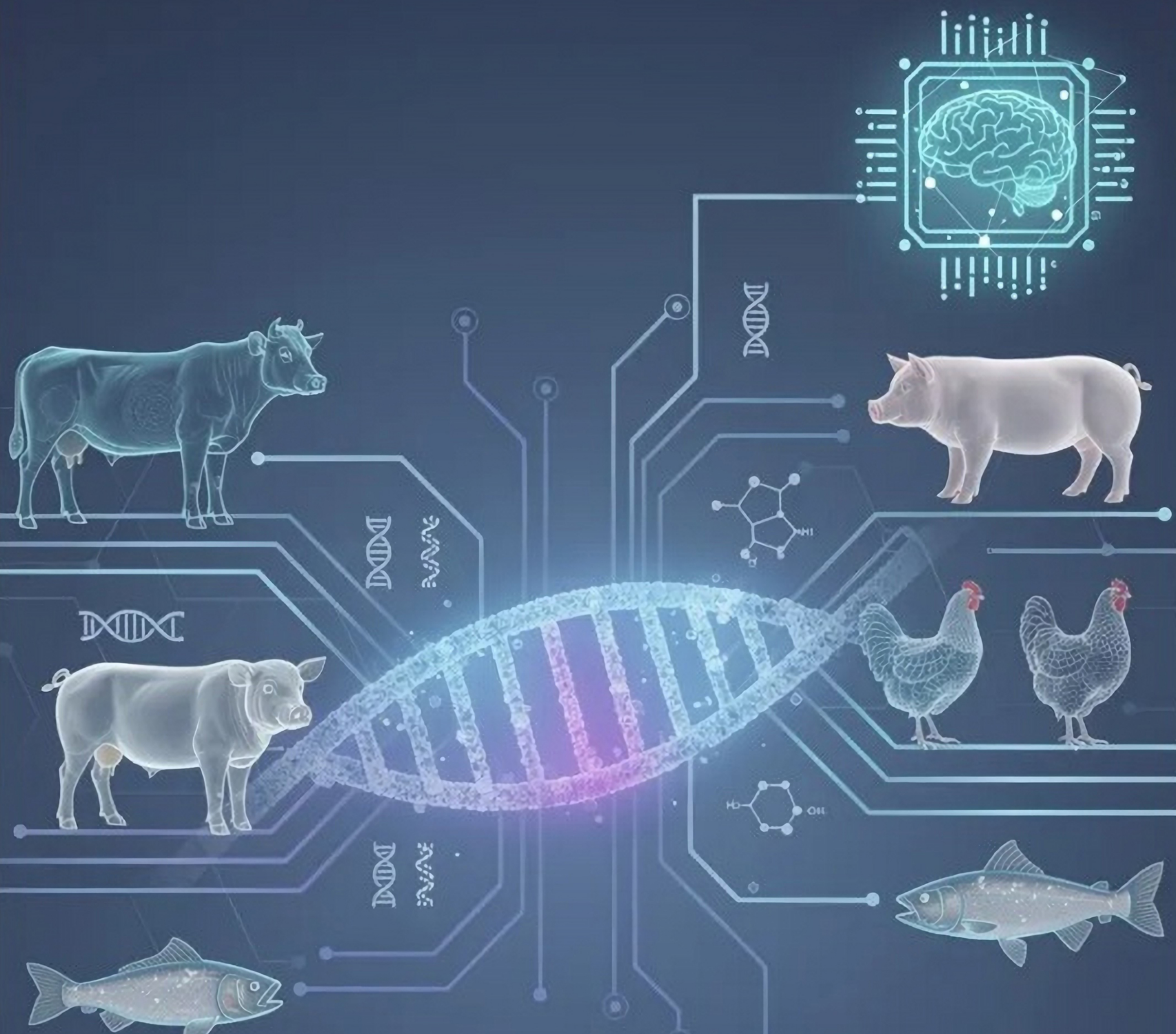

GENOMIC SELECTION IN LIVESTOCK AND AQUACULTURE:

INTEGRATION OF MULTI-OMICS AND ARTIFICIAL INTELLIGENCE

Raziye IŞIK KALPAR

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Raziye IŞIK KALPAR[1]

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1. INTRODUCTION

Genomic selection (GS) has rapidly emerged as a pivotal field within contemporary livestock genomics, becoming an essential component of animal breeding strategies over the past two decades. Following the seminal work of Meuwissen, Hayes, and Goddard (2001), which introduced prediction models utilizing all genome-wide markers simultaneously, many limitations inherent in classical selection methods were effectively addressed. With the widespread adoption of high-density SNP panels, this innovative approach became routine in the dairy cattle industry beginning in 2008 and subsequently expanded to the swine, poultry, and small ruminant sectors (Goddard & Hayes, 2009). Today, genomic selection has evolved beyond a genotype-based tool; it has transformed into a multidimensional selection platform supported by multi-omics integration, artificial intelligence, big data analytics, sensor technologies, disease-resistance genomics, and climate-adaptation research.

Given the intricate genetic architecture underlying economically significant traits, the majority of phenotypic variation in livestock can be attributed to the aggregate effects of numerous loci, each contributing minimally (Hill, Goddard & Visscher, 2008). Consequently, genomic selection (GS) offers considerable advantages over traditional marker-assisted selection (MAS), particularly for polygenic traits. For example, genomic data has been demonstrated to enhance prediction accuracy by 20–50% for traits with low heritability, such as milk yield, reproductive performance, health traits, resilience, and behavior (VanRaden et al., 2009). This improvement not only increases the reliability of genomic estimated breeding values (GEBVs) but also fundamentally transforms breeding programs—most notably by obviating the necessity for progeny testing in dairy bulls.

The increasing complexity of livestock genomics in recent years can be largely attributed to the rapid advancement of multi-omics technologies. Beyond genotypic data, the integration of transcriptomic (RNA-seq), epigenomic (DNA methylation and histone modifications), metagenomic (rumen microbiome), proteomic, and metabolomic datasets into genomic prediction models facilitates a more comprehensive understanding of the molecular mechanisms underlying animal performance (Kadarmideen, 2014). This multi-layered approach presents new opportunities for predicting complex phenotypes, including disease resistance, environmental stress tolerance, feed efficiency, and adaptive capacity.

Concurrently, the swift advancement of artificial intelligence (AI) and machine learning (ML) has significantly augmented the predictive capabilities of genomic selection models. Beyond traditional GBLUP and Bayesian methodologies, algorithms such as random forests, gradient boosting, support vector machines, and multilayer neural networks are increasingly implemented in livestock breeding programs (Gianola & Rosa, 2015). Notably, deep learning models leverage the hierarchical architecture of neural networks to discern intricate, high-dimensional genomic patterns, resulting in marked enhancements in prediction accuracy (Montesinos-López et al., 2018). Given the heterogeneous nature of multi-omics data, deep learning-based data-fusion frameworks have emerged as a pivotal area of research.

Another notable advancement in genomic selection (GS) is the widespread adoption of digital phenotyping and sensor-based data collection systems. The rapid integration of Internet of Things (IoT)-enabled technologies into modern agricultural practices facilitates high-frequency phenotypic measurements, thereby improving the precision of environmental variation modeling (Halachmi, 2019). As a result, genomic prediction models can more accurately account for both genetic and environmental sources of variation. Genomic selection also has significant economic and social implications. Substantial evidence suggests that genomic evaluation provides considerable economic benefits in large commercial herds by enhancing fertility, herd health, and feed efficiency, ultimately reducing production costs (Schaeffer, 2006). However, the ethical and socio-economic aspects of GS require careful consideration. Issues such as technology access for small-scale farmers, preservation of local breeds, long-term genetic diversity, and data privacy necessitate thorough examination (Fraser, 2019). In this context, genomic selection should be regarded not merely as a breeding tool but as a multidimensional ecosystem encompassing data science, artificial intelligence, molecular biology, systems biology, and ethical frameworks. This book chapter aims to comprehensively evaluate all components of this evolving ecosystem.

2. HISTORICAL DEVELOPMENT OF GENOMIC SELECTION

The development of genomic selection has been a transformative journey shaped by decades of scientific progress and technological innovation. Initially, breeding programs relied heavily on phenotypic and pedigree-based selection, where observable traits and family lineage were the primary criteria for selecting superior individuals. This traditional approach, while foundational, was limited by its dependence on visible characteristics and the slow pace of genetic gain. The subsequent introduction of Marker-Assisted Selection (MAS) marked a significant advancement by enabling breeders to use molecular markers linked to desirable traits, thereby improving selection accuracy and efficiency. However, MAS was constrained by the limited number of markers and the complexity of polygenic traits, which often involve many genes with small effects.

The emergence of genomic selection revolutionized breeding by leveraging dense genome-wide markers to predict the genetic potential of individuals more comprehensively. This approach allowed for the capture of the cumulative effects of numerous loci, enhancing prediction accuracy and accelerating breeding cycles. In the modern era, genomic selection has evolved further through the integration of artificial intelligence (AI) and multi-omics data, including genomics, transcriptomics, proteomics, and metabolomics. These advancements enable the analysis of complex biological interactions and environmental influences on traits, supported by big data analytics and machine learning algorithms. Together, these innovations have culminated in highly sophisticated breeding systems that optimize genetic improvement with unprecedented precision and speed.

This section reviews the historical evolution of genomic selection in four major phases:

(1) phenotypic and pedigree-based selection, (2) Marker-Assisted Selection (MAS), (3) the emergence of genomic selection, and (4) the modern era characterized by artificial intelligence and multi-omics integration.

2.1. Phenotype and Pedigree-Based Selection (1930–1990)

Between 1930 and 1960, the field of animal breeding predominantly relied on phenotypic measurements, with selection processes based on the comparison of individual performance records. However, substantial environmental variation posed significant constraints on genetic advancement. A pivotal development during this period was the introduction of the Best Linear Unbiased Prediction (BLUP) methodology by Henderson in the 1970s (Henderson, 1975). BLUP enhanced prediction accuracy by incorporating both pedigree and phenotypic data, rapidly establishing itself as the standard method in livestock breeding.

The phenotype and pedigree-based selection method possesses several advantages, including operational simplicity, a well-established statistical framework, and the standardization of progeny testing in dairy cattle. Nevertheless, this approach also exhibits certain limitations, such as extended generation intervals (e.g., 5–6 years required for bull daughter performance testing), diminished accuracy for traits with low heritability, and susceptibility to errors in pedigree recording. These limitations underscore the necessity for molecular tools that can provide additional genetic information beyond what is available from pedigree data.

2.2. Marker-Assisted Selection (QTL and MAS Era, 1990–2005)

Since the early 1990s, the extensive application of microsatellite markers and quantitative trait loci (QTL) mapping techniques marked the advent of the Marker-Assisted Selection (MAS) era. MAS has achieved significant success in traits governed by major genes, particularly those associated with disease resistance (Dekkers, 2012). Notable examples include: the DGAT1 K232A mutation linked to milk fat percentage, MSTN (myostatin) mutations affecting muscle development in cattle and sheep, and PRLR (prolactin receptor) variants related to milk production. However, despite these achievements, MAS has proven inadequate for addressing complex traits controlled by hundreds or thousands of loci with minor effects (Goddard & Hayes, 2009).

The limitations of Marker-Assisted Selection (MAS) include the inability to identify effective Quantitative Trait Loci (QTLs) for all traits, low prediction accuracy for polygenic traits, and a significant portion of genetic variance remaining unexplained. These shortcomings have led to the development of approaches capable of simultaneously evaluating the entire genome.

2.3. Genomic Selection (2001–2010): A Paradigm Shift

The pivotal advancement in genomic selection was marked by the work of Meuwissen, Hayes, and Goddard (2001), who introduced prediction models utilizing genome-wide marker information. This innovation facilitated the concurrent estimation of effects for thousands of markers, each presumed to exert a minor influence. Core components of genomic selection include a genotyped reference population, high-quality phenotypic data, and a statistical prediction model (e.g., GBLUP, BayesA/B/C), culminating in the Genomic Estimated Breeding Value (GEBV). The most transformative benefit of genomic selection was the substantial reduction in the generation interval. For instance, in dairy cattle, breeding values could be estimated without the necessity of waiting for daughters' performance data (VanRaden, 2008).

2008–2012: Initial Large-Scale Commercial Implementations

The formal adoption of genomic evaluations within the North American Holstein population (VanRaden et al., 2009) marked a significant advancement. Concurrently, the initiation of genomic data sharing among European countries was facilitated through Interbull. Additionally, genomic testing was adopted by swine, poultry, and sheep breeding companies. This period was catalyzed by the decreasing cost of genotyping, with medium-density panels such as the BovineSNP50 becoming central tools for routine genomic selection.

2010–2015: Growth of big data and new prediction models

The development of high-density SNP panels (HD 700K), improvements in imputation accuracy, and the introduction of single-step GBLUP (ssGBLUP) (Legarra et al., 2014), alongside the widespread use of low-density panels for cost-effective genotyping, have collectively facilitated the establishment of genomic selection as a standard practice in large commercial breeding programs.

2.4. Whole-Genome Sequencing and the Omics Era (2015–2023)

Following 2015, the field of livestock genomics experienced significant advancements due to the increased accessibility of whole-genome sequencing (WGS) data. The contributions of WGS to genomic selection include the identification of rare variants, the characterization of regulatory region variation, the incorporation of structural variants (SVs) into prediction models, and the enhanced resolution of linkage disequilibrium (LD) blocks. Notably, the 1000 Bull Genomes Project has become a global benchmark for bovine genomics (Hayes & Daetwyler, 2019). During this period, additional omics layers—such as transcriptomics, methylomics, proteomics, and metagenomics—were also integrated into prediction frameworks.

2.5. Artificial Intelligence, Multi-Omics, and Digital Phenotyping (2020–Present)

Since 2020, genomic selection has advanced significantly beyond SNP-based models. Contemporary breeding programs now incorporate deep learning algorithms, multi-omics data fusion approaches, sensor-based real-time phenotyping, rumen microbiome profiling, and environmental data alongside G×E modeling. Deep learning methodologies (Montesinos-López et al., 2021) facilitate the identification of nonlinear interactions and intricate genomic patterns. Concurrently, sensor technologies (IoT) provide high-frequency measurements of behavior, feed intake, activity, and physiological status, thereby enhancing genomic prediction models (Halachmi et al., 2020).

2.6. Historical Overview and Emerging Trends

Genomic selection has become a pivotal component of livestock breeding, primarily due to its capacity to achieve high prediction accuracy, shorten generation intervals, reduce phenotyping costs, and integrate diverse biological data layers. The historical progression of genomic selection clearly illustrates its ability to transcend the limitations inherent in classical genetic evaluation. Over the next decade, significant advancements are anticipated, driven by AI-enhanced prediction systems, multi-omics data fusion, and autonomous phenotyping technologies.

3. GENETIC ARCHITECTURE AND GENOMIC DATA STRUCTURES

Achieving success in livestock genomic selection is contingent upon the precise characterization of the genetic architecture of traits that hold economic significance. Genetic architecture refers to the number of contributing loci, effect sizes, allele frequencies, interactions such as epistasis, and the genomic distribution of causal variants (Mackay, 2001). As contemporary genomic prediction models strive to encapsulate this complexity, the type, density, and quality of input data have a direct impact on prediction accuracy. This section provides a systematic review of the genetic basis of complex traits, genomic data sources, marker technologies, variant types, linkage disequilibrium (LD) patterns, and the contributions of modern sequencing technologies to selection models.

3.1. Genetic Architecture of Complex Traits

Numerous economically significant traits in livestock, such as milk yield, growth rate, feed efficiency, fertility, and disease resistance, are polygenic in nature. This means that these traits are controlled by the combined influence of hundreds or even thousands of genetic loci, each contributing a relatively small effect rather than a single gene having a major impact (Hill et al., 2008). The polygenic architecture of these traits results in continuous variation within populations, making their genetic improvement more complex compared to traits governed by single genes. Understanding the polygenic basis is essential for implementing effective breeding strategies, such as genomic selection, which leverages information from numerous genetic markers across the genome to predict an animal's genetic merit. This approach enables more accurate selection decisions, accelerating genetic progress for these complex traits in livestock populations.

Genetic architecture encompasses several critical components that collectively influence the heritability and expression of complex traits. The effect size distribution highlights that most genes contribute small effects, consistent with the infinitesimal model originally proposed by Fisher (1918), which underpins many regression-based genomic prediction methods like GBLUP. This model assumes an essentially infinite number of loci, each with minuscule effects, facilitating the prediction of phenotypes based on additive genetic variance. However, while rare variants can have larger individual effects, their overall impact on prediction accuracy tends to be limited due to their low frequency in reference populations, as noted by Goddard et al. (2010).

Beyond additive effects, dominance and epistatic interactions play important roles, particularly in traits related to fitness and health (Varona et al., 2018). Although additive variance generally explains the bulk of phenotypic variance, these nonlinear genetic interactions can influence trait expression in complex ways. Advanced nonlinear models, such as deep learning approaches, are better suited to capture these complexities. Additionally, variants within functional genomic regions—such as promoters, enhancers, and miRNA binding sites—affect gene regulation and expression. Incorporating functional annotations into predictive models has been shown to improve accuracy by prioritizing biologically relevant variants (Zhang et al., 2021), thereby enhancing the understanding and prediction of genetic contributions to complex traits.

3.2. Genomic Data Sources and SNP Technologies

The cornerstone of genomic selection is the utilization of SNP marker data, although the discovery of variants through sequencing methods is becoming increasingly prevalent. Due to their low cost and high accuracy, SNP chips have become the standard in livestock genomics since 2008 (Matukumalli et al., 2009)(Table 1).

Table 1. Common SNP panel densities

Panel Type	**Density**	**Application**
Low density (LD)	3K–20K	Inexpensive genotyping + imputation
Medium density (MD)	35K–80K	Standard for cattle, sheep, swine
High density (HD)	600K–900K	High resolution, improved LD estimation
WGS	20–30 million SNPs	Research, rare variant detection

The use of SNP chips in genetic studies provides several significant benefits that make them a popular choice for genotyping. Their low cost enables large-scale studies to be conducted more affordably, while the low error rate ensures reliable and reproducible data. Additionally, SNP chips are highly effective for cross-population comparisons because they target common variants shared across diverse groups. This broad applicability is further enhanced by imputation techniques, which increase marker density and resolution, allowing researchers to infer genotypes at untyped loci and thus achieve finer-scale genetic mapping without the need for more expensive sequencing.

Despite these advantages, SNP chips have important limitations that restrict their utility in certain contexts. The panels are primarily designed to capture common variants, which means they provide limited information on rare or population-specific alleles, particularly in indigenous or underrepresented breeds. This bias reduces their effectiveness in studies aiming to understand genetic diversity in such populations. Moreover, SNP chips do not detect structural variations (SVs) such as insertions, deletions, or copy number variations, which can have substantial functional impacts. Consequently, while SNP chips are valuable for many applications, complementary approaches like whole-genome sequencing may be necessary to capture the full spectrum of genetic variation, especially in diverse or less-studied populations.

3.3. Whole-Genome Sequencing (WGS)

WGS technologies allow comprehensive characterization of genomic variation (Daetwyler et al., 2012), capturing rare variants, regulatory mutations, and structural variants that SNP chips cannot detect.

Contributions of WGS

- Detection of rare variants
- High-accuracy imputation reference panels
- Identification of functional mutations (e.g., in enhancers, promoters, intronic regulatory regions)
- Structural variant (SV) analysis, including CNVs, inversions, and translocations

3.4. Linkage Disequilibrium (LD) and Population Structure

LD refers to the nonrandom association of alleles at different loci and plays a central role in genomic selection success (Flint-Garcia et al., 2003).

Importance of LD

- Markers act as proxies for QTLs
- Determines required SNP panel density
- Longer LD in small populations allows cheaper genotyping

Species comparisons

- **Cattle:** long-range LD → 35K–50K panels are sufficient
- **Sheep and goats:** LD varies significantly among breeds
- **Chickens:** short LD → require dense SNP panels
- **Pigs:** high LD in commercial lines, lower in indigenous breeds
- **Salmon:** LD varies by strain → 50K panels often sufficient for GS, but some populations benefit from ≥100K density.

Population structure (e.g., breed differences) also influences prediction accuracy because LD patterns differ between breeds (Hayes et al., 2009).

3.5. Variant Types and Functional Annotations

Modern genomic analyses incorporate a diverse range of variant types:

- **SNPs (Single Nucleotide Polymorphisms)** – the core of genomic selection
- **Indels** – may alter gene transcription or translation
- **CNVs (Copy Number Variations)** – influence growth, immunity, and adaptation (Zhou et al., 2014)
- **Structural variants** – inversions, translocations, large deletions
- **Regulatory variants** – promoters, enhancers, miRNA-binding sites, CpG methylation regions

Incorporating functional annotations into models (e.g., BayesRC) improves prediction accuracy (Edwards et al., 2019).

3.6. Genomic Data Integration

Integrating multiple genomic data sources strengthens prediction models.

Major integration strategies

- **Imputation:** Enhancing low-density genotypes to high-density levels
- **Functional weighting:** Allocating greater prior weights to variants located in functional regions
- **Multi-omics fusion:** Integrating genotypes with RNA-seq, methylation, proteome, and metagenome data
- **Across-population analyses**: Augmenting accuracy through the utilization of shared reference populations

4. STATISTICAL AND MACHINE LEARNING MODELS IN GENOMIC SELECTION

Genomic selection relies heavily on advanced statistical frameworks that can manage high-dimensional genomic data, enabling the simultaneous evaluation of thousands to millions of markers across the genome. These models not only capture the direct associations between marker genotypes and phenotypic traits but also adjust for confounding factors such as population stratification and relatedness among individuals. Key considerations in model design include the extent of linkage disequilibrium (LD) within the population, which affects how well markers tag causal variants, as well as marker density and sample size, both of which influence the power and accuracy of predictions. Traditional linear mixed models, such as genomic best linear unbiased prediction (GBLUP), have been widely used due to their robustness and interpretability in capturing additive genetic effects (Sillanpää, 2010).

The integration of machine learning (ML) and deep learning techniques into genomic selection frameworks has introduced greater flexibility and improved predictive performance, especially for complex traits influenced by non-additive genetic architectures and gene-by-environment interactions. ML models, including random forests, support vector machines, and gradient boosting, can capture nonlinear relationships and interactions without explicit parametric assumptions. Deep learning approaches, such as convolutional neural networks and recurrent neural networks, further enhance the ability to model hierarchical and temporal genomic patterns by learning multi-layered feature representations directly from raw genotype data. These innovations have expanded the methodological repertoire for genomic prediction, enabling more accurate selection decisions and accelerating breeding programs across diverse species (Montesinos-López et al., 2021).

4.1. Classical Linear Models

Classical linear models in genomic prediction primarily utilize linear regression frameworks to estimate the effects of genetic markers on complex traits. These models assume that the relationship between marker genotypes and phenotypic values is additive, meaning that the total genetic effect is the sum of individual marker effects without considering interactions or dominance effects. This additive assumption simplifies the genetic architecture and allows for straightforward interpretation and computation, making these models computationally efficient and broadly applicable. Consequently, they have become foundational in animal breeding programs, particularly in major livestock species where additive genetic variance is a key driver of trait heritability (Azodi et al., 2019).

Despite their simplicity, classical linear models remain highly effective for many quantitative traits due to the predominance of additive genetic variance in livestock populations. They enable breeders to predict genomic breeding values by leveraging dense marker information, thus accelerating genetic gain through more accurate selection decisions. However, these models may have limitations in capturing non-additive genetic effects such as epistasis or dominance, which can be important for certain traits. Nonetheless, their robustness, ease of implementation, and proven success have sustained their widespread use in the genomic prediction landscape, often serving as a baseline for comparison with more complex nonlinear or machine learning approaches (Hay, 2024).

4.1.1. Genomic Best Linear Unbiased Prediction (GBLUP)

GBLUP is one of the most widely used models in genomic selection. It represents a genomic extension of the BLUP framework developed by Henderson (1975), incorporating a genomic relationship matrix (G-matrix) constructed from SNP marker data (VanRaden, 2008). GBLUP aligns with the infinitesimal model (Goddard et al., 2010), which assumes that many loci contribute small additive effects.

GBLUP (Genomic Best Linear Unbiased Prediction) is highly valued for its computational efficiency and ability to scale effectively with large datasets, making it particularly suitable for modern genomic selection programs where vast amounts of marker data are common. Its robust performance across a wide range of polygenic traits—those influenced by many genes each with small effects—has established GBLUP as the standard model in commercial breeding, where reliability and speed are critical for practical implementation (Karaman et al., 2018).

However, the model's assumption that all marker effects have equal variance can limit its predictive accuracy for traits governed by major quantitative trait loci (QTL) with large effects. This equal variance assumption means GBLUP may underperform when genetic architecture is dominated by a few loci with substantial influence, as it tends to distribute genetic variance uniformly across markers. Consequently, alternative models that allow for heterogeneous marker variances may be more appropriate in such cases to capture the true genetic signal more effectively (Tiezzi & Maltecca, 2015).

4.1.2. Single-Step Genomic BLUP (ssGBLUP)

The single-step Genomic Best Linear Unbiased Prediction (ssGBLUP) method represents an advanced approach in genetic evaluation by seamlessly integrating genomic, pedigree, and phenotypic data within a single analytical framework. This integration allows for more accurate estimation of breeding values by leveraging the complementary information contained in each data type. Unlike traditional BLUP, which relies solely on pedigree and phenotypic records, ssGBLUP incorporates dense marker information from genomic data, enhancing the precision of genetic evaluations especially for individuals without extensive phenotypic records (Vallejo et al., 2017).

By combining the strengths of BLUP and Genomic BLUP (GBLUP), ssGBLUP improves prediction accuracy and genetic gain in breeding programs. It achieves this by constructing a unified relationship matrix that blends pedigree-based relationships with genomic relationships, thereby capturing both the historical and realized genetic relationships among individuals. This unified approach simplifies the evaluation process, reduces bias, and enables the inclusion of genotyped and non-genotyped individuals simultaneously, making ssGBLUP a powerful tool for modern animal and plant breeding applications (Gowane et al., 2019).

4.2. Bayesian Models

Bayesian models are particularly advantageous in genomic selection due to their ability to accommodate heterogeneous marker effects by assigning distinct prior distributions to each marker. This flexibility allows them to effectively model genetic architectures where only a subset of markers has significant influence, capturing sparse effect patterns that traditional models may overlook. For instance, Bayes A assumes marker effects follow a t-distribution, which helps identify markers with large effects, while Bayes B posits that many markers have zero effect, making it suitable for traits governed by sparse genetic architectures. Bayes Cπ builds on Bayes B by introducing the π parameter, which explicitly defines the probability that a marker has no effect, further refining the model's capacity to represent genetic sparsity (Stock et al., 2020).

More advanced Bayesian approaches like Bayes R and BayesRC extend this framework by incorporating mixture distributions and functional genomic information, respectively. Bayes R uses a mixture of normal distributions with different variances to model varying effect sizes, providing greater flexibility for complex quantitative trait loci (QTL) architectures. BayesRC enhances this by integrating functional annotations into the prior distributions, such as assigning higher prior probabilities to single nucleotide polymorphisms (SNPs) located in coding or enhancer regions, or weighting markers based on population-specific biological relevance. This integration of functional genomic data represents a significant advancement, enabling more biologically informed genomic predictions and improving the accuracy of selection by leveraging prior knowledge about marker functionality (Macleod et al., 2016).

4.3. Sparsity and Regularization-Based Models

Sparsity and regularization-based models are essential tools in genomic prediction, particularly for handling high-dimensional data where the number of predictors exceeds the number of observations. LASSO (Least Absolute Shrinkage and Selection Operator) applies an L1 penalty, which induces sparsity by shrinking some marker effect estimates exactly to zero. This feature selection property makes LASSO especially useful for traits influenced by a few major quantitative trait loci (QTL), as it effectively identifies and retains only the most relevant markers, similar in principle to marker-assisted selection (MAS). In contrast, Ridge regression (also known as RRBLUP in genomic contexts) uses an L2 penalty that shrinks all marker effects towards zero uniformly without setting any coefficients exactly to zero. This approach is mathematically equivalent to genomic best linear unbiased prediction (GBLUP) and is more suitable for traits governed by many small-effect loci, as it retains all markers but controls overfitting by shrinking their effects (Meher et al., 2022).

The Elastic Net method integrates both L1 and L2 penalties, combining the strengths of LASSO and Ridge regression. By balancing variable selection and effect shrinkage, the Elastic Net can handle correlated predictors better than LASSO alone, which tends to arbitrarily select one marker from a group of correlated variables. This makes it particularly effective for polygenic traits where numerous loci with small to moderate effects contribute to the phenotype. The Elastic Net's flexibility allows it to perform robust variable selection while maintaining predictive accuracy, especially in complex genetic architectures where both sparsity and shrinkage are beneficial. This combination enhances model stability and interpretability, making the Elastic Net a valuable approach in genomic prediction frameworks (Waldron et al., 2011).

4.4. Machine Learning Models

Machine learning (ML) models have become increasingly popular in genomic prediction due to their ability to capture complex, nonlinear relationships and interactions among genetic markers that traditional linear models may overlook. Random Forests, for example, leverage an ensemble of decision trees to model epistatic effects naturally and provide robust variable importance measures, which help identify key markers influencing traits. Their stability across large datasets makes them suitable for genomic contexts; however, their predictive performance can suffer when faced with extremely high-dimensional marker sets, and they may underperform compared to genomic best linear unbiased prediction (GBLUP) models when traits are predominantly controlled by additive genetic effects (Li et al., 2024).

Support Vector Regression (SVR) extends the capacity to model nonlinear relationships by employing kernel functions, making it well-suited for medium-density marker datasets and traits with significant non-additive genetic components. By transforming input data into higher-dimensional feature spaces, SVR can capture complex patterns that linear models cannot. This flexibility allows SVR to address genetic architectures where interactions and dominance effects play a substantial role, although its performance depends on careful tuning of kernel parameters and may be computationally intensive for very large datasets (Li et al., 2024).

4.5. Deep Learning Models

Deep learning has emerged as a powerful approach in genomic prediction, particularly effective for handling the complexity and high dimensionality of genomic datasets. Multilayer Perceptrons (MLPs) serve as foundational models that capture nonlinear interactions through fully connected layers; however, their effectiveness depends heavily on the availability of large training populations and the application of appropriate regularization techniques to prevent overfitting. Convolutional Neural Networks (CNNs) extend this capability by interpreting single nucleotide polymorphisms (SNPs) as sequential genomic features, enabling the capture of linkage disequilibrium (LD) blocks and haplotype structures, which has been shown to improve prediction accuracy in several studies (Li, 2024).

Recurrent Neural Networks (RNNs) further leverage the sequential nature of genomic data, making them well-suited to model complex biological phenomena such as epistasis, long-range LD, and regulatory motifs that influence gene expression and trait variation. Meanwhile, Deep Gaussian Process Models provide an advanced framework that combines nonlinear modeling with uncertainty estimation, offering a promising alternative for genomic prediction tasks where quantifying prediction confidence is critical. Together, these deep learning architectures represent a versatile toolkit for advancing genomic prediction by accommodating the intricate patterns and dependencies inherent in genetic data (Mcdermott & Wikle, 2019).

4.6. Comparative Performance of Models

Table 2. General tendencies across trait architectures

Trait Type	**Preferred Model(s)**
Highly polygenic traits	GBLUP / RRBLUP
Traits with major QTL	Bayes B, Bayes R
When functional data are available	BayesRC
Traits with epistasis	Random Forest, CNN
Highly nonlinear genetic architectures	Deep learning models
Small reference populations	ssGBLUP

Several additional factors critically influence the performance of predictive models in genetic studies (Table 2). Sample size plays a fundamental role, as larger datasets generally provide more statistical power, enabling models to capture complex genetic architectures more accurately and reduce overfitting. Marker density, or the number of genetic markers used, affects the resolution with which models can detect associations; higher marker density improves the ability to capture linkage disequilibrium patterns and genetic variation but may also increase computational complexity. Phenotype accuracy is equally important, as precise and reliable measurement of traits ensures that the models learn from valid signals rather than noise, directly impacting predictive reliability (Liu et al., 2015).

Population structure is another key factor that can affect model outcomes. Differences in allele frequencies and genetic backgrounds across subpopulations can introduce biases if not properly accounted for, potentially leading to spurious associations or reduced prediction accuracy. Models that incorporate or adjust for population stratification tend to perform better in diverse or structured populations. Together, these factors—sample size, marker density, phenotype accuracy, and population structure—interact to determine the robustness and generalizability of genetic prediction models, underscoring the need for careful experimental design and data preprocessing in genomic research (Guo et al., 2014).

5. DATA INTEGRATION AND MULTI-OMICS APPROACHES IN GENOMIC SELECTION

Traditional genomic selection models have predominantly depended on SNP genotypes; nevertheless, the intricacy of biological systems cannot be comprehensively elucidated by DNA sequence variation alone. Phenotypic variation is influenced by multifaceted biological processes, including gene expression, epigenetic regulation, protein–protein interactions, metabolic pathways, microbiome dynamics, and environmental factors (L. Zhao et al., 2025). Consequently, the integration of multi-omics data has emerged as a pivotal research frontier to enhance predictive accuracy and deepen mechanistic understanding in livestock genomics (Li et al., 2022). This chapter examines the principal types of multi-omics data, integration strategies, computational frameworks, artificial intelligence–based unified modeling approaches, and their applications in livestock breeding.

5.1. Types of Multi-Omics Data

Multi-omics data encompass various biological layers that elucidate the structure and function of living systems. The most pertinent omics categories for genomic selection are outlined below.

5.1.1. Genomics (DNA-seq) Data

Genomic data refer to the various types of DNA-level variations that exist within the genome and serve as critical inputs for genomic prediction models. These variations include single nucleotide polymorphisms (SNPs), which are changes at a single base pair; insertions and deletions (Indels), which involve the addition or loss of small DNA segments; structural variants, encompassing larger rearrangements such as inversions or translocations; and copy number variations (CNVs), which represent changes in the number of copies of particular DNA regions. Together, these diverse forms of genetic variation provide a comprehensive landscape of genomic differences that influence phenotypic traits and disease susceptibility (Hinds et al., 2005).

The integration of these genomic variations into prediction models enables researchers to identify genetic markers associated with complex traits and improve the accuracy of trait prediction across populations. By leveraging high-throughput sequencing and genotyping technologies, large-scale genomic datasets capturing these variations are generated, facilitating the development of statistical and machine learning models that can predict outcomes such as disease risk, treatment response, and agricultural trait performance. Thus, genomic data form the foundational basis for advancing personalized medicine, crop improvement, and evolutionary studies through precise and data-driven genomic predictions (Moler et al., 2018).

5.1.2. Epigenomics (DNA Methylation, Histone Modifications)

Epigenetic modifications constitute a dynamic and reversible layer of gene regulation that does not alter the underlying DNA sequence but profoundly influences cellular function and identity. DNA methylation typically involves the addition of a methyl group to cytosine residues, often leading to transcriptional repression when occurring in gene promoter regions. Histone modifications, such as acetylation and methylation, alter chromatin structure by modulating the accessibility of DNA to transcriptional machinery; for example, histone acetylation generally promotes gene activation by loosening chromatin, whereas specific histone methylation marks can either activate or repress transcription depending on the context. Additionally, miRNA–mRNA interactions regulate gene expression post-transcriptionally by targeting messenger RNAs for degradation or translational inhibition, adding another layer of fine-tuning in tissue-specific gene expression (Auverlot et al., 2024).

These epigenetic mechanisms are highly responsive to environmental cues, enabling organisms to adapt to changing conditions without permanent genetic changes. In livestock, such epigenomic plasticity has been linked to phenotypic variation in traits critical for production, such as growth rate, milk yield, and stress resilience. Environmental stressors like temperature fluctuations, nutrition, and disease exposure can induce epigenetic changes that influence gene expression patterns, thereby affecting animal health and productivity. Understanding these epigenetic adaptations offers promising avenues for improving livestock breeding and management strategies by integrating epigenomic information alongside traditional genetic selection. (Gao et al., 2021)

5.1.3. Transcriptomics (RNA-seq) Data

Gene expression plays a fundamental role in shaping phenotypic traits by regulating the functional output of the genome. RNA sequencing (RNA-seq) data provide a comprehensive snapshot of gene activity, enabling researchers to capture dynamic expression patterns that underlie complex traits. Incorporating transcriptomic information into genomic prediction models enhances their predictive power by directly linking gene expression profiles to phenotypic variation. This integration allows for more precise modeling of gene expression–phenotype associations, which improves the identification of causal genes and pathways influencing traits of interest (Lee, 2018).

Additionally, RNA-seq facilitates the mapping of expression quantitative trait loci (eQTLs), which are genomic regions that regulate gene expression levels. By overlaying eQTL data with genomic markers, researchers can uncover regulatory variants that contribute to phenotypic diversity. The construction of tissue-specific regulatory networks using transcriptomic data further refines predictions by accounting for the context-dependent nature of gene regulation (Battle & Montgomery, 2014). Moreover, RNA-seq supports feature selection by highlighting genes with significant expression changes relevant to the trait, thereby reducing noise and focusing the model on biologically meaningful variables. Collectively, these mechanisms contribute to a 10–25% improvement in genomic prediction accuracy, as demonstrated in multiple studies (Dutta et al., 2020).

5.1.4. Proteomics Data

Protein abundance serves as a crucial indicator of biological function because it directly reflects the presence and activity of proteins that execute cellular processes, unlike genomic or transcriptomic data, which represent potential or intermediate stages of gene expression. While genomic and transcriptomic analyses provide valuable insights into genetic variation and gene expression patterns, they do not always correlate precisely with protein levels due to post-transcriptional and post-translational modifications, protein degradation, and other regulatory mechanisms. Therefore, proteomics offers a more accurate snapshot of the functional state of cells and tissues, enabling better understanding of phenotypic traits and disease mechanisms.

However, the integration of proteomics into routine genomic selection programs faces significant hurdles. The high costs associated with proteomic measurements, including sample preparation, instrumentation, and data analysis, limit large-scale application, especially in breeding populations where extensive sample sizes are needed for robust statistical power. Additionally, current proteomic techniques may have lower throughput and reproducibility compared to genomic methods. Despite these limitations, proteomics has successfully identified key biomarkers linked to important traits such as metabolic syndrome, mastitis, and immune response, demonstrating its potential to complement genomic data and enhance selection accuracy by providing functional validation and mechanistic insights (Bonnet et al., 2020).

5.1.5. Metabolomics Data

Metabolites represent the end products of cellular metabolism and provide a direct snapshot of the physiological state of an organism. Because they reflect the integrated output of gene expression, protein activity, and environmental influences, metabolites are valuable as biomarkers for assessing complex biological traits. In livestock and animal science, metabolite profiling through metabolomics enables the identification of biochemical signatures associated with feed efficiency, helping to optimize nutrition and reduce production costs. Additionally, metabolites can indicate an animal's ability to tolerate environmental stressors, such as heat or disease, thereby supporting strategies to improve resilience and welfare (Clemmons et al., 2017).

The application of metabolomics extends beyond performance traits to encompass animal health monitoring and disease diagnosis. By capturing dynamic changes in metabolic pathways, metabolite analysis can reveal early signs of metabolic disorders or infections before clinical symptoms arise. This capacity makes metabolomics a powerful tool for precision livestock farming, facilitating targeted interventions and improving overall productivity. The comprehensive insights gained from metabolomics complement genomic and proteomic data, offering a holistic understanding of physiological processes and enabling more effective management practices in animal agriculture (Lecchi et al., 2019).

5.1.6. Microbiome Data

The rumen microbiota is integral to the overall health and productivity of ruminant animals, influencing key physiological processes that affect feed utilization and environmental impact. The specific composition of these microbial communities determines how efficiently feed is broken down and converted into energy, directly impacting growth rates and milk production. Furthermore, the diversity within the rumen microbiome plays a crucial role in modulating methane emissions, a potent greenhouse gas, thereby linking microbial ecology to both agricultural sustainability and climate change mitigation efforts (Bowen et al., 2020).

Advancements in metagenomic technologies have allowed for the integration of detailed microbial data into genomic prediction models, significantly improving the accuracy of these models by up to 15% (Wallace et al., 2019). This integration provides a more comprehensive understanding of the genetic and microbial factors that influence ruminant traits, enabling more precise selection and breeding strategies. Ultimately, leveraging metagenomic insights enhances the potential for optimizing animal performance while reducing environmental footprints, marking a significant step forward in the field of animal genetics and microbiome research (Montesinos-López et al., 2024).

5.2. Strategies for Multi-Omics Integration

Several integration strategies have been developed to effectively combine heterogeneous omics datasets, each addressing different challenges inherent in multi-omics analysis. Early integration involves merging all omics data types into a single unified feature matrix, enabling a comprehensive analytical model that naturally captures interactions across omics layers such as SNPs, gene expression, and methylation. This approach benefits from a holistic view of the data but faces challenges due to high dimensionality, which can increase the risk of overfitting, and issues related to missing data that may impair model performance (Flores et al., 2023).

Late integration, by contrast, models each omics type separately using specialized methods optimized for that data, such as GBLUP for SNPs, BayesR for CNVs, and artificial neural networks for expression data, before combining the results through ensemble techniques. This allows for tailored modeling of heterogeneous datasets but introduces computational complexity and increases the burden of managing multiple models. Intermediate integration offers a balanced alternative by applying dimensionality reduction techniques like principal component analysis (PCA) or autoencoders to extract latent features from each omics layer prior to integration. This strategy reduces dimensionality and noise, facilitating more efficient and interpretable multi-omics analyses, and is widely adopted in deep learning frameworks designed for multi-omics data fusion (Zhao et al., 2022).

6. ARTIFICIAL INTELLIGENCE AND BIG DATA ANALYTICS IN GENOMIC SELECTION APPLICATIONS

The exponential growth in data generation within livestock genomics has transformed breeding programs into complex, data-intensive ecosystems. This data diversity, ranging from single nucleotide polymorphism (SNP) arrays and whole-genome sequencing (WGS) to transcriptomic profiles from RNA-seq and microbiome analyses, is further complemented by continuous streams of phenotypic information collected via on-animal sensors and digital phenotyping platforms. Managing and integrating this multi-dimensional data requires not only vast computational resources but also sophisticated analytical frameworks capable of handling high dimensionality, heterogeneity, and dynamic data structures (Wójcik-Gront et al., 2024). Traditional statistical models, which often assume linearity and independence, are increasingly inadequate for capturing the intricate biological interactions and environmental influences that shape complex traits in livestock (Montesinos-López et al., 2021).

To address these challenges, artificial intelligence (AI) and machine learning (ML) techniques have been rapidly adopted in genomic selection pipelines. These approaches facilitate enhanced prediction accuracy by uncovering nonlinear relationships and complex patterns embedded within large-scale datasets. Moreover, AI-driven phenotyping methods enable real-time, high-throughput trait measurement, improving the resolution and reliability of phenotype data. Integrating big data analytics with scalable learning algorithms also supports the development of dynamic decision-support systems that can adapt to evolving datasets and breeding goals. This convergence of AI and big data analytics not only accelerates genetic gain but also deepens biological understanding, ultimately enabling more precise and sustainable livestock breeding strategies (Wójcik-Gront et al., 2024).

6.1. The Big Data Ecosystem in Genomic Selection

The contemporary stage of genomic selection operates within an environment where multi-layered biological and sensor-derived data are continuously generated. The principal components of this big data infrastructure are outlined below.

6.1.1. Genotype Data

Modern genotyping platforms have revolutionized genetic research by enabling the generation of extraordinarily large and diverse datasets. These platforms encompass a range of technologies, from low- to high-density single nucleotide polymorphism (SNP) arrays, which provide varying resolutions of genetic variation across the genome. Additionally, whole-genome sequencing (WGS) techniques produce comprehensive datasets containing 20 to 30 million variants per individual, offering an unprecedented depth of genetic information. Beyond SNPs and small-scale variants, these datasets also capture complex structural variations (SVs) such as copy number variations (CNVs) and chromosomal inversions, which play critical roles in genomic diversity and disease susceptibility (Cooper et al., 2008; Hou et al., 2011).

The scale and complexity of these datasets pose significant challenges and opportunities for data storage, processing, and analysis. The integration of haplotype-based variation further enriches the genetic landscape by allowing researchers to study combinations of alleles inherited together, which can be crucial for understanding population genetics and linkage disequilibrium patterns. Collectively, these advances result in terabyte-scale datasets that demand sophisticated computational tools and analytical frameworks to extract meaningful biological insights, thereby driving forward precision medicine and genomics research (Wójcik-Gront et al., 2024).

6.1.2. Phenotype Data and Digital Phenotyping

Precision livestock systems have evolved significantly by integrating a wide array of sensor technologies that extend beyond traditional phenotypic measurements. These systems utilize tools such as RFID tracking to monitor animal location and movement patterns, infrared thermography to detect temperature variations indicative of health status, and accelerometers coupled with IoT-based activity sensors to capture detailed behavioral data. Automated feed intake measurement devices provide continuous, precise records of consumption, while acoustic sensors enable real-time respiratory monitoring. Robotic milking systems further contribute by automating routine tasks and collecting data on milk yield and quality. Collectively, these technologies produce an immense volume of data points daily, offering granular insights into each animal’s physiological and behavioral states (Bailey et al., 2021; Lamanna et al., 2025; Tzanidakis et al., 2023).

The data generated by these advanced sensors exhibit the key characteristics of big data: high volume, velocity, and variety. The continuous and rapid stream of diverse data types—from spatial movement to physiological signals—requires sophisticated data management and analytical approaches to extract meaningful information (Neethirajan & Kemp, 2021a). This integration facilitates more precise and timely decision-making in livestock management, improving animal welfare, productivity, and disease detection. By harnessing such comprehensive datasets, precision livestock farming moves towards a data-driven paradigm that enhances sustainability and operational efficiency within the agricultural sector (Halachmi et al., 2020).

6.1.3. Multi-Omics Data

Crucial high-dimensional omics layers encompass diverse biological data types that capture different aspects of cellular and molecular function. RNA sequencing (RNA-seq) provides comprehensive profiles of gene expression, revealing which genes are active under specific conditions or in particular cell types. The methylome reflects epigenetic modifications, such as DNA methylation patterns, that regulate gene activity without altering the underlying DNA sequence. The microbiome characterizes the composition and dynamics of microbial communities inhabiting various environments, including the human body, which can influence host physiology and disease states. Proteomics and metabolomics analyze the biochemical phenotypes by quantifying proteins and metabolites, respectively, offering insights into functional pathways and metabolic states (Acharya & Mukhopadhyay, 2024; Wu et al., 2024)

Integrating these heterogeneous datasets poses significant analytical challenges due to their high dimensionality, varying data structures, and complex interdependencies. Each omics layer generates vast amounts of data with distinct measurement scales, noise profiles, and biological contexts, requiring sophisticated computational and statistical methods for effective integration and interpretation. Addressing these challenges is essential for uncovering comprehensive molecular mechanisms, identifying biomarkers, and advancing precision medicine. Multimodal analysis frameworks and advanced machine learning approaches are increasingly employed to harness the full potential of these layered omics data, enabling a more holistic understanding of biological systems (Acharya & Mukhopadhyay, 2024).

6.2. Big Data Analytics Frameworks

Several computational frameworks have been specifically designed to handle the challenges posed by genomics and multi-omics big data, which often involve massive datasets requiring scalable and efficient processing. Platforms such as Hadoop, Apache Spark, Dask, Delta Lake, and distributed implementations of TensorFlow and PyTorch offer robust solutions by enabling parallel processing and distributed computation across clusters of machines. These frameworks facilitate the management of high-throughput sequencing data and complex multi-omics datasets by providing fault tolerance, scalability, and optimized resource utilization, thereby accelerating data analysis workflows in genomics research (Liu et al., 2023).

Among these, Spark-based genomic frameworks like HAIL and ADAM have gained significant traction due to their ability to integrate distributed computing with domain-specific optimizations. HAIL, for example, is designed to simplify the analysis of large-scale genetic data by providing high-level APIs that abstract complex distributed operations, while ADAM offers a genomics-focused data model and processing pipeline built on Apache Spark. Such tools enable researchers to perform variant calling, genotype imputation, and other computationally intensive tasks more efficiently, supporting large cohort studies and population-scale analyses. Together, these frameworks represent a critical infrastructure component for advancing precision medicine and large-scale genomic investigations (Xu et al., 2025).

6.3. Artificial Intelligence–Based Genomic Prediction Models

AI-based genomic prediction models differ from classical linear approaches by capturing nonlinear relationships, epistatic effects, and complex multi-dimensional data structures.

6.3.1. Deep Learning Approaches

Deep learning has revolutionized genomic prediction by enabling models to automatically learn hierarchical and complex features directly from high-dimensional genomic data. Various architectures are employed for this purpose, including Multilayer Perceptrons (MLPs), Convolutional Neural Networks (CNNs), Recurrent Neural Networks (RNNs) such as Long Short-Term Memory (LSTM) and Gated Recurrent Units (GRU), Deep Gaussian Processes, and Transformer-based models. Each architecture leverages unique strengths: CNNs efficiently identify linkage disequilibrium (LD) blocks by capturing local spatial patterns; RNNs exploit the sequential nature of genomic data to model dependencies along the genome; and Transformers excel at capturing long-range interactions, which are critical for understanding complex genomic architectures (Liu et al., 2019).

The advantages of deep learning in genomics include its adaptive learning capacity, which allows models to capture nonlinear and intricate interactions among genetic variants that traditional linear models might miss. Additionally, these methods facilitate the integration of multi-omics data, enabling a more holistic understanding of biological systems. However, challenges remain, such as the requirement for large labeled datasets to effectively train deep models, which can be a limiting factor in many genomic studies. Furthermore, the high computational cost associated with training and tuning deep architectures can be prohibitive. Another significant limitation is the limited interpretability of these models, which complicates biological insight extraction and hinders trust and adoption in clinical settings. Addressing these challenges is crucial for the broader application of deep learning in genomic prediction (Abimannan et al., 2023; Mienye et al., 2024).

6.4. Machine Learning–Based Prediction Models

Machine learning models have become essential tools in genomic selection due to their ability to capture complex nonlinear relationships and epistatic interactions among genetic markers that traditional linear models may fail to detect. Algorithms such as Random Forest, Gradient Boosting frameworks (including XGBoost and LightGBM), Support Vector Machines (SVM/SVR), and k-Nearest Neighbors are commonly employed because they can model intricate patterns in high-dimensional genomic data. Ensemble learning approaches, which combine predictions from multiple models, further enhance predictive accuracy by reducing variance and bias, making them particularly effective in capturing the multifaceted genetic architecture of traits (Perez et al., 2022; Wang & Zhang, 2024).

These machine learning methods often outperform linear models when traits are influenced by significant non-additive genetic effects, such as dominance and epistasis, which involve interactions between different loci. By leveraging their flexibility and capacity to model complex interactions without explicit parametric assumptions, ML models provide more accurate genomic predictions, improving selection decisions in breeding programs (Li et al., 2024). This advantage is supported by studies like Ortuño et al. (2019), which demonstrate superior performance of ML models over linear approaches in scenarios where genetic effects deviate from additivity, highlighting their growing importance in modern genomic selection frameworks.

6.5. AI-Driven Sensor Data Analysis

The integration of Internet of Things (IoT) sensor data with genomic prediction represents a significant advancement in precision livestock breeding by enabling environmentally responsive genomic selection. Through the deployment of diverse sensor technologies, such as computer vision, accelerometers, and behavioral analytics, AI-driven systems can continuously monitor key physiological and behavioral traits. For example, automated feed intake prediction leverages deep learning applied to visual data, while accelerometer-based sensors track rumen activity to provide insights into digestive health. Early detection of heat stress, disease surveillance via cough detection and gait analysis, and reproduction monitoring through activity spikes further enrich the phenotypic data captured in real time (Cooper & Messina, 2021; Lamanna et al., 2025).

Incorporating these dynamic environmental and behavioral indicators directly into genomic prediction models enhances the modeling of genotype-by-environment (G×E) interactions, which are critical for accurate selection decisions under variable conditions. By capturing the complex interplay between an animal's genetic potential and its immediate environment, this approach improves the precision of breeding value estimates and supports more resilient and productive livestock populations. This synergy of AI-analyzed sensor data with genomic tools thus offers a powerful framework for optimizing animal performance and welfare in diverse production systems (Cooper et al., 2020).

6.8.1. Digital Twin–Enabled Livestock Systems

Emerging research in precision livestock farming is increasingly centered on the full integration of artificial intelligence (AI) to optimize animal management and productivity. A key innovation in this domain is the development of digital twins—virtual replicas of individual animals that leverage comprehensive datasets to simulate and predict performance outcomes. These digital twins integrate multiple data layers, including genomic architecture, which provides insights into the genetic potential and predispositions of the animal; phenotypic history, capturing observable traits and past performance; real-time sensor data, offering continuous monitoring of physiological and behavioral parameters; and detailed health records, documenting medical history and treatments (Arulmozhi et al., 2024; Vallée, 2024).

By synthesizing this diverse information, digital twins enable the generation of accurate virtual simulations that can forecast growth, health status, and productivity under varying environmental and management conditions. This holistic approach facilitates precision decision-making, allowing farmers to tailor interventions such as nutrition, breeding, and healthcare on an individual basis. The integration of AI-driven digital twins thus represents a transformative step toward sustainable and efficient livestock farming, enhancing animal welfare while maximizing resource use and economic returns (Monteiro et al., 2018; Neethirajan & Kemp, 2021b).

7. SPECIES-SPECIFIC APPLICATIONS OF GENOMIC SELECTION

The efficacy of genomic selection in livestock breeding is contingent upon several critical factors that are specific to each species. The genetic architecture, encompassing the number, effect size, and distribution of genes influencing traits, is pivotal in determining the effectiveness of genomic information in predicting breeding values. Species characterized by simpler genetic architectures or traits governed by fewer genes typically exhibit higher prediction accuracies. Furthermore, population size and structure significantly impact the degree of linkage disequilibrium (LD) between genetic markers and causal variants, thereby influencing the reliability of genomic predictions. Larger, well-characterized populations with robust LD patterns enable more precise genomic evaluations. The availability and quality of phenotyping infrastructure are equally crucial, as accurate and consistent trait measurement is fundamental to the training of genomic prediction models (Heffner et al., 2011; Liu et al., 2019).

The economic significance of traits targeted by genomic selection also varies across species and production systems, influencing breeding priorities and investment in genomic tools. For instance, traits such as milk yield and quality are of paramount importance in dairy cattle, whereas growth rate and feed efficiency may be prioritized in pigs and poultry. This chapter systematically examines how these factors affect implementation strategies, prediction accuracies, and realized genetic gains in cattle, sheep, goats, poultry, and pigs. It further elucidates species-specific challenges, such as the relatively limited genomic resources in small ruminants compared to cattle or the complex breeding structures in poultry, emphasizing the necessity for tailored approaches to optimize the benefits of genomic selection across diverse livestock species (Nayak et al., 2024; Strandén et al., 2019).

7.1. Cattle (Dairy and Beef)

Cattle have emerged as the leading species for genomic selection in livestock breeding, owing to several synergistic factors that have facilitated its rapid and effective implementation. A primary enabler is the establishment of extensive reference populations, which offer a large and diverse genetic dataset crucial for the precise estimation of marker effects. These populations are bolstered by robust, standardized phenotypic recording systems that ensure high-quality and consistent trait measurements across animals, thereby enhancing the reliability of genomic predictions. Moreover, cattle populations exhibit long-range linkage disequilibrium (LD), allowing genetic markers to reliably tag causal variants across broader genomic regions, thus augmenting the efficacy of genomic selection models (Esrafili Taze Kand Mohammaddiyeh et al., 2023; Strandén et al., 2019).

Additionally, the widespread commercial availability and adoption of genotyping technologies have reduced costs and increased accessibility for producers, expediting the integration of genomic information into breeding programs. The economic incentives are also substantial, as production traits in cattle—such as milk yield, growth rate, and feed efficiency—possess high financial value, motivating investment in genomic tools to enhance these traits efficiently. Collectively, these factors have created an optimal environment for genomic selection to flourish in cattle, establishing a benchmark for other livestock species seeking to leverage genomic advancements for genetic improvement (Wiggans et al., 2016; Wiggans & Carrillo, 2022).

7.1.1. Dairy Cattle Genomic Selection

Since its introduction in North America and Europe around 2008, genomic selection in dairy breeds such as Holstein, Jersey, and Brown Swiss has significantly transformed breeding programs. This method utilizes dense single nucleotide polymorphism (SNP) arrays, typically comprising 50K to 150K markers, in conjunction with extensive genomic databases like CDCB and EuroGenomics, to estimate breeding values with markedly enhanced accuracy. The reported accuracies for genomic estimated breeding values (GEBVs) differ by trait category, with milk yield exhibiting the highest accuracy range of 50–70%, followed by fertility traits at 30–50%, and health and robustness traits at 25–45% (VanRaden, 2008). These advancements in prediction accuracy facilitate more precise selection decisions, thereby accelerating genetic gain across economically significant traits (Wiggans et al., 2016).

The economic impact of genomic selection is substantial, primarily due to a significant reduction in the generation interval from the traditional 5–6 years to approximately 2 years. This reduction enables a more rapid turnover of superior genetics within the population, thereby enhancing overall herd performance more swiftly. Furthermore, the widespread adoption of genomic indices by artificial insemination (AI) companies has enabled the large-scale dissemination of genetically superior sires. Key factors contributing to this success include standardized phenotyping protocols that ensure consistent trait measurements, high imputation accuracies that facilitate cost-effective genotyping even with lower-density arrays, and the integration of comprehensive genomic and phenotypic data. Collectively, these elements have established genomic selection as a fundamental component of contemporary dairy cattle breeding strategies (Brito et al., 2020a; Mrode et al., 2019).

7.1.2. Beef Cattle Genomic Selection

Genomic selection in beef cattle breeds, including Angus, Hereford, Charolais, and Limousin, has experienced significant growth, albeit at a slower pace compared to dairy cattle. This slower advancement is primarily attributed to several challenges inherent in beef production systems. Beef breeds display more heterogeneous phenotypes than dairy cattle, complicating the capture of consistent genetic signals across populations. Furthermore, the recording of key traits such as feed efficiency and survival is more complex in extensive or pasture-based systems, thereby limiting the availability of high-quality phenotypic data. The smaller size of reference populations in beef cattle further constrains the accuracy and robustness of genomic predictions, as fewer animals with both genotypic and phenotypic data are available for model training (Esrafili Taze Kand Mohammaddiyeh et al., 2023).

Despite these challenges, recent advancements have enhanced the precision of genomic predictions for significant traits in beef cattle. Noteworthy progress has been achieved in predicting feed efficiency, a critical factor for reducing production costs and minimizing environmental impact. Additionally, improvements have been realized in carcass quality traits, which directly affect meat value and consumer preferences. Furthermore, adaptation to pasture-based systems, a crucial element for many beef production environments, has become more predictable through genomic tools. These advancements reflect ongoing efforts to expand and refine reference populations and integrate diverse data sources, thereby enhancing the utility of genomic selection in beef breeds (Boichard et al., 2015).

7.2. Sheep

Genomic selection in sheep has lagged behind cattle primarily due to several genetic and practical challenges. One major factor is the substantial variation in linkage disequilibrium (LD) patterns across different sheep breeds, which complicates the transferability and accuracy of genomic predictions. Additionally, sheep populations tend to have highly heterogeneous structures, often influenced by diverse breeding practices and geographic isolation, further limiting the effectiveness of uniform genomic selection models. Compounding these issues are incomplete or inconsistent phenotypic records in many countries, which reduce the reliability of training datasets needed for robust genomic evaluations (Larkin et al., 2019; Prieur et al., 2017).

The introduction of the 50K Sheep HD SNP array (Kijas et al., 2012) represented a significant advancement, enabling more precise genotyping and facilitating the application of genomic selection in sheep breeding. This technology has been successfully applied to improve key traits such as parasite resistance (e.g., fecal egg count), wool yield and fiber quality, growth and carcass characteristics, and reproductive performance. National breeding programs like Australia's MERINOSelect and New Zealand's Sheep Improvement Ltd (SIL) have incorporated genomic tools into their selection schemes, often employing hybrid statistical models such as BayesR and GBLUP to enhance prediction accuracy and genetic gain. These developments underscore the growing integration of genomic technologies in sheep breeding, despite the earlier challenges (Bolormaa et al., 2015; Daetwyler et al., 2010).

7.3. Goats

Genomic selection in goats has advanced at a slower rate compared to cattle and sheep, primarily due to several limiting factors. These factors include the limited availability of reference populations, which constrains the accuracy and robustness of genomic predictions, as well as inaccuracies in pedigrees that undermine the reliability of genetic evaluations. Furthermore, small herd sizes and inconsistent phenotyping practices have impeded the accumulation of high-quality data necessary for effective genomic selection (Carillier-Jacquin et al., 2018). Despite these challenges, significant advancements have been made in dairy goat breeds, particularly in France, where genomic selection programs have been successfully implemented for Saanen and Alpine breeds. These programs have demonstrated genomic estimated breeding value (GEBV) accuracies ranging from 30% to 60% for key milk production traits, indicating promising potential for genetic improvement (Boichard et al., 2015; Teissier et al., 2018).

Despite advancements, the development of genomic tools in goats continues to encounter challenges, notably the significant variation in linkage disequilibrium (LD) patterns across different breeds, which complicates the transferability of genomic information. Additionally, the lack of a centralized phenotyping infrastructure restricts the consistency and scale of data collection. To mitigate cost-related barriers, the implementation of low-density single nucleotide polymorphism (SNP) arrays, in conjunction with imputation techniques, has been instrumental in reducing genotyping expenses. This strategy has broadened the accessibility of genomic selection programs to a wider array of herds, thereby facilitating more extensive implementation. Furthermore, genomic models targeting traits such as mastitis resistance have been developed, reflecting efforts to enhance animal health alongside production traits.

Collectively, these advancements contribute to the gradual yet significant integration of genomic selection in goat breeding programs (De Lima et al., 2020; Larkin et al., 2019).

7.4. Poultry

Poultry represents the second most advanced livestock species in the implementation of genomic selection, following cattle. This advancement is primarily attributed to the commercial poultry industry's integration of genomic tools, facilitated by the species' rapid generational turnover and large population sizes. The genomic architecture of poultry is characterized by short-range linkage disequilibrium (LD), necessitating the employment of higher-density single nucleotide polymorphism (SNP) panels to adequately capture genetic variation. Furthermore, the complex population structure, shaped by multiple distinct breeding lines, presents unique challenges and opportunities for genomic selection strategies (Aslam et al., 2012; Dekkers, 2012; Goddard et al., 2010).

Genomic selection in poultry has successfully improved a variety of economically significant traits, including egg production and quality, growth rate, feed conversion efficiency, mortality rates, robustness, and health-related traits such as tibial dyschondroplasia and heat tolerance. Leading breeding companies, such as Hy-Line, Aviagen, and Cobb, intensively utilize genomic selection to accelerate genetic gain while effectively managing inbreeding levels. Their use of advanced genomic tools facilitates more precise selection decisions, thereby enhancing overall productivity and sustainability within the poultry industry (De Beukelaer et al., 2017; Liu et al., 2018; Wolc et al., 2015).

7.5. Aquaculture

In the past decade, genomic selection in aquaculture has undergone substantial advancements, driven by the rapid expansion of global aquaculture production and the increasing demand for genetically improved stocks. Compared to terrestrial livestock, aquaculture species often exhibit higher fecundity, larger effective population sizes, and shorter generation intervals, creating an ideal environment for the application of genomic-based breeding strategies. However, challenges such as high within-family variance, limited pedigree accuracy, and the widespread use of mass spawning in hatcheries underscore the need for genomic tools to enhance the accuracy of breeding value estimation (Houston et al., 2020; Yáñez et al., 2015). The development of species-specific SNP arrays, including those for Atlantic salmon, rainbow trout, tilapia, and shrimp, has facilitated reliable genome-wide marker coverage, thereby enabling more precise genomic predictions (Correa et al., 2015; Palaiokostas et al., 2016).

Genomic selection has facilitated significant advancements in various economically important aquaculture traits, including disease resistance, growth performance, feed efficiency, fillet quality, and stress tolerance. Among these, disease resistance has emerged as a primary focus due to the substantial economic losses associated with pathogens in farmed fish populations. For instance, genomic selection for resistance to Piscirickettsia salmonis in Atlantic salmon has achieved prediction accuracies up to twofold higher than those obtained through pedigree-based BLUP methods, indicating the considerable genetic gain achievable for health traits (Yáñez et al., 2014; Barría et al., 2018). Similarly, genomic prediction for sea lice resistance has been successfully integrated into breeding programs, contributing to reduced parasite loads and diminishing the necessity for chemical treatments (Tsai et al., 2016). In species such as tilapia, genomic models have enhanced the accuracy of breeding values for growth and carcass traits, despite the complex mating systems and limited pedigree information typical of many tilapia hatcheries (Joshi et al., 2020).

The integration of genomic technologies into aquaculture is steadily advancing as the costs associated with sequencing decrease and high-throughput phenotyping tools—such as automated imaging, hyperspectral sensors, and environmental monitoring platforms—are increasingly utilized. However, several challenges persist, including the high cost of genotyping for species with low economic value, the requirement for large and diverse reference populations, and the complexity of implementing genomic selection in species with polyploid genomes, such as sturgeon and certain oyster species. Despite these constraints, the growing body of evidence demonstrating enhanced genetic gain, improved disease resilience, and increased production efficiency underscores genomic selection as a transformative approach poised to drive the next generation of breeding advancements in aquaculture (Houston, 2017; Robledo et al., 2018).

7.6. Cross-Species Comparative Assessment

The Table 3, summarizes species-specific differences in genomic selection implementation.

Table 3. Species-specific differences in genomic selection implementation

Species	Implementation Level	Reference Population Size	LD Pattern	Key Challenges
Cattle	Very high	Very large	Long LD	G×E, health traits
Sheep	Moderate	Medium	Highly breed-dependent	Pedigree gaps, population heterogeneity
Goats	Low–moderate	Small	Short LD	Poor phenotyping, small herds
Poultry	Very high	Extremely large	Short LD	Between-line variability
Aquaculture	Moderate	Very large	Short LD	Mass spawning causing pedigree uncertainty; high within-family variance; limited phenotyping infrastructure; polyploidy in some species

7.7. Future Directions in Species-Specific Genomic Selection

The future of livestock genomics is poised to benefit significantly from the routine implementation of Whole-Genome Sequencing (WGS). This advanced sequencing technique will greatly enhance the identification of genetic variants and improve the precision of genomic predictions across diverse species. WGS facilitates the accurate detection of genetic markers associated with traits of economic and biological significance. In addition to WGS, the integration of multi-omics data—including microbiome profiles, metabolomics, and epigenetic modifications—will be essential for unraveling the intricate biological pathways that govern traits influenced by a combination of genetic and environmental factors. This comprehensive approach provides a deeper insight into trait architecture and supports the development of more effective selection strategies (Liu et al., 2023; Nayak et al., 2024; Xu et al., 2025; Ye et al., 2020).

Concurrently, advancements in artificial intelligence, particularly through convolutional neural networks (CNNs), Transformer architectures, and hybrid deep learning models, are poised to revolutionize the identification of causal single nucleotide polymorphisms (SNPs) and functional genomic regions by capturing intricate patterns within large-scale genomic datasets. The development of cross-species genomic models, which leverage shared reference populations and multi-species prediction frameworks, is expected to further reduce costs and enhance prediction accuracies by facilitating knowledge transfer across related species. Moreover, as climate change intensifies, there will be an increasing focus on breeding climate-resilient and heat-tolerant livestock. Genomic research will prioritize adaptation traits to ensure sustainable productivity and animal welfare under changing environmental conditions, marking a critical shift in breeding objectives (Ehret et al., 2015; Haque et al., 2024; Meuwissen et al., 2016; Rasal et al., 2024).

8. INTEGRATION OF GENE-EDITING TECHNOLOGIES (CRISPR, PRIME EDITING) WITH GENOMIC SELECTION

Genomic selection has markedly advanced livestock breeding by facilitating the swift identification and propagation of advantageous genetic traits within populations. This methodology utilizes extensive genomic data to predict breeding values, thereby expediting genetic gain without necessitating phenotypic evaluation of each individual. Nevertheless, its efficacy is inherently constrained by the genetic variation already present within the breeding pool. Gene-editing technologies address this limitation by directly modifying the genome to introduce novel alleles or rectify deleterious mutations that are either absent or rare in the population. These technologies provide precise, targeted interventions that can augment genomic selection by broadening the genetic diversity available for breeding programs (Bishop & Van Eenennaam, 2020; Lu et al., 2024).

Contemporary gene-editing technologies, including CRISPR-Cas systems, base editors, and prime editors, offer versatile platforms for the precise and efficient manipulation of livestock genomes. The CRISPR-Cas system facilitates targeted DNA cleavage followed by repair, enabling the insertion, deletion, or replacement of specific genetic sequences. Base editing allows for the conversion of individual nucleotides without causing double-strand breaks, thereby minimizing off-target effects and enhancing safety. Prime editing further refines this capability by permitting precise insertions, deletions, and various base substitutions with minimal unintended modifications. The integration of these gene-editing techniques with genomic selection strategies can expedite the development of livestock exhibiting enhanced traits, such as disease resistance, productivity, and environmental adaptability. However, the application of these technologies necessitates careful consideration of ethical issues, animal welfare, and regulatory frameworks to ensure their responsible use in livestock breeding (Rodriguez-Villamil et al., 2024; Wani et al., 2022).

8.1. Fundamentals of Gene-Editing Technologies

Gene editing encompasses a suite of biotechnological tools that enable targeted cutting, modification, or replacement of DNA sequences within the genome.

8.1.1. CRISPR-CAS9

CRISPR-Cas9’s versatility stems from its modular design, allowing researchers to easily customize the single guide RNA (sgRNA) to target virtually any DNA sequence of interest. This adaptability facilitates a wide range of genetic manipulations, including gene knockouts, insertions, and corrections, which are invaluable for functional genomics studies and the development of gene therapies. Moreover, the system's ability to introduce multiplexed edits—simultaneous targeting of multiple genomic sites—enables complex genetic modifications that were previously challenging or impossible with earlier genome-editing technologies such as zinc finger nucleases (ZFNs) or transcription activator-like effector nucleases (TALENs). This capability accelerates research workflows and expands the scope of potential applications (Ferreira & Choupina, 2022; Naeem et al., 2020).

CRISPR-Cas9 technology has emerged as a transformative tool in animal breeding, offering unprecedented precision and efficiency for modifying genomic regions associated with economically important traits. By enabling targeted editing of specific loci, CRISPR-Cas9 allows breeders to introduce beneficial alleles, eliminate deleterious variants, and accelerate genetic improvement far beyond the limits of traditional selection and even genomic selection alone. One of the most prominent applications in livestock is the correction or introduction of functional variants that confer disease resistance, such as editing the *CD163* gene in pigs to generate complete resistance to Porcine Reproductive and Respiratory Syndrome (PRRS), or modifying viral entry receptors in poultry to enhance influenza resistance. Similarly, editing the *PRNP* gene in cattle has demonstrated the potential to mitigate the risk of transmissible spongiform encephalopathies (Cigan et al., 2024; Islam et al., 2020; Ruan et al., 2017).

Beyond disease resistance, CRISPR-Cas9 is being deployed to manipulate traits linked to productivity, animal welfare, and environmental adaptability. Notably, the introduction of the naturally occurring SLICK allele into beef cattle has significantly improved heat tolerance, a trait of growing importance under global climate change (Harris et al., 2020). Likewise, targeted disruption of the *MSTN* (myostatin) gene in cattle, sheep, and goats has resulted in increased muscle mass, offering potential benefits for meat production, although these modifications require careful evaluation to avoid unintended physiological consequences. Gene editing has also facilitated improvements in reproductive efficiency and stress tolerance by fine-tuning endocrine, metabolic, or thermoregulatory pathways (Kim et al., 2020; Pozzebon et al., 2024; Zhu et al., 2020; Carlson et al., 2016).

Despite these promising advances, several challenges continue to shape the responsible implementation of CRISPR-Cas9 in livestock breeding. Potential off-target effects, mosaicism, variable editing efficiency, and the need for reliable delivery systems—particularly in large domestic animals—remain areas of active investigation. Ethical and regulatory considerations further influence the deployment of edited animals in commercial production, with global policies differing markedly in their treatment of gene-edited livestock. Nevertheless, when integrated with genomic selection, multi-omics data, and precision phenotyping, CRISPR-Cas9 is poised to redefine the trajectory of animal breeding, enabling rapid, targeted genetic progress that aligns with the goals of sustainability, animal health, and agricultural resilience (Hennig et al., 2020; Salvesen et al., 2024; Zhou et al., 2014).

CRISPR-Cas9 has rapidly become one of the most influential technologies in aquaculture genetics, offering precise manipulation of loci controlling growth, disease resistance, sterility, and environmental tolerance. In salmonids, CRISPR-mediated knockout of the **dead end (dnd1)** gene has successfully produced germline-sterile Atlantic salmon, providing a powerful strategy for preventing genetic introgression between farmed and wild stocks and enhancing the sustainability of aquaculture systems (Wargelius et al., 2016). Similarly, targeted editing of the **slc45a2** pigmentation gene in Atlantic salmon and Nile tilapia has validated the efficiency and specificity of CRISPR tools for functional genomics and trait mapping in teleost species (Edvardsen et al., 2014; Li et al., 2021). A major focus of gene-editing research in aquaculture is the improvement of disease resistance—an economically critical trait due to high mortality from viral and bacterial infections. For example, CRISPR-Cas9 knockout of the **pou2f1b** gene in catfish has conferred enhanced resistance to *Edwardsiella ictaluri*, while editing of immune-related loci such as **tnfrsf11b** and **tlr5** in common carp and grass carp has significantly increased resilience against bacterial pathogens (Khalil et al., 2017; Wang et al., 2018). In addition to disease resistance, gene editing has been effectively used to enhance growth performance, as demonstrated by CRISPR-induced mutations in the **myostatin (mstn)** gene in channel catfish and tilapia, which resulted in increased muscle accretion and accelerated growth rates (Zhong et al., 2016; Coogan et al., 2022). Beyond targeted gene knockouts, CRISPR has become instrumental in developing strains with improved thermal tolerance and salinity adaptation by modulating endocrine and osmoregulatory pathways central to aquaculture productivity (Dehler et al., 2016). Despite these achievements, limitations such as mosaicism, variable editing efficiency, and ethical constraints regarding the commercial release of gene-edited fish continue to shape regulatory and scientific discussions. Nevertheless, with expanding genomic resources, improved delivery methods, and integration with genomic selection and multi-omic datasets, CRISPR-Cas9 is expected to become a cornerstone technology for accelerating genetic gain, improving animal health, and enhancing sustainability across global aquaculture systems.

8.2. Applications of Gene Editing in Livestock and Aquaculture

Gene-editing technologies have been successfully applied across multiple livestock species and aquaculture. Advancements in livestock genetic engineering have enabled the development of cattle with enhanced disease resistance, such as those resistant to Bovine Viral Diarrhea Virus (BVDV). A notable example includes the knockout of the PRNP gene, which confers resistance to transmissible spongiform encephalopathies, a group of fatal neurodegenerative diseases. These genetic modifications hold significant promise for improving herd health and reducing economic losses caused by infectious diseases (Antos et al., 2021; Brunelle et al., 2007; Kuile et al., 2017).

In addition to disease resistance, genetic improvements targeting environmental adaptability and physical traits have been successfully implemented. These innovations demonstrate the potential of precise genome editing to improve both animal welfare and production efficiency (Proudfoot et al., 2014).

Genome editing has shown significant potential in enhancing disease resistance and production traits across various livestock species. For example, editing the CD163 receptor in pigs has been demonstrated to confer complete resistance to Porcine Reproductive and Respiratory Syndrome Virus (PRRSV), a major swine pathogen, thereby improving animal health and reducing economic losses (Whitworth et al., 2016). Similarly, knocking out the MSTN (myostatin) gene in pigs leads to increased muscle mass, presenting opportunities for improved meat yield. In xenotransplantation research, multi-locus genome editing has been employed to modify pig genes to reduce immunological incompatibility with human recipients, advancing the prospects of using pig organs for human transplantation (Wang et al., 2022).

In small ruminants like sheep and goats, targeted genome editing strategies have focused on enhancing muscularity through MSTN knockouts and improving disease resistance by editing immune-related genes associated with Ovine Progressive Pneumonia Virus (OPPV) and scrapie. In poultry, editing viral entry receptors has been explored to confer resistance against avian influenza, a critical disease affecting poultry health and production. Additionally, targeted mutations aim to improve laying performance and egg quality, supporting both productivity and animal welfare in the poultry industry. These examples collectively illustrate how precise genetic modifications can address key challenges in animal agriculture by enhancing disease resistance and production efficiency (Wang et al., 2015; Zhou et al., 2022).

For example, targeted edits of immune-related genes such as **tnfaip8l3** in zebrafish have demonstrated enhanced resistance to bacterial infections, supporting the development of genetically resilient strains (Wang et al., 2018; Liu et al., 2019). Additionally, gene editing has been applied to modify traits associated with environmental adaptability. For instance, altering endocrine pathway genes in salmonids has shown potential to improve thermal tolerance, an increasingly important trait under climate change pressures (Dehler et al., 2016). Collectively, these innovations demonstrate that gene-editing technologies offer transformative potential in aquaculture by enhancing disease resistance, growth performance, environmental resilience, and stock management efficiency.

9. CHALLENGES, RISKS, AND FUTURE PERSPECTIVES IN GENOMIC SELECTION

Genomic selection (GS) has significantly transformed livestock genetics by facilitating more rapid and precise breeding decisions. However, it encounters substantial limitations that impede its full potential. Biologically, challenges include the intricate genetic architecture of traits, genotype-by-environment interactions, and the difficulty of capturing rare variants or epistatic effects with current models. From a computational perspective, the integration and analysis of extensive, heterogeneous datasets necessitate advanced algorithms and considerable computational resources. Economically, the expense associated with generating high-quality genomic and phenotypic data can be prohibitive for numerous breeding programs, particularly in developing regions. Furthermore, social acceptance and ethical concerns emerge from the application of genome editing and data-driven breeding approaches, encompassing issues related to animal welfare, biodiversity loss, and equitable access to technology (Alali & Wardat, 2024; Bhat et al., 2023; Elufioye et al., 2024; Mmbando & Ngongolo, 2024).

The future of genomic selection (GS) is set to undergo significant transformation through the integration of big data analytics, artificial intelligence-driven prediction systems, multi-omics integration, and genome editing technologies. These advancements hold the potential to enhance predictive accuracy, expedite genetic gain, and facilitate precision breeding tailored to specific environmental conditions and production objectives. However, they also introduce new complexities and risks, including concerns related to data privacy, algorithmic biases, and unintended ecological consequences. Ethical and socio-economic considerations must be meticulously addressed to ensure responsible implementation, encompassing transparent governance, stakeholder engagement, and policies that balance innovation with sustainability. Future research should prioritize the development of robust, interpretable models, the improvement of data sharing frameworks, and the exploration of the long-term impacts of advanced genomic technologies on livestock populations and farming communities (Aboelhassan & Abozaid, 2024; Lu et al., 2024; Quteishat, 2024).

9.1. Genetic and Biological Challenges

9.1.1. Complexity of Polygenic Traits

Many economically important livestock traits, including fertility, health, behavior, and feed efficiency, exhibit a highly polygenic architecture characterized by the involvement of numerous genetic loci, each contributing a small effect. This complexity, combined with their typically low heritability, poses significant challenges for genetic evaluation and breeding programs. The cumulative influence of many small-effect loci makes it difficult to accurately capture the genetic variance underlying these traits, which in turn limits the predictive accuracy of genomic estimated breeding values (GEBVs). Although modern genomic selection (GS) programs utilize high-density single nucleotide polymorphism (SNP) markers to capture genetic variation comprehensively, the polygenic nature of these traits inherently restricts the performance of prediction models (Calus & Veerkamp, 2007; Goddard et al., 2010; Liu et al., 2011).

Furthermore, environmental factors play a substantial role in shaping the phenotypic expression of these traits, adding another layer of complexity to prediction efforts. Traits with strong environmental influence tend to exhibit greater phenotypic variability that is not attributable to genetic differences, thereby diluting the genetic signal available for selection. This environmental noise reduces the reliability of GEBVs, especially when the genetic architecture is highly polygenic. Consequently, despite technological advances in genotyping and statistical modeling, the interplay between polygenicity and environmental variation remains a primary bottleneck in achieving high accuracy in genomic predictions for these economically critical traits. Addressing these challenges requires continued refinement of models that can better integrate genetic and environmental data to improve prediction reliability (Habier et al., 2013; Jayasinghe et al., 2024).

9.1.2. Genotype–Environment Interaction (G×E)

In production systems characterized by substantial environmental variation, the accuracy of genomic predictions often suffers due to the complex interactions between genotype and environment (G×E). For instance, in heat-stressed environments, thermoregulatory responses can significantly influence gene expression patterns, thereby altering phenotypic outcomes and reducing the predictive power of genomic models that do not account for such stressors. Similarly, variable feeding regimes can modify metabolic pathways, leading to differential gene expression and physiological adaptations that challenge the stability of genomic predictions. Extensive production systems with heterogeneous management practices further exacerbate this variability, as diverse environmental conditions and management inputs create a broad spectrum of phenotypic responses that are difficult to capture with standard genomic prediction models (Calus et al., 2016; Slater et al., 2022).

To address these challenges, future genomic selection (GS) frameworks must explicitly incorporate G×E interaction models to enhance prediction robustness across diverse and fluctuating environments. Integrating environmental covariates and interaction terms into GS models will enable a more accurate representation of how genotypes perform under varying conditions, improving the reliability of selection decisions. This approach will facilitate the development of breeding strategies that are resilient to environmental heterogeneity, ultimately optimizing genetic gain in real-world production settings. By embracing G×E models, breeders can better predict performance stability and adaptability, which are critical for sustainable genetic improvement in complex, variable production environments (Morais Júnior et al., 2018; Mulder, 2016).

9.2. Modeling Challenges

Linkage disequilibrium (LD) reflects the non-random association of alleles at different loci and varies considerably among breeds, lines, and composite populations due to their unique breeding histories, effective population sizes, and selection pressures. This variability in LD patterns poses significant challenges for genomic prediction models, as models trained on one population often fail to generalize effectively to others. The problem is particularly acute in species like sheep, goats, and poultry, where populations tend to be highly structured and fragmented, with reference datasets typically limited to specific breeds. Such population stratification reduces the accuracy of across-breed genomic predictions because the underlying LD structure and allele frequencies differ substantially between populations (Daetwyler et al., 2012; Ma et al., 2024; Song et al., 2019).

To overcome these limitations, enhancing across-breed prediction accuracy requires leveraging more comprehensive genomic information beyond single-marker effects. Incorporating deeper genomic features such as functional annotations—identifying regions of the genome with biological significance—and haplotype-based models that consider blocks of linked variants can capture the shared genetic architecture more effectively across diverse populations. These approaches enable models to exploit conserved genomic segments and functional elements that transcend breed boundaries, thereby improving the transferability of prediction models. Developing methodologies that integrate these richer genomic data layers is essential for advancing genomic selection in fragmented populations and for achieving robust, cross-population predictive performance (Ma et al., 2024).

9.3. Capturing Non-linear Genetic Relationships

Traditional linear models like GBLUP operate under the assumption that genetic effects are additive, which limits their capacity to capture more complex genetic phenomena such as dominance, epistasis, and higher-order interactions. These non-additive genetic effects can contribute significantly to the genetic architecture of complex traits, making purely additive models insufficient for accurate genomic prediction in many cases. Consequently, there is a growing need for more flexible modeling approaches that can accommodate these complex relationships to improve predictive performance (Dos Santos et al., 2016; Duenk et al., 2019).

Deep learning (DL) models offer a promising alternative due to their ability to model nonlinear and intricate patterns in genomic data. However, their application in genomic selection (GS) is hindered by several challenges. The "black-box" nature of DL algorithms results in limited interpretability, making it difficult to trace decision pathways, understand biological relevance, or identify causal variants underlying predictions. This opacity complicates error diagnosis and reduces user trust. Explainable AI (XAI) methods are therefore critical for enhancing transparency and interpretability in DL-based GS. Additionally, DL models demand large, diverse training datasets to prevent overfitting and ensure generalizability. In livestock species with small or limited reference populations—particularly in small ruminants and minor breeds—this data requirement restricts the practical utility of DL approaches, underscoring the need for strategies to overcome these limitations (Singh et al., 2024; Zhang et al., 2022).

10.CONCLUSION AND GENERAL EVALUATION

Genomic selection has revolutionized livestock breeding by enabling the prediction of an animal's genetic potential with unprecedented precision and efficiency. By leveraging dense genome-wide markers, breeders can now capture the effects of numerous quantitative trait loci simultaneously, which significantly enhances the accuracy of estimated breeding values compared to traditional pedigree-based methods. The establishment of large, well-characterized reference populations has been critical in calibrating these genomic prediction models, allowing for robust estimation of marker effects across diverse breeds and populations. Furthermore, advancements in statistical modeling, including Bayesian approaches and machine learning algorithms, combined with AI-driven frameworks, have facilitated the integration of complex genomic data and improved the prediction of economically important traits, such as growth rate, disease resistance, and fertility (Chakraborty et al., 2022; Wellmann & Bennewitz, 2012)

Beyond the core genomic data, the integration of multi-omics layers—such as transcriptomics, proteomics, and metabolomics—holds great promise for further refining selection accuracy and understanding the biological mechanisms underlying complex traits. This holistic approach enables breeders to incorporate functional genomic information, thereby enhancing the ability to predict phenotypes under varying environmental conditions and management practices. Economically, genomic selection accelerates genetic gain while reducing generation intervals and costs associated with progeny testing, ultimately improving productivity and sustainability in livestock systems. Looking ahead, continued innovation in data collection technologies, computational methods, and the expansion of global genomic resources will drive the evolution of genomic selection, fostering precision breeding strategies that address emerging challenges in animal agriculture (Choudhary et al., 2024; Li et al., 2024).

10.1. Strengthening of Scientific Foundations

The success of genomic selection has been propelled by significant advancements in molecular genetics that have enhanced the resolution and accuracy of genetic analyses. Key developments include a refined understanding of genome structure and the delineation of linkage disequilibrium (LD) blocks, which enable more precise identification of genomic regions associated with traits of interest. The discovery and mapping of quantitative trait loci (QTL) have provided critical targets for selection, while the creation of high-density single nucleotide polymorphism (SNP) genotyping arrays has allowed for comprehensive and cost-effective genotyping across diverse populations. Collectively, these innovations have improved the characterization of genetic diversity and the establishment of robust reference populations in economically important livestock species such as cattle, sheep, goats, pigs, and poultry, thus facilitating more efficient and reliable genomic predictions (Hayes & Goddard, 2010; Iheshiulor et al., 2016).

Moreover, the integration of multi-omics datasets—encompassing transcriptomics, epigenomics, microbiomics, proteomics, and metabolomics—has enriched the biological context underlying genomic selection. These multi-layered data sources reveal complex interactions between gene expression, regulatory elements, and phenotypic traits, providing a holistic view of the genetic architecture of complex traits. By linking molecular mechanisms to observed phenotypes, researchers can better understand gene regulation, pleiotropy, and environmental influences, thereby enhancing the predictive power and functional interpretation of genomic selection models. This systems-level approach, as highlighted by Roukos et al. (2021), supports the development of more precise breeding strategies that consider not only genetic markers but also the dynamic biological pathways influencing trait variation (Hay, 2024; Ma et al., 2024).

10.2. Evolution of Statistical Models

In the early stages of genomic selection, linear models such as GBLUP, Bayesian Ridge Regression, and BayesA/B/C were foundational due to their simplicity and interpretability. These models assume additive genetic effects and linear relationships between markers and traits, which limits their ability to capture the complexity inherent in biological systems. As genomic datasets grew larger and more complex, researchers recognized the need for more flexible modeling approaches capable of representing non-linear and interactive genetic architectures (Hay, 2024).

The advent of machine learning (ML) and deep learning (DL) methods marked a significant evolution in genomic prediction. These approaches can model complex patterns such as epistatic interactions (interactions between genes), gene–environment interactions, and other non-linear genetic relationships that linear models cannot adequately capture. Kernel-based methods extend this flexibility by implicitly mapping data into higher-dimensional spaces, enhancing predictive performance. Additionally, the integration of explainable artificial intelligence (XAI) tools has improved the interpretability of these complex models, allowing researchers to better understand the biological significance of predictions. Collectively, these second-generation genomic prediction methods have substantially increased prediction accuracy for complex traits, enabling more effective selection strategies in breeding programs (Montesinos-López et al., 2021).

10.3. Role of Digital Phenotyping and Sensor Technologies

Modern livestock production increasingly leverages IoT-based sensor technologies to gather continuous, high-resolution data on various animal traits such as activity levels, feed consumption, rumination behavior, health indicators, and other behavioral characteristics. These sensors enable the collection of dynamic phenotypic data in real time, providing a detailed and nuanced understanding of individual animal status and performance. When this wealth of phenotypic information is combined with AI-driven analytical frameworks, it substantially improves the precision of predictive models, especially for traits related to health, behavior, and welfare. This enhanced predictive capability supports more timely and informed decision-making in livestock management, allowing for early detection of health issues, optimization of feeding strategies, and overall improvement of animal well-being (Lamanna et al., 2025; Neethirajan, 2023).

The integration of continuous phenotypic monitoring with genomic selection marks a significant evolution in breeding and farm management practices. Traditionally, genomic selection has been a static process focused on genetic evaluation based on historical data. However, by incorporating real-time sensor data analyzed through AI models, genomic selection transforms into a dynamic decision support system. This system can adapt to changing conditions on the farm, providing actionable insights that guide management interventions and breeding decisions in near real time. Such a shift not only enhances the accuracy of genetic evaluations but also bridges the gap between genetic potential and actual animal performance, ultimately contributing to more sustainable, efficient, and welfare-conscious livestock production (Fatoki et al., 2024; Vlaicu et al., 2024).

10.4. Economic and Sustainability Benefits

Genomic selection drives economic gains primarily by shortening the generation interval, which accelerates genetic progress across livestock populations. Enhanced prediction accuracy allows breeders to identify superior animals more reliably, leading to improved traits such as feed efficiency and disease resistance. These improvements reduce production losses and lower overall costs, directly benefiting profitability. For example, in dairy cattle, the implementation of genomic selection has been quantified to yield an annual economic advantage of approximately 50–100 USD per cow, reflecting significant returns on investment in breeding programs (Wiggans et al., 2011).

From a sustainability standpoint, genomic selection contributes to climate-positive livestock production by mitigating environmental impacts and promoting animal health. Reduced methane emissions and decreased reliance on antibiotics help address key concerns related to greenhouse gases and antimicrobial resistance. Additionally, the development of heat-tolerant and climate-resilient breeds supports adaptation to changing environmental conditions, while efforts to preserve genetic diversity ensure long-term population viability. Together, these factors position genomic selection as a strategic tool for advancing both economic and ecological goals in modern animal agriculture (Sachdeva et al., 2025; Strandén et al., 2019).

10.5. Challenges and Areas Requiring Further Development

Despite its transformative potential, genomic selection faces several significant challenges that hinder its widespread and effective application in breeding programs. One major limitation is the generally low accuracy of across-population predictions, which restricts the transferability of genomic prediction models between different genetic backgrounds or environments. This issue is exacerbated for traits with low heritability, where the genetic signal is weak and difficult to capture accurately. Additionally, the scarcity of large, high-quality phenotypic and genotypic datasets, often compounded by sensor errors and inconsistencies in data collection, limits the robustness and reliability of genomic predictions. The high costs associated with genotyping and maintaining the necessary data infrastructure also pose substantial barriers, particularly for breeding programs with limited resources (Barwant et al., 2024; Demircioglu, 2024).

Beyond technical and economic constraints, genomic selection raises ethical and regulatory concerns, including the risk of genetic erosion and increased inbreeding as selection intensifies within narrower genetic pools. These challenges underscore the need for sustainable breeding strategies that not only aim for genetic gain but also preserve long-term population resilience. Addressing these issues will require concerted efforts to develop larger and more genetically diverse reference populations, facilitated by international data-sharing initiatives that enhance the breadth and depth of available data. Furthermore, breeding programs must integrate practices that balance short-term improvements with the conservation of genetic diversity to mitigate risks associated with inbreeding and maintain adaptability to future environmental changes (Clark et al., 2013; De Beukelaer et al., 2017).

10.6. The Future Selection Paradigm

Over the past decade, genomic selection has evolved through the integration of diverse biological data types and advanced computational methods, significantly enhancing the precision and scope of breeding programs. Multi-omics data fusion now enables the simultaneous analysis of genomic, epigenomic, transcriptomic, microbiome, and metabolomic information, providing a holistic view of the biological systems that underpin traits of interest. This integrative approach, combined with AI-driven predictive frameworks, facilitates more accurate and robust predictions of complex traits by capturing interactions across multiple biological layers. Hybrid models that merge deep learning with explainable AI (XAI) techniques further advance this field by not only improving predictive accuracy but also offering biological interpretability, which is crucial for understanding the underlying genetic mechanisms and ensuring trust in AI-assisted decisions (Hu et al., 2019; Xu et al., 2025).

In parallel, technological innovations in phenotyping and genome editing are transforming breeding strategies. Autonomous phenotyping platforms employ automated camera systems, RFID sensors, thermal imaging, and behavioral classifiers to collect high-resolution, real-time data on animal traits and behaviors, vastly increasing throughput and reducing human error. The integration of genome editing tools such as CRISPR and prime editing into breeding programs allows for precise genetic modifications that complement genomic selection, accelerating genetic gains while maintaining genetic diversity. Additionally, the concept of digital twin livestock—virtual replicas that integrate genomic, phenotypic, and environmental data—enables simulation-driven optimization of breeding decisions under varying scenarios. Collectively, these advancements herald the era of Precision Breeding, characterized by data-rich, sustainable, and AI-assisted genetic improvement systems that promise to revolutionize animal breeding with unprecedented accuracy and efficiency (Brito et al., 2020b; Klingström et al., 2024).

10.7. General Conclusion

Genomic selection has revolutionized livestock breeding by enabling the use of comprehensive genetic information to predict the breeding value of animals with unprecedented accuracy. This approach leverages large-scale genomic data and advanced computational models to accelerate genetic gain far beyond what traditional selection methods could achieve. The integration of data-intensive techniques allows breeders to make rapid, informed decisions, optimizing traits that enhance productivity, disease resistance, and environmental adaptability.

Consequently, genomic selection not only improves economic returns by increasing efficiency and output but also supports sustainability by promoting traits that reduce the environmental footprint of livestock production.

Moreover, the convergence of genomic technologies with artificial intelligence further amplifies the potential of livestock improvement programs. AI-driven analytics can uncover complex genetic interactions and predict outcomes under diverse environmental conditions, facilitating more precise and adaptive breeding strategies. This synergy is critical in addressing global challenges such as food security and climate change, as it enables the development of resilient livestock populations tailored to evolving production systems. Ultimately, genomic selection forms the cornerstone of a future livestock industry that is integrated, intelligent, and sustainable, ensuring long-term viability and responsiveness to societal needs.

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