



Genomic Testing; A Modern Perspective in Bull Selection for Breed Improvement

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Abstract: Genomic selection; A Modern perspective in Animal breeding which has revolutionized the Dairy and Beef industry. It has enabled us to predict the genetic merit of candidate animals early and accurately by means of Genome Wide testing technologies. This review article focuses on the key advancements in genomic selection methodologies, prediction models and their positive results like genetic gain, reduction of generation intervals productivity etc. Moreover, Applications of GS in milk yield, fat and protein content and climate resilience are discussed along with its role in crossbreeding programs and conservation of genetic diversity. Genomic selection still faces some challenges. Breeders need large and diverse reference populations for accurate predictions. The cost of genotyping is high. Some researchers also talk about some collateral damage of GS on the biodiversity of the gene pool. Future work should focus on using functional variants and whole-genome sequencing. Reproductive technologies like embryo selection can also improve results. Overall, genomic selection is a strong tool to improve productivity and sustainability

INTRODUCTION

From Centuries, the breed improvement strategies were centered on choosing the bulls having exceptional phenotypic characters and regressively using them in the populations. While these methods were useful but they were slow costly and often taking years to evaluate a bull's true genetic potential (VanRaden, 2020). Genomic selection has revolutionized this process. Genomics is the study of structure, function, and inheritance of the genetic material (the genome) of an organism such as dairy cattle. The genetic material is contained within DNA, which, among other things, consists of parts of nucleotides. Breeders can now predict a young bull's genetic merit accurately by using dense DNA markers across the genome, accurately and timely. This led to an accelerated genetic gain and reduction in generation intervals (Yuan et al., 2025; Curzon et al., 2024). This approach also allows selection for traits that appear in later stages of life or are limited to one sex. such as fertility, Milk production, disease resistance, and adaptability to environment. (Ogunbawo et al., 2024).

Recent studies emphasize on developing genomic tools for diverse cattle populations. To ensure precise predictions in tropical systems, for example, certain *Bos indicus* breeds need specific SNP arrays and reference genomes which is one of the biggest challenge in adopting this system for different breeds (Ogunbawo et al., 2024). Genomic selection is also being used more and more in crossbreeding programs, where sire choice has a major impact on production and efficiency outcomes. These developments show how

genomic selection is affecting the selection of bulls around the world, from smallholder to intensive dairy systems. Concerns about preserving genetic diversity, the high cost of genotyping, and the scarcity of reference populations in native breeds are ongoing issues. These issues are anticipated to be coped up by whole genome sequencing expanding the reference populations and data interpretations by AI models.

HISTORICAL BACKGROUND

The switch from traditional approaches to genomic selection in bull breeding gained popularity in the beginning of 2010 as genotyping technologies evolved and reference populations expanded. In traditional models BLUP (Best Linear Unbiased Prediction) that is basically a prediction model of bull's potential was derived on the basis of pedigree and progeny evaluations. Recent research has demonstrated that adding genetic data (marker-based associations) significantly improved accuracy compared to pedigree-based BLUP, particularly for characteristics with low to moderate heritability. In Hanwoo beef cattle, a study comparing PBLUP (pedigree-based BLUP), GBLUP (Genomics-based BLUP), and single-step ssGBLUP (having a combined effect of both pedigree and genomics) for body measurement traits found that ssGBLUP delivered on average 43% higher accuracy than GBLUP and about 33% higher than PBLUP, illustrating how combining pedigree and genotype data enabled more reliable selection of young bulls long before progeny are evaluated. (Cho et al., 2020).

A recent study on the Holstein herd book showed that ssGBLUP works well, even in smaller herds. Even though the herd was smaller than usual, the accuracy of predictions was still high. The prediction costs were also low when all the available genetic and performance data were used. (Curzon et al., 2024) Another study found that using functional SNPs helped improve predictions for fat and protein percentages by about 3%, even with fewer markers. This suggests that concentrating on biologically meaningful genes may compensate for lower marker density (e.g., using 16,000 markers vs full-density panels up to 90,000 markers). Furthermore, these efforts have revealed more breed-specific genetic markers and the preservation of genetic diversity (Li et al., 2024). In the meanwhile, computational analyses demonstrated that marker density and reference population size are crucial; higher-density SNP panels and bigger reference populations produced significantly better genomic EBVs (Pryce et al., 2015; Meuwissen, Hayes, & Goddard, 2016).

PRINCIPLES OF GENOMIC SELECTION

Genomic selection is based on the principal that genetic merit in an animal can be predicted from DNA markers spread across the entire genome. Unlike traditional practices, based on pedigrees and daughter records. Genomic selection uses large panels of single nucleotide polymorphisms (SNPs) Arrays for detection of genetic variations between individuals. A DNA microarray called an SNP array is used to find polymorphisms in a population. It is the most common type of variation seen throughout DNA. This SNP array is used to find polymorphisms in a population. The most common type of variation seen throughout the genome is an SNP, which is variation at a single location in DNA. These panels are sold commercially for a variety of breeds. It functions under the premise that linkage disequilibrium exists, making SNPs substitutes for gene-affecting functions. Breeders may forecast genomic estimated

breeding values (GEBVs) with high accuracy, even in young bulls without offspring, by adding thousands of these markers into prediction algorithms (Meuwissen et al., 2016; VanRaden, 2020).

The principle of genomic selection is to construct prediction equations of the genetic merit of individuals by utilizing both genotypic and phenotypic data available in the reference population (Boichard, D et al., 2016). The core of genomic selection is the reference population. precision of prediction in other words larger and better representable sets of references have higher GEBV reliability, especially for low-heritability traits such as fertility, disease resistance, and longevity (Goddard, 2016; Liu et al., 2022). Cross-population studies also report that if the reference population is very different from the focus population (for example using Holsteins as references for predicting Jersey animals), prediction precision is much reduced due to differences in patterns of linkage disequilibrium (Lund et al., 2014). Resultantly, there should be a greater investment in the breed-specific or region-specific reference population.

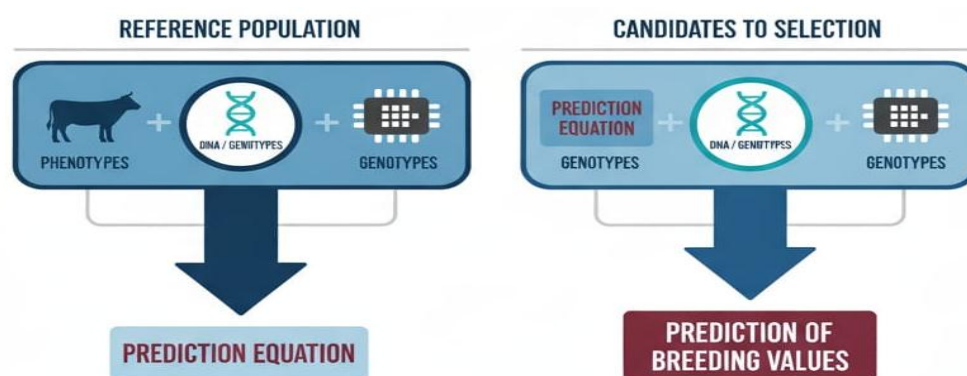


Figure 1.1: The flowchart illustrates the principle of genomic selection; the phenotypic data and genotypic data coming from reference population is used to form the prediction equation which would be ultimately used for combining with the genotype of candidate animal to declare estimated Breeding Values

The statistical foundation for genomic selection is based on models such as GBLUP (Genomic Best Linear Unbiased Prediction) and Bayesian methods. GBLUP assumes all SNPs have slight effects and builds a genomic relationship equation to measure actual genetic similarity between animals (Wiggans et al., 2017). Bayesian models (BayesA, BayesB, BayesR) are less conservative and permit a mixture of some SNPs with significant effects for traits with a few major genes (Pérez & de los Campos, 2022). More recent single-step GBLUP (ssGBLUP) integrates pedigree and genomic data and is practical for national breeding programs with not all animals being genotyped (Misztal et al., 2020; Curzon et al., 2024).

APPLICATIONS IN BULL SELECTION

Production Traits

Historically, production traits such as milk yield, fat, and protein content were evaluated through long-term progeny testing, which required waiting for daughters to provide records before a bull's genetic potential could be determined. Genomic selection has revolutionized

this process by enabling accurate predictions of Genomic Estimated breeding values (GEBVs) at a very young age, often before the bull has sired any offspring. For example, genome complementarity studies in beef-on-dairy crossbreeds have shown that selective sire choice can maintain high carcass weight and growth performance while reducing genomic inbreeding (BMC Genomics, 2024). Genes like NCAPG and LCORL have been pinpointed as key drivers of growth and body size, providing molecular targets for selection. Genomic selection has also enabled the identification of milk protein variants, particularly the A1/A2 beta-casein gene, which affects both milk quality and human health. Studies show that the A1 beta casein protein releases a peptide known as Bet casamorphin-7 during digestion which leads to digestive discomfort and bloating. So, any bull containing the A1 allele in its gene pair would not be considered for selection and genomic testing helps us to do so. By incorporating the A1/A2 genotype into selection indices, breeding programs can select bulls that not only maximize yield but also enhance milk quality for consumers (He, Yang, Suo, & Song, 2025; Novika et al., 2025). Additionally, functional variant analyses have shown consistent improvements in prediction of fat and protein percentages, outperforming traditional SNP panels (Alemu et al., 2025). Incorporating this genomic data helps breeding programs achieve economic goals and genetic gains faster in dairy cattle (Garcia-Ruiz et al., 2016; VanRaden, 2020).

Fertility and Health Traits

Fertility and health traits have historically been difficult to improve because they are expressed later in life and have low heritability. But now Genomic selection helps in the identification of young bulls with superior reproductive and health potential. This is possible a long before progeny records are available. Recent studies in tropically adapted bulls have identified SNPs on X chromosomes and chromosome number 5 linked to semen quality, sperm morphology, and scrotal circumference. These are the direct markers for reproductive performance (Tan et al., 2023).

In Holsteins, computed sequence-level genotypes have revealed QTLs (quantitative trait loci) that are related to calving ease, days open, and conception rates. When these traits were observed they were added into the fertility indices like Health weighted index (HWI) and sustainability Index. Genomic tools also help detect deleterious haplotypes and prenatal loss causes, enabling AI centers to avoid risky mating and reduce inbreeding (Fritz et al., 2013). According to early estimates, GS in dairy cattle would increase the annual genetic gain by 70 -108%, depending on the breeding plan used (Scott, Haile-Mariam, Cocks, & Pryce, 2021)

Reliability			
Trait	Parent Average	Genomic Values	Parentavg+ Genmic Values
Lactation No. Milk	35%	24%	59%
Milk	39%	31%	70%
Fat	39%	36%	75%
Production Life	33%	33%	66%
Daughter Pregnancy Rate	33%	20%	53%

Holstein Reliability Value: Comparing Traditional To Genomic

Adaptation and Resilience

One of the biggest challenges of the upcoming time is climate change which should be taken seriously in the selection of the animals that could survive in extremes. Genomic studies in indigenous and crossbred populations have identified genes related to heat tolerance, cold hardiness, immune response, and feed efficiency. These traits are main part of the EBV index known as sustainability index (SI) (Porto-Neto et al., 2020; Hayes et al., 2021). For example, comparative genome sequencing of Mongolian cattle and their crossbreeds discovered the genes like TRPM8 for extreme colds and some immune related genes which could be taken as selection strategy in that breed. The local breeds of an area could be made genomically tested for their native gene pools (Tian et al., 2023). Similarly, indigenous Belahi cattle have shown selection signals in genes like IL2, IL21, and DNAJB13, which are associated with immune function and stress response, offering valuable information for breeding resilient bulls in harsh environments (Chavan et al., 2025). By including these markers into bull selection, genomic selection improves dairy and beef herd productivity as well as long-term adaptation.

Reliability of Genomic Predictions

Reliability of a breeding program lies in the genetic gain ΔG . Four factors determine the annual genetic gain for every domestic species (I) genetic variability of the Trait σ^2_g (ii) generation interval GI (iii) selection intensity SI (iv) Accuracy Of prediction (r). (Ibtisham, F et al., 2017)

$$\Delta G = I * r * \sigma^2_g / IG$$

Through genetic selection, the latter three can be altered. Genomic selection's primary benefit is that candidates can be assessed and chosen without relying on their own phenotypic data or that of their offspring. As a result, selection can be done shortly after birth or even very early on can be used on embryos. Thus, a shorter generation interval may be necessary for genomic selection in a variety of species and production settings. The shorter the generation interval the more the number of animals taken in reference population so the second and third factor are interrelated. Moreover, by increasing the size of reference population, selection intensity could increase. Talking about the fourth factor that is Accuracy of prediction or genetic Evaluation Precision directly depends upon the accuracy of the SNP effect, their linkage disequilibrium between the SNPs and the causal variants leading to greater Accuracy of prediction (Scott, Haile-Mariam, Cocks, & Pryce, 2021).

Cost-benefit Considerations for Breeding Programs

In underdeveloped nations, small-scale nucleus dairy breeding initiatives can make enough money to ensure their sustainability in the future. Additionally, GS schemes will perform better than PT schemes in terms of economic and genetic gains. Shorter generating intervals, lower operation expenses, and reduced revenue all contribute to GS's superior performance. Breeding programs can save money by storing sperm and eliminating bulls early on. Ultimately, implementation of a breeding program and choice of selection strategy will be determined by the ability to generate profit. Genetic selection programs have larger

gross margins than PT schemes and require less infrastructure and performance documentation. (Kariuki, Brascamp, Komen, Kahi, & Van Arendonk, 2017)

LIMITATION AND FUTURE DIRECTIONS

The high expense of DNA testing often prevents its widespread adoption. As costs decrease, DNA testing will become more widely used. This will help to create larger and more current reference populations. Unrecorded qualities will continue to pose an issue. One-step evaluations are expected to become the standard. This is due to improved EBV accuracy and cost-effectiveness of DNA testing, which will increase the number of animals examined. Future methods for calculating genomic EBVs may include two approaches. The evaluation could be within the breed (wbGS) or multiple breeds (abGS). To calculate the prediction equation for wbGS medium- or low-density SNPs can be employed using G- or SNP-BLUP. In other case, the reference population could include many breeds and crosses (abGS). Dense SNPs and nonlinear approaches for calculating the prediction equation can improve the accuracy of EBVs. For wbGS, there appears to be minimal possibility to improve predictions without increasing the number of reference populations. AbGS has several opportunities for improvement. Genome sequencing data provides more accurate EBVs than dense SNPs as it includes causative variants and eliminates the need for Linkage Disequilibrium. Understanding the effects of mutations at each place in the genome can help identify causative variants (Meuwissen, Hayes, & Goddard, 2016).

Genomic selection provides two opportunities that have not been effectively utilized. Combining GS with reproductive technology can significantly reduce generation duration. When paired with multiple ovulation and embryo transfer (MOET), GS can aid in selection. Select the best embryos for the future generation of animals, rather than random embryos. To improve accuracy, the prediction equation might be trained on commercial animals rather than stud (Pure Bred elite) animals that have already been tested for key features. Commercial animals, such as crossbreds, often face harsher conditions than purebred stud animals. Additionally, we can collect data on qualities not assessed at the stud level, like as meat quality and disease resistance. Due to a decrease in phenotypic and pedigree recording and an increase in the cost of creating the reference dataset, this suggests a decrease in costs at the stud level. This shift may also be expected as costs of practical trait recording and genotyping will keep decreasing with advent of new recording technologies like automatic milk record sensors in parlors. There is currently no clear commercial vehicle to finance this transition.

CONCLUSION

As the global population grows, the demand for high-quality protein, fats, and micronutrients from livestock is expected to rise. Increased food demand requires faster and more efficient ways. Genomic selection is a promising strategy for enhancing animal output through genetic gain, notwithstanding its early stages. Advancements in research and technology have made it possible to simply acquire the genetic data of livestock species for breeding purposes at a reasonable cost. While genomic selection is less developed in other livestock species than dairy cow, it is expected to become an effective method for producing superior animals as research progresses.

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