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Genomic prediction in Cattle: How It Works and Its Role in Genetic Improvement

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Introduction

The discovery of deoxyribonucleic acid (DNA) in 1953 by Watson and Crick marked a major breakthrough in molecular genetics. This discovery helped scientists understand the fundamental building blocks of life and the mechanisms through which cells function and pass information from one generation to the next. Watson and Crick emphasized that the structure of DNA possessed properties of significant biological importance.

Nearly three decades later, Alec Jeffreys developed the technique of genetic fingerprinting, which allows individuals to be identified based on their unique genetic code. Today, genetic testing is considered one of the strongest forms of scientific evidence and is widely used in forensic investigations, cancer screening, and paternity testing. These developments have also opened new opportunities for genetic improvement in livestock species, particularly cattle.

DNA-based technologies have greatly enhanced genetic evaluation programs in cattle. They enable more accurate estimation of genetic relationships, reliable parentage verification, and direct identification of genes influencing economically important traits. As a result, genomic testing has become an important tool in modern cattle breeding programs.

The introduction of genomic selection (GS) transformed animal breeding by drastically increasing the accuracy of breeding value prediction. The availability of high-density genome-wide markers allowed breeders to capture the genetic variation underlying complex traits much more effectively. Studies such as those by VanRaden et al. (2009) demonstrated the tremendous impact of GS in dairy cattle, enabling rapid genetic gains and reshaping breeding programs globally.

The conceptual foundation of GS was laid by Meuwissen et al. (2001), who proposed the concept of using dense genomic information to predict breeding values through Bayesian models that estimate SNP effects and compute direct genomic values (DGVs). Subsequently,

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VanRaden (2008) introduced the genomic BLUP (GBLUP) method, which uses a genomic relationship matrix (**G**) instead of pedigree relationships to predict genomic breeding values.

Testing of Inherited Traits

Genetic testing is based on the basic principles of inheritance. Some traits are controlled by a single gene (Coat colour and horn status) or a small number of genes i.e. polygenes (most of the production and reproduction traits – quantitative in nature).

For example, coat color in Angus cattle is controlled by a single gene with two possible alleles: black and red. Each animal inherits one allele from its sire and one from its dam. The black allele is dominant over the red allele, meaning that animals with at least one black allele will appear black. Animals must inherit two red alleles to express a red coat color. A similar inheritance pattern exists for horn status, where the horned condition is recessive.

Parentage Testing in Cattle

The concept that each parent contributes one allele to its offspring forms the basis of parentage testing in cattle. Parentage testing is particularly useful in herds where multiple bulls are used or when cleanup bulls are introduced after artificial insemination. By genotyping animals, breeders can accurately identify the true sire of a calf.

Unlike simple inherited traits, parentage testing uses multiple DNA markers to compare calves with potential parents, providing a high degree of certainty. Table 1 presents a simplified example of how DNA markers can be used to determine the true sire of a calf.

Table 1. Simplified example of parentage testing using a single genetic marker.

	Calf	Dam	Sire 1	Sire 2
Allele 1	A	B	A	B
Allele 2	B	B	B	B
Result	AB	BB	AB	BB
Conclusion	—	—	True sire	Excluded

Genomic Testing in Cattle

Recent advancements in genomic testing have introduced high-throughput technologies that can analyze tens of thousands of DNA markers, known as single nucleotide polymorphisms (SNPs), from a single animal. DNA samples can be collected from blood, hair roots, or tissue. Hair samples must include the root to ensure successful DNA extraction, with tail switch hair being the most commonly recommended source.

Figure 1. Blood sample collection for genomic testing in cattle.

After DNA extraction, samples are analyzed in specialized laboratories using SNP chips. The most commonly used bovine SNP chip evaluates approximately 50,000 DNA markers across the genome (**Figure 2**). SNPs represent variations in the DNA sequence that contribute to genetic differences among animals.

Figure 2. Bovine SNP chip used for genomic testing.

The ability to analyze thousands of SNPs is particularly valuable because most economically important traits, such as milk yield, calving ease, feed intake, and feed efficiency, are controlled by many genes rather than a single gene. Genomic testing allows for more accurate prediction of genetic potential at an early age, although phenotypic performance remains an important indicator of genetic merit.

Molecular Breeding Values and Genomic EPD

Initially, genomic test results were reported as molecular breeding values (MBV). MBVs are calculated as the sum of the effects of individual SNPs present in an animal's genome. **Figure 3** presents a simplified example of MBV calculation using three SNPs.

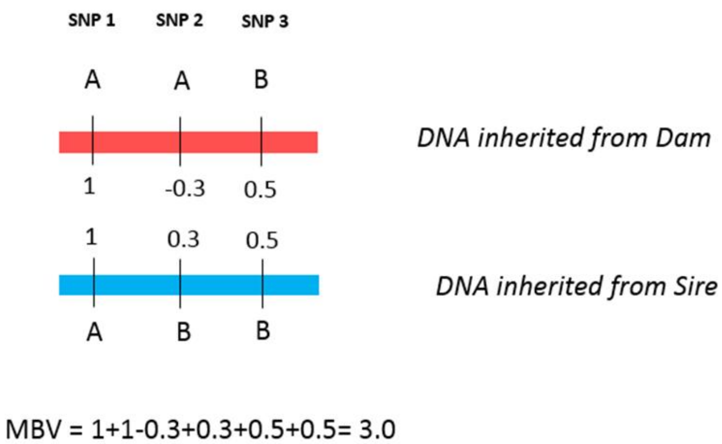

Figure 3. Simplified example showing the calculation of molecular breeding values (MBV) using three SNPs.

Over time, MBVs were combined with traditional expected progeny differences (EPD) to produce genomic-enhanced EPD (GE-EPD). This integration improves accuracy because SNP markers do not capture all genetic variation, whereas EPDs incorporate pedigree and performance information.

Single-Step Genomic Evaluation (ssGBLUP)

A major advancement in genomic evaluation was the development of the single-step genomic best linear unbiased prediction (ssGBLUP) method. Unlike earlier multi-step approaches, ssGBLUP integrates pedigree, performance, and genomic information into a single evaluation system.

Misztal *et al*., 2009 introduced an approach based on the GBLUP architecture called single-step genomic best linear unbiased prediction (ssGBLUP), which utilises simultaneously all pedigree, genotypic and phenotypic information from both genotyped and non-genotyped individuals. This approach combines the Numerator relationship matrix based on pedigree and genotypes into a single matrix called (H). Fitting H^{-1} in Henderson MME gives the single step genomic BLUP.

$$H^{-1}=A^{-1}+\begin{bmatrix}0 & 0\\0 & G^{-1}-A_{22}^{-1}\end{bmatrix}$$

Where, A_{22}^{-1} was inverse of numerator of genotyped animals.

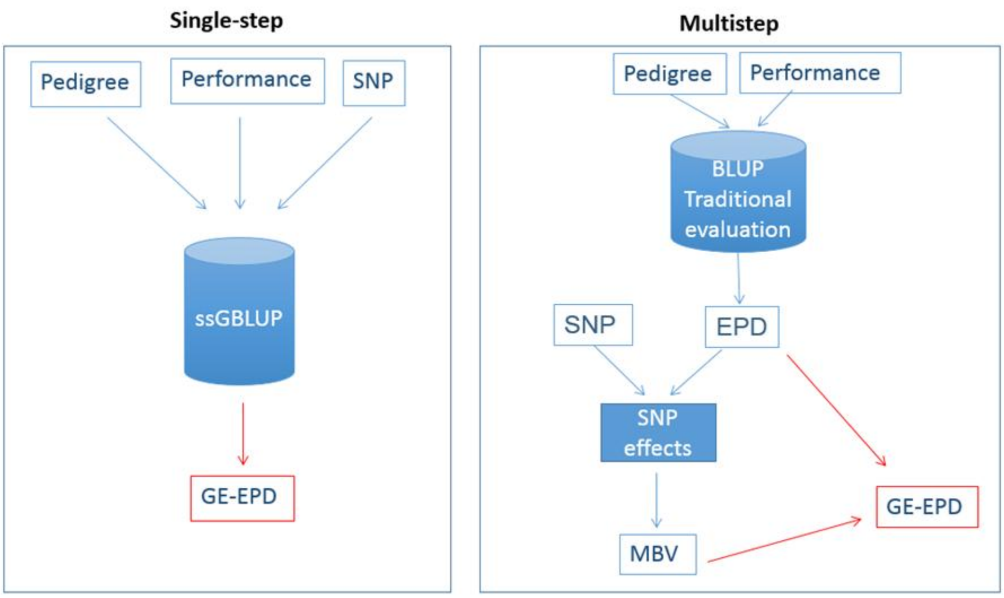

Figure 4. Comparison of multi-step and single-step genomic evaluation methods.

In the single-step approach, both genotyped and non-genotyped animals benefit from genomic information if they are connected through pedigree relationships. Since its development in 2009, ssGBLUP has been widely adopted by major cattle breed associations worldwide.

An important advantage of the single-step genomic best linear unbiased prediction (ssGBLUP) approach is that breeding values can be estimated for all animals, even when pedigree or phenotypic records are incomplete. Using the animal model implemented in BLUPF90+ software (Misztal *et al*., 2015), ssGBLUP allows the simultaneous incorporation of available pedigree, phenotypic and genomic information. This feature is particularly valuable under Indian conditions, where most farmers maintain small herds and systematic phenotypic recording is often limited. In addition, economic constraints usually prevent genotyping of all animals in the population. However, even when only a subset of recent animals is genotyped, ssGBLUP can effectively combine genomic data from these animals with pedigree information from the entire population to estimate genomic breeding values. Several studies have shown that partial genotyping, when integrated with pedigree data, can still lead to a meaningful improvement in the accuracy of breeding value estimation. Overall, the major advantages of genomic selection using ssGBLUP include reduced generation interval, increased accuracy of selection and enhanced genetic gain.

Accuracy of Genomic-Enhanced EPD

Young animals often have low EPD accuracy due to the lack of performance or progeny records. Genomic testing significantly improves accuracy by providing information equivalent to several progeny records. As accuracy increases, EPD estimates move closer to the true genetic value, whether the estimate increases or decreases.

Conclusion

Genomic testing has transformed genetic evaluation in cattle by enabling early and more accurate prediction of genetic merit. As the cost of genomic technologies continues to decline, their adoption is expected to increase further. However, breeders must carefully evaluate the economic benefits of genomic testing to ensure its effective and sustainable use in cattle breeding programs.

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