

Genomic Selection in Animal Breeding: Principles, Applications, and Future Perspectives

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Received:- 04 July 2026/ Revised:- 17 July 2026/ Accepted:- 25 July 2026/ Published: 31-07-2026

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Abstract— Genomic selection (GS) has transformed modern animal breeding by enabling the prediction of genetic merit using dense genome-wide molecular markers rather than relying solely on pedigree and phenotypic information. Since its conceptual introduction in 2001, GS has become a cornerstone of genetic improvement programs in livestock species, particularly dairy cattle, and has subsequently expanded to beef cattle, sheep, goats, swine, poultry, and aquaculture. The integration of high-density single nucleotide polymorphism (SNP) genotyping with advanced statistical prediction models has substantially increased the accuracy of breeding value estimation, shortened generation intervals, and accelerated rates of genetic gain. Compared with conventional best linear unbiased prediction (BLUP) and marker-assisted selection (MAS), genomic selection captures the combined effects of thousands of loci distributed throughout the genome, making it highly effective for complex quantitative traits governed by many genes of small effect. Recent advances, including single-step genomic BLUP, Bayesian prediction methods, whole-genome sequence analysis, functional genomics, multi-omics integration, artificial intelligence, and precision livestock farming technologies, have further enhanced the scope and efficiency of genomic prediction. These innovations are facilitating simultaneous improvement in productivity, fertility, feed efficiency, disease resistance, animal welfare, and environmental sustainability. Moreover, genomic information is increasingly being integrated with genome editing technologies such as CRISPR to support precision breeding strategies. This review summarizes the historical evolution, fundamental principles, methodological developments, and practical applications of genomic selection in livestock breeding while highlighting emerging innovations and future research directions that are expected to shape next-generation animal improvement programs.

Keywords— Genomic selection; Genomic estimated breeding value; Genomic prediction; Single nucleotide polymorphism; Livestock breeding; Genomic BLUP; Animal genetics; GBLUP; ssGBLUP; Quantitative genetics; Marker-assisted selection; SNP; Heritability.

I. INTRODUCTION

Genetic improvement has long been one of the primary drivers of increased productivity, efficiency, and profitability in livestock production. Traditionally, breeding programs have relied on phenotypic performance records, pedigree information, and statistical methods such as Best Linear Unbiased Prediction (BLUP) to estimate breeding values. Although these approaches have generated substantial genetic progress over the past several decades, their effectiveness is constrained by long generation intervals, delayed availability of phenotypic records, and reduced prediction accuracy for traits with low heritability or those expressed late in life [1, 2].

The rapid development of molecular genetics and high-throughput genotyping technologies has fundamentally changed animal breeding strategies. The availability of dense genome-wide single nucleotide polymorphism (SNP) markers has enabled direct estimation of genomic relationships among individuals and facilitated prediction of breeding values based on DNA information

rather than pedigree alone [1, 3]. This strategy, known as genomic selection (GS), estimates the combined effects of thousands of markers distributed across the entire genome, thereby capturing the genetic architecture underlying complex quantitative traits.

Unlike conventional marker-assisted selection, which focuses on a limited number of significant quantitative trait loci (QTL), genomic selection simultaneously exploits information from all available genome-wide markers regardless of their individual statistical significance [1, 4]. This approach has markedly improved the accuracy of genomic estimated breeding values (GEBVs), particularly for young selection candidates without phenotypic records, enabling earlier and more reliable selection decisions [2, 5].

The widespread adoption of genomic selection in dairy cattle since 2008 has demonstrated remarkable increases in annual genetic gain, reduced breeding costs, and shortened generation intervals. Similar advances are now being realized in beef cattle, sheep, goats, swine, poultry, and aquaculture species through continued improvements in genomic resources, computational methodologies, and sequencing technologies [3, 6–8]. Consequently, genomic selection has become one of the most influential innovations in modern quantitative genetics and animal breeding, laying the foundation for sustainable and precision livestock improvement.

II. EVOLUTION OF GENOMIC SELECTION

The evolution of animal breeding has been characterized by continuous advances in quantitative genetics, statistical methodologies, and molecular biology. For much of the twentieth century, selection decisions were based primarily on observable phenotypes and pedigree records. The introduction of Best Linear Unbiased Prediction (BLUP) in the 1970s revolutionized genetic evaluation by integrating pedigree and performance information to estimate breeding values with greater accuracy. Although conventional BLUP substantially improved selection efficiency, it remained dependent on extensive phenotypic recording and accurate pedigree information, limiting genetic progress for traits expressed late in life, those with low heritability, or traits difficult or expensive to measure [1, 3].

The rapid development of molecular genetics during the 1990s generated considerable enthusiasm for marker-assisted selection (MAS), which aimed to improve breeding efficiency by identifying quantitative trait loci (QTL) associated with economically important traits. While several major genes with large effects were successfully identified, MAS generally failed to achieve widespread implementation because most economically important traits, including milk yield, growth rate, fertility, and disease resistance, are polygenic and controlled by numerous loci with individually small effects. Consequently, only a small proportion of the total genetic variance could be explained by significant QTL, limiting the overall effectiveness of MAS in commercial breeding programs [9].

A major breakthrough occurred when Meuwissen, Hayes, and Goddard proposed the concept of genomic selection (GS) in 2001. Rather than identifying only statistically significant markers, genomic selection assumes that all markers distributed across the genome contribute to the prediction of genetic merit. Dense genome-wide single nucleotide polymorphism (SNP) markers are used simultaneously to estimate marker effects, enabling the calculation of Genomic Estimated Breeding Values (GEBVs) without requiring prior knowledge of the causal mutations [1]. This paradigm shift fundamentally changed livestock breeding by exploiting linkage disequilibrium between markers and quantitative trait loci throughout the genome.

The practical implementation of genomic selection became feasible following several technological advances. High-density SNP genotyping arrays, such as the bovine 50K SNP chip introduced in 2008, enabled rapid and cost-effective genome-wide genotyping of thousands of animals [10]. Simultaneously, improvements in computational algorithms and mixed-model methodologies facilitated efficient estimation of genomic breeding values in large breeding populations [5]. As a result, genomic selection was rapidly adopted in dairy cattle breeding programs across North America, Europe, Australia, and New Zealand, where it substantially reduced generation intervals while improving prediction accuracy and annual rates of genetic gain [3, 11].

Since its successful implementation in dairy cattle, genomic selection has expanded to beef cattle, sheep, goats, pigs, poultry, and aquaculture species. Continuous improvements in sequencing technologies, genotype imputation, whole-genome sequence data, and large international reference populations have further enhanced prediction accuracy and broadened the scope of genomic applications across livestock species [4, 6].

III. PRINCIPLES OF GENOMIC SELECTION

Genomic selection is founded on the principle that dense genome-wide molecular markers capture the majority of genetic variation influencing complex quantitative traits. Unlike traditional pedigree-based evaluations, genomic selection estimates realized genomic relationships among individuals using thousands of SNP markers, thereby providing a more accurate representation of shared genetic inheritance [1, 5].

A genomic selection program begins with the establishment of a reference (training) population, consisting of animals possessing both reliable phenotypic records and genome-wide SNP genotypes. Statistical models are developed using this population to estimate the effects of individual markers distributed throughout the genome. These estimated marker effects are subsequently applied to a validation or candidate population, where animals are genotyped but may not yet possess phenotypic records. The resulting Genomic Estimated Breeding Values (GEBVs) enable selection decisions at an early age, substantially shortening the generation interval and increasing the rate of genetic improvement [1, 4].

The accuracy of genomic prediction depends on several interrelated factors, including the size and quality of the reference population, marker density, the extent of linkage disequilibrium (LD) between markers and causal variants, trait heritability, and the statistical prediction model employed [5, 6]. Linkage disequilibrium refers to the non-random association of alleles at different loci, which allows markers to serve as proxies for nearby causal variants. Dense SNP coverage ensures that virtually every quantitative trait locus is in LD with one or more markers, allowing the cumulative effects of thousands of loci to be incorporated into genomic evaluations. Consequently, genomic selection is particularly effective for complex traits controlled by many genes of small additive effect, where conventional marker-assisted selection performs poorly.

Compared with pedigree-based BLUP, genomic selection captures Mendelian sampling variation among full siblings, allowing genetically superior individuals to be identified before phenotypic performance becomes available. This improvement has significantly increased selection intensity while reducing breeding costs associated with progeny testing. Modern genomic evaluation systems now combine pedigree, phenotypic, and genomic information within unified statistical frameworks, providing more reliable genetic evaluations across diverse livestock populations and production systems [3, 11].

IV. GENOMIC SELECTION METHODOLOGY

Genomic selection (GS) integrates genome-wide molecular information with quantitative genetic models to predict the genetic merit of animals. Unlike conventional pedigree-based evaluations, GS uses thousands of single nucleotide polymorphism (SNP) markers distributed across the genome to estimate Genomic Estimated Breeding Values (GEBVs). The methodology begins with the establishment of a reference (training) population, comprising animals with both reliable phenotypic records and dense SNP genotypes. Marker effects estimated from this population are subsequently used to predict GEBVs for validation or candidate populations, which generally possess genotype data but limited or no phenotypic information [1, 5].

A prerequisite for successful genomic prediction is the presence of linkage disequilibrium (LD) between SNP markers and the underlying quantitative trait loci (QTL). Dense marker panels ensure that most causal variants are associated with nearby markers, allowing statistical models to capture the cumulative effects of thousands of loci influencing complex quantitative traits [12]. Prediction accuracy is determined by several factors, including the size and genetic diversity of the reference population, marker density, trait heritability, genetic relationships between training and validation populations, and the statistical model employed [13].

Several statistical approaches have been developed for genomic prediction. Genomic Best Linear Unbiased Prediction (GBLUP) replaces the pedigree-based relationship matrix with a genomic relationship matrix (G) constructed from SNP genotypes, thereby estimating realized genomic relationships among individuals [11]. Because GBLUP assumes equal variance across marker effects, it is computationally efficient and has become the standard method in many livestock breeding programs. An important advancement is the single-step GBLUP (ssGBLUP) methodology, which combines pedigree, phenotypic, and genomic information into a unified evaluation system through the H matrix, enabling simultaneous evaluation of genotyped and non-genotyped animals without bias [14].

Bayesian genomic prediction methods—including BayesA, BayesB, BayesC π , and Bayesian LASSO—allow heterogeneous marker variances and are particularly useful when a limited number of loci exert relatively large effects. These methods improve prediction accuracy for certain economically important traits but require greater computational resources than GBLUP [15, 16]. More recently, machine learning and deep learning algorithms have emerged as complementary tools capable of

modeling nonlinear interactions, dominance effects, epistasis, and high-dimensional genomic datasets, particularly when integrated with whole-genome sequence information and other omics data [17].

TABLE 1
COMPARISON OF GENOMIC PREDICTION METHODS

Method	Key Feature	Advantages	Limitations
GBLUP	Equal variance across markers	Computationally efficient	Assumes equal marker effects
ssGBLUP	Combines pedigree + genomic info	Unified evaluation of genotyped and non-genotyped animals	Requires accurate pedigree
BayesA	Heterogeneous variances	Captures large effects	Computationally intensive
BayesB	Mixture model with some zero effects	Better for traits with few QTL	Complex implementation
BayesC π	Variable selection approach	Flexible model	Requires tuning
Bayesian LASSO	Shrinkage estimation	Handles many markers	Computationally demanding
Machine Learning	Nonlinear interactions	Models epistasis and dominance	Requires large datasets

Advances in genotype imputation, whole-genome sequencing, transcriptomics, metabolomics, and functional genomics are further enhancing the biological interpretation and predictive performance of genomic evaluations. These developments are expected to improve the identification of causal variants while supporting more precise selection strategies for complex traits associated with productivity, health, fertility, resilience, and environmental sustainability [8].

V. APPLICATIONS OF GENOMIC SELECTION

5.1 Dairy Cattle

Dairy cattle breeding represents the most successful application of genomic selection. The introduction of genomic evaluations around 2008 revolutionized sire selection by allowing accurate prediction of breeding values shortly after birth, thereby replacing lengthy and expensive progeny-testing programs [11]. The reduction in generation interval from approximately five years to less than two years has nearly doubled the annual rate of genetic gain for economically important traits, including milk yield, milk composition, fertility, longevity, feed efficiency, and disease resistance [8]. Contemporary dairy breeding programs increasingly employ single-step GBLUP, large multinational reference populations, and whole-genome sequence data to improve prediction accuracy further while supporting selection for methane reduction, heat tolerance, and improved animal welfare.

5.2 Beef Cattle

The adoption of genomic selection in beef cattle has accelerated genetic improvement for growth rate, carcass quality, feed efficiency, fertility, calving ease, and disease resistance. Beef breeding often involves multiple breeds with smaller reference populations than dairy cattle, creating additional challenges for prediction accuracy. Nevertheless, genomic information substantially improves selection decisions, particularly for young bulls and replacement females lacking progeny records. International collaborations and breed-specific genomic reference populations continue to enhance genomic prediction across commercial beef production systems [18].

5.3 Sheep and Goats

Genomic selection has become increasingly valuable in sheep and goat breeding, particularly for traits that are difficult, expensive, or impossible to measure directly on selection candidates. These include resistance to gastrointestinal parasites, milk production, reproductive efficiency, wool quality, growth performance, and adaptation to harsh production environments. Although relatively small population sizes and limited phenotypic recording have slowed implementation compared with dairy cattle, declining genotyping costs and international reference populations are expanding genomic breeding programs in small

ruminants. Genomic evaluations are also facilitating conservation and genetic improvement of indigenous breeds possessing valuable adaptive characteristics [8].

5.4 Swine

Commercial swine breeding has rapidly incorporated genomic selection into nucleus breeding programs. Genomic evaluations improve prediction accuracy for growth performance, feed conversion efficiency, carcass composition, reproductive performance, robustness, and disease resistance while reducing generation intervals. Because pigs produce large family sizes and have relatively short reproductive cycles, genomic selection enables rapid dissemination of superior genetics throughout commercial production systems. Integration of genomic prediction with reproductive technologies further accelerates cumulative genetic gain [15].

5.5 Poultry

The poultry industry has widely adopted genomic selection to improve egg production, egg quality, growth rate, feed efficiency, carcass yield, skeletal health, immune competence, and resistance to infectious diseases. Poultry breeding programs generate extensive pedigree and phenotypic datasets, making them highly suitable for genomic prediction. Genomic information also enables selection for sex-limited traits and traits expressed late in life, which are difficult to evaluate using conventional breeding approaches. Emerging applications integrating genomic selection with precision livestock farming, sensor technologies, artificial intelligence, and genome editing are expected to further enhance sustainable poultry production under changing environmental conditions [19].

5.6 Aquaculture

Genomic selection is increasingly being applied in aquaculture species, including Atlantic salmon, rainbow trout, tilapia, and shrimp. In Atlantic salmon, genomic selection has been used to improve growth rate, disease resistance (particularly against infectious pancreatic necrosis and sea lice), and flesh quality traits. In rainbow trout, genomic prediction has been applied to enhance resistance to bacterial cold-water disease and improve fillet yield. In tilapia, genomic selection is being explored for growth performance and salinity tolerance. Shrimp breeding programs are increasingly incorporating genomic information to select for resistance to white spot syndrome virus and other pathogens. Although reference populations in aquaculture are generally smaller than in terrestrial livestock, declining genotyping costs and the development of species-specific SNP arrays are accelerating the adoption of genomic selection in this sector [8, 20].

TABLE 2
APPLICATIONS OF GENOMIC SELECTION ACROSS LIVESTOCK SPECIES

Species	Key Traits Improved	Reference Population Size	Adoption Status
Dairy Cattle	Milk yield, composition, fertility, longevity, feed efficiency	Large (10,000+)	Widely adopted
Beef Cattle	Growth rate, carcass quality, feed efficiency, fertility	Moderate to large	Increasing adoption
Sheep and Goats	Parasite resistance, milk production, wool quality, growth	Small to moderate	Emerging
Swine	Growth, feed conversion, carcass composition, reproduction	Large	Widely adopted
Poultry	Egg production, growth, feed efficiency, carcass yield	Large	Widely adopted
Aquaculture	Growth, disease resistance, flesh quality	Small to moderate	Emerging

VI. ADVANTAGES OF GENOMIC SELECTION

Genomic selection (GS) has fundamentally transformed livestock improvement by enabling the estimation of genetic merit directly from genome-wide marker information. Compared with conventional pedigree-based Best Linear Unbiased Prediction (BLUP), GS substantially increases the accuracy of breeding value estimation, particularly for young animals lacking phenotypic records or progeny information [3]. The ability to identify genetically superior individuals shortly after birth considerably shortens the generation interval, thereby accelerating annual rates of genetic gain.

One of the greatest advantages of GS is its effectiveness for complex quantitative traits controlled by numerous genes of small effect. Unlike marker-assisted selection (MAS), which targets only a limited number of major quantitative trait loci (QTL), GS simultaneously utilizes information from thousands of single nucleotide polymorphisms (SNPs) distributed throughout the genome. Consequently, genomic prediction captures a much larger proportion of additive genetic variance, resulting in more reliable Genomic Estimated Breeding Values (GEBVs) for economically important traits [9].

Genomic selection has also broadened breeding objectives beyond productivity alone. Modern breeding programs increasingly incorporate fertility, longevity, feed efficiency, disease resistance, heat tolerance, methane emission, resilience, and animal welfare into genomic evaluations. These traits are often difficult or expensive to measure using conventional breeding methods but become more amenable to improvement through genomic prediction. Furthermore, the adoption of single-step GBLUP, genotype imputation, and international reference populations has enhanced prediction accuracy while reducing implementation costs, allowing genomic selection to be extended to multiple livestock species [14].

Economic benefits include reduced expenditure on progeny testing, faster dissemination of superior genetics, and greater efficiency of breeding programs. In dairy cattle, genomic selection has nearly doubled the annual rate of genetic improvement while reducing generation intervals from approximately five years to less than two years. Similar benefits are increasingly being realized in beef cattle, sheep, goats, pigs, poultry, and aquaculture species [8].

VII. CHALLENGES AND LIMITATIONS

Despite its considerable advantages, genomic selection faces several biological, computational, and economic challenges. The accuracy of genomic prediction depends heavily on the size, quality, and genetic diversity of the reference population. Small or poorly characterized reference populations often produce lower prediction accuracy, particularly for low-heritability traits or across genetically distant breeds [4].

Prediction accuracy also declines when genomic evaluations are applied across populations with different linkage disequilibrium structures or allele frequencies. Consequently, many breeding programs require breed-specific reference populations, increasing both logistical complexity and cost. In developing countries, limited infrastructure, insufficient phenotypic recording systems, and the high cost of large-scale genotyping remain major barriers to widespread implementation [7].

Another important limitation involves the use of dense SNP panels, which primarily capture linkage disequilibrium with causal variants rather than the causal mutations themselves. Recombination over successive generations gradually weakens marker–QTL associations, requiring periodic updating of reference populations and re-estimation of marker effects. In addition, conventional genomic prediction models predominantly estimate additive genetic effects, whereas dominance, epistasis, genotype-by-environment interactions, and epigenetic influences remain incompletely characterized [11].

The growing availability of whole-genome sequence data presents both opportunities and challenges. Although sequence information may improve identification of causal variants, it substantially increases computational demands, data storage requirements, and statistical complexity. Efficient integration of high-dimensional genomic datasets with transcriptomic, proteomic, metabolomic, and phenomic information remains an active area of research [19].

Ethical and societal considerations also merit attention. The increasing use of genomic information in breeding decisions raises questions about data privacy, intellectual property, and the potential for reduced genetic diversity in breeding populations. Balancing the benefits of genomic selection with ethical considerations will be important for sustainable implementation [20].

VIII. FUTURE PERSPECTIVES

Future developments in genomic selection will increasingly integrate whole-genome sequencing, functional genomics, and multi-omics technologies to improve the biological interpretation of genomic predictions and enhance the identification of causal variants. Rather than relying solely on linkage disequilibrium between markers and quantitative trait loci, future genomic evaluations are expected to incorporate transcriptomic, epigenomic, metabolomic, and proteomic information into unified predictive models [17].

Artificial intelligence (AI), machine learning, and deep learning algorithms are emerging as powerful tools for analyzing complex genomic datasets and modeling nonlinear genetic interactions that are not adequately captured by traditional statistical approaches. Simultaneously, precision livestock farming technologies—including automated sensors, wearable devices,

computer vision, and real-time health monitoring systems—will generate high-quality phenotypic data that can be integrated with genomic information to improve prediction accuracy and accelerate genetic progress.

Another promising direction involves combining genomic selection with CRISPR/Cas-mediated genome editing, enabling the identification and precise modification of favorable alleles associated with disease resistance, feed efficiency, climate resilience, and product quality. Although ethical, regulatory, and societal considerations remain important, the integration of genome editing with genomic selection has the potential to accelerate sustainable livestock improvement [20].

Global breeding objectives are also shifting toward sustainability. Future breeding programs will increasingly emphasize reduced greenhouse gas emissions, improved nitrogen utilization, enhanced resilience to climate change, improved animal welfare, antimicrobial resistance, and adaptation to emerging diseases. International collaboration, open genomic databases, and expanding multinational reference populations are expected to improve prediction accuracy across breeds and production environments while making genomic technologies more accessible worldwide [6].

IX. CONCLUSION

Genomic selection represents one of the most significant innovations in modern animal breeding, fundamentally transforming genetic evaluation through the use of genome-wide molecular information. By combining dense SNP genotyping with advanced statistical prediction models, genomic selection has substantially improved the accuracy of breeding value estimation, accelerated genetic gain, and reduced generation intervals across livestock species. Its successful implementation in dairy cattle has stimulated rapid adoption in beef cattle, sheep, goats, swine, poultry, and aquaculture, where continued improvements in genotyping technologies and computational methodologies are expanding its practical applications.

Recent advances such as single-step GBLUP, Bayesian genomic prediction, whole-genome sequencing, multi-omics integration, artificial intelligence, and precision livestock farming are further enhancing the efficiency and scope of genomic selection. Nevertheless, challenges related to reference population size, computational demands, across-breed prediction, and implementation costs remain important considerations. Continued international collaboration, improved phenotypic recording, and integration of functional genomics with genome editing technologies are expected to further strengthen genomic breeding programs. Consequently, genomic selection will remain a central component of sustainable livestock improvement, supporting increased productivity, improved animal health and welfare, enhanced environmental resilience, and long-term global food security.

CONFLICT OF INTEREST

The authors declare no conflict of interest.

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