validation of the POLLED Celtic variant in South African Bonsmara and Drakensberger beef cattle breeds. Livest Sci 217, 136–139.

Nicholas, F. W., Tammen, I., & Sydney Informatics Hub. 1995. Online Mendelian Inheritance in Animals (OMIA). https://doi.org/https://doi.org/10.25910/2AMR-PV70.

Nicholas, J. E., Tammen, I., & Sydney Informatics Hub. 2023. OMIA:0004839913: Online Mendelian Inheritance of Animals (OMIA).

Reding, J. J., Theron, H. E., & van der Westhuizen, R. R. 2021. Genebox: A three-dimensional tool to visualise cattle breed differences through principal component clustering. Page: 54 in 52nd Annual SASAS Congress. Pretoria.

Van Marle-Köster, E., & Visser, C. 2018. Genomics for the advancement of livestock production: A South African perspective. S Afr J Anim Sci 48 https://doi.org/10.4314/sajas.v48i5.2.