

Recent trends in genomic selection for livestock

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KEY WORDS: artificial intelligence, genomic selection, livestock breeding, multi-omics, whole genome sequencing

Received: 8 August 2025
Revised: 17 September 2025
Accepted: 29 September 2025

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ABSTRACT. Genomic selection (GS) has emerged as a transformative tool in livestock breeding, enabling the accurate and efficient improvement of genetic traits. This review provides a comprehensive overview of the recent advancements in GS technologies, focusing on key innovations such as high-density single nucleotide polymorphism arrays, whole genome sequencing, and advanced imputation methods. Our review examines how GS is being applied across major livestock species, including cattle, swine, and poultry. These applications enhance productivity traits, while simultaneously improving disease resistance and environmental adaptability. This review highlights the integration of multi-omics data, spanning from genomics to microbiomics. Additionally, we emphasize the growing role of artificial intelligence in refining genetic evaluation models. The development of new trends holds promise for accelerating genetic improvements and broadening the range of traits that can be enhanced. The implementation of GS brings about hurdles such as requiring enhanced multi-omics data integration and improved genomic prediction models, while resolving ethical issues related to advanced breeding technologies, including genome editing. GS is poised to be an essential element for achieving sustainable livestock production. Improving the efficiency and climate resilience it will contribute to global food security and support long-term sustainability of animal agriculture.

Introduction

The field of livestock breeding has undergone significant changes in recent decades, transitioning from traditional selection based on visible traits and ancestry records to modern genomic selection (GS) techniques (Meuwissen et al., 2001; VanRaden, 2008). The emergence of molecular genetics along with high-throughput sequencing technologies has advanced the discovery of genetic markers for economically vital traits that have enhanced breeding programs through improved precision and efficiency (Goddard and Hayes, 2007; Hayes et al., 2009). GS uses single nucleotide polymorphism (SNP) markers across the genome to determine estimated

genomic breeding values, which helps breeders make early and better-informed decisions during animal development (Meuwissen et al., 2001).

Traditional breeding methods depend mainly on phenotypic selection and pedigree-based genetic assessments, along with limitations caused by environmental factors and lengthy generation intervals, which produce inaccurate breeding value estimates (Hill and Mackay, 2004). Marker-assisted selection, which represents the first step toward molecular breeding, is limited by its reliance on a small number of markers, which have been proven insufficient to capture the polygenic nature of complex traits (Lander and Botstein, 1987; Meuwissen et al., 2001; Visscher et al., 2006).

Several key technological advancements have underpinned the success of GS. The development of high-density SNP arrays has facilitated cost-effective genotyping of large populations (Goddard and Hayes, 2007), whereas whole-genome sequencing (WGS) has provided a more comprehensive view of genetic variation (VanRaden, 2008). Statistical approaches such as genomic best linear unbiased prediction (GBLUP) and Bayesian models have been developed to enhance the estimation of genomic estimated breeding values with high precision (Meuwissen et al., 2001; VanRaden, 2008). These models use extensive genomic and phenotypic datasets for enhanced accuracy of predicted breeding values. Innovations in computational methods, such as mixed linear models and regularization techniques, have improved prediction models by enhancing their scalability for processing large datasets (Hayes et al., 2009; Habier et al., 2013).

GS offers several benefits over conventional breeding approaches. It utilizes genome-wide markers to lower environmental uncertainty, while increasing the precision of breeding value predictions (Hayes et al., 2009). Early-life genotyping enables breeders to make selection decisions prior to reproductive maturity, thereby accelerating cumulative genetic progress through shorter generational intervals and the evaluation of more generations (Goddard and Hayes, 2007). Although marker-assisted selection focuses on specific loci, GS simultaneously evaluates multiple small-effect loci, which makes it effective for complex traits, such as milk yield, feed efficiency, and disease resistance (Meuwissen et al., 2001; Visscher et al., 2006). GS has multiple benefits; however, it encounters numerous challenges. It requires considerable investment in both genotyping and computational infrastructure, which present limitations for smaller breeding operations (VanRaden, 2008; Hayes et al., 2009). Genomic prediction accuracy depends on well-established reference populations that require extensive genotyping and phenotyping efforts requiring significant time and resources (Meuwissen et al., 2001). The use of genomic data in intense selection processes can reduce genetic diversity, leading to significant inbreeding depression and decreased adaptability to environmental changes (Hill and Mackay, 2004; Visscher et al., 2006). Ongoing improvements in GS are expected to have multiple transformative effects on livestock breeding practices. Breeding efficiency

and selection accuracy can be improved by integrating GS with real-time phenotypic monitoring using wearable sensors and automated systems (Goddard and Hayes, 2007; VanRaden, 2008). Although SNP-based GS remains a common practice, structural variants, including copy number variations and insertions or deletions, have a significant impact on trait variation and should be integrated into selection models (Visscher et al., 2006; McCarthy et al., 2008). The increasing challenges of global climate change in livestock production demand the use of GS to identify and spread traits that enhance heat tolerance and reduce methane emissions and drought resistance (Meuwissen et al., 2001; Hayes et al., 2009). The evolution of genomic technologies requires livestock breeders to manage the integrated complexities of GS and new developments in artificial intelligence, genome editing, and multi-omics tools. The next phase of research should aim to refine genomic prediction models, while growing reference populations and creating affordable genotyping methods to enhance GS benefits in various livestock sectors (Figure 1).

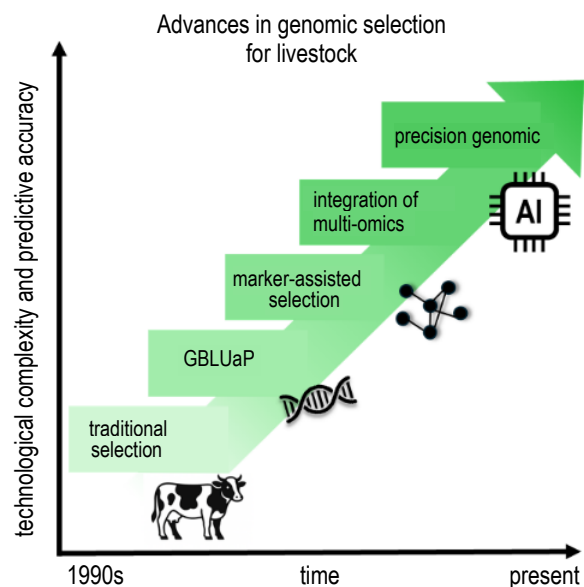


Figure 1. Advances in genomic selection for livestock

Conceptual illustration of the progressive development of genomic selection (GS) technologies for livestock. A visual staircase depicts the transition from traditional phenotypic and pedigree-based selection to genomic best linear unbiased prediction (GBLUaP), marker-assisted selection, and integration of multi-omics data. The final step represents the advancement of precision genomic selection supported by artificial intelligence (AI). Each stage reflects an increased genetic prediction accuracy and the incorporation of more complex biological information into breeding programs.

Advances in genomic selection technologies

High-density SNP arrays and whole-genome sequencing

The evolution of genotyping technology plays a crucial role in the success of GS through the development and adoption of high-density SNP arrays and WGS (Hayes et al., 2009). The first SNP arrays were limited in their marker count, which restricted their resolution and ability to detect comprehensive genomic variations in livestock populations (Goddard and Hayes, 2007). Recent improvements in chip design and progress in manufacturing have enabled scientists to produce high-density SNP panels containing hundreds of thousands to millions of markers (Matukumalli et al., 2009). High-density SNP arrays have enhanced the accuracy of genomic evaluation because of their ability to generate detailed genetic diversity maps and linkage disequilibrium patterns (Guo et al., 2021). The falling expenses and growing efficiency of sequencing technologies have enabled livestock researchers and breeders to utilize WGS more easily (Elsik et al., 2009). WGS delivers comprehensive genetic data by identifying common and rare variants, as well as structural variations and novel polymorphisms that traditional array-based genotyping tends to overlook (Liu and Bickhart, 2012). WGS improves genomic predictions when combined with existing SNP array data through gap filling, mutation detection, and imputation accuracy (Howie et al., 2012). Imputation has become vital for data standardization across genotyping platforms, while maximizing genomic resource utility using reference panels to predict missing genotypes (Marchini and Howie, 2010). These advancements help improve the accuracy of genomic breeding value (Daetwyler et al., 2008) and allow researchers to detect trait-related loci and explore intricate gene networks (Mackay et al., 2005). Modern livestock breeding programs rely on high-density SNP genotyping combined with WGS to create a scalable and high-resolution genomic foundation that enables genetic progress tracking and selection response improvement, while enhancing the understanding of the genetic structure of economically important traits' genetic structure (Woolliams et al., 2015).

Development of genomic prediction models in livestock breeding

Development and refinement of genomic prediction models are pivotal for translating raw

genomic data into meaningful breeding values that guide selection decisions (Meuwissen et al., 2001). Among the foundational models, best linear unbiased prediction has long served as the standard method for estimating breeding values based on pedigree and phenotypic information (Henderson, 1984). However, the integration of genomic data has necessitated an extension of this approach, giving rise to GBLUP (VanRaden, 2008). The use of genomic relationship matrices from SNP data within GBLUP enhances breeding value prediction accuracy through the use of actual genetic relationships rather than relying solely on pedigree-based expected relationships (Hayes et al., 2009). This new approach will enable breeders to capture greater portions of the true genetic variance responsible for complex traits (Goddard and Hayes, 2009). Bayesian models have been identified as effective substitutes for GBLUP, particularly for genetic traits affected by several loci with significant effects and many loci with minimal effects (Heffner et al., 2009). Bayesian methods such as BayesA, BayesB, BayesC, and BayesR employ distinct strategies for modelling SNP effect distributions and setting prior assumptions about these effects, according to a previous study (Habier et al., 2013). BayesA operates under the assumption that every marker has an effect and uses a scaled t-distribution for these effects, whereas BayesB applies a prior probability that some markers have no effect, resulting in sparse solutions that are better suited to specific traits (Shi et al., 2021). BayesR developed these concepts by enabling marker effects to come from multiple normal distributions that possess different levels of variance, creating an adaptable framework that aligns well with the specific genetic structure of the analysed trait (Erbe et al., 2012). Artificial intelligence (AI)-based methods in livestock breeding require further refinement and validation, yet they show potential for better prediction outcomes and the discovery of new genetic information that conventional methods fail to reveal (Abdollahi-Arpanahi et al., 2020). Future genomic prediction models need to maintain an equilibrium between their predictive accuracy, interpretability, and computational efficiency, while also advancing in their methodological development (de Los Campos et al., 2013; Eraslan et al., 2019). Future livestock breeding strategies will likely combine traditional statistical methods and the complex problem-solving capabilities of modern machine learning techniques into hybrid models (Figure 2) (Nayeri et al., 2019).

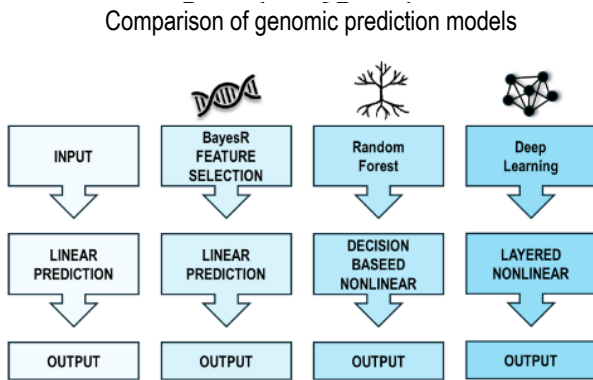


Figure 2. Comparison of genomic prediction models

Comparative scheme of genomic prediction models applied to livestock breeding. The figure outlines the progression from traditional linear models (e.g., genomic best linear unbiased prediction (GBLUP)) to Bayesian methods (e.g., BayesR with feature selection) and further to machine-learning approaches, including Random Forest and Deep Learning. However, GBLUP and BayesR produce linear predictions based on genomic features, Random Forest utilizes decision-based nonlinear structures, and Deep Learning leverages multilayered nonlinear transformations to capture complex genetic architectures. This reflects the increasing capacity of newer models to handle high-dimensional and nonadditive genetic effects.

The maturation of GS reveals that integrating multi-omics data is crucial for improving predictive power and biological relevance (Chaisson et al., 2015). The incorporation of transcriptomic, epigenomic, proteomic, metabolomic, and microbiome data analyses provides a complete picture of the molecular processes driving complex traits (Cohen et al., 2017). The multi-omics approach provides specific insights into gene regulatory mechanisms and expression patterns that affect epigenetic and host-microbiome interactions, resulting in phenotypic diversity among livestock species (Biscarini et al., 2020). Researchers can capture gene expression patterns linked to advantageous traits across different physiological and environmental settings using transcriptomic tools, such as RNA sequencing (Conesa et al., 2016). Epigenomic research has demonstrated reversible heritable changes, such as DNA methylation and histone modifications, which alter gene expression patterns without changing the underlying DNA sequence (Kelsey et al., 2017). Environmental elements influence epigenetic markers, which in turn determine phenotypic characteristics (Feil and Fraga, 2012).

Wang et al. (2020) demonstrated that the gut microbiome affects feed efficiency, immune system performance, and disease resistance. Functional genomic methods have been used to identify causal genetic variants and networks (de Souza Fonseca et al., 2022). The expression Quantitative Trait Loci

mapping establishes connections between genetic variants and gene expression levels according to Albert and Kruglyak (2015).

Multi-omics integration marks a groundbreaking advancement in GS according to Ye et al. (2020). However, certain challenges still remain (Subramanian et al., 2020). These findings suggest substantial potential benefits (Yan et al., 2021).

Applications of genomic selection in livestock

The integration of GS into livestock breeding practices has allowed breeders to perform accurate genetic assessments of several animal species (Lee et al., 2024). The implementation of GS produces quantifiable benefits in productivity, health, and efficiency, and each species is associated with specific challenges and opportunities (Mukherjee et al., 2024). This section examines how GS is applied to cattle, swine, and poultry as well as its transformative effects on modern animal farming practices. The dairy and beef cattle industries have experienced significant genetic improvements owing to GS techniques. Through the use of GS in dairy cattle, early detection of superior genetic merits has gained accuracy in milk yield, composition (including fat and protein content), and disease resistance traits such as mastitis and lameness (Boichard et al., 2012). Resultantly, productivity levels have risen and animal welfare standards have enhanced. Genetic advancement has accelerated because calf genotyping lowers the dependence on progeny testing, resulting in shorter generation intervals (Boichard et al., 2012). GS in beef cattle targets important traits such as carcass quality, growth rate, and feed efficiency (Nwogwugwu et al., 2020). Traits that hold economic value present challenges to traditional measurements. Through genomic tools, breeders can now evaluate the genetic potential of key traits in young animals, leading to improved mating choices, better meat quality, and increased profitability (Van Eenennaam et al., 2014). Swine breeding programs have achieved substantial development through GS, which improved the growth rate, feed conversion efficiency, and reproductive performance. Swine breeding programs display rapid reproductive cycles with short generational gaps, enabling rapid progress in genomic research. The integration of genomic data enables breeders to recognize elite animals at an earlier stage with higher accuracy (Jones and Wilson, 2022). The incorporation of genomic data has produced better daily weight gain outcomes and lower feed expenses, while improving reproductive

performance through larger litter sizes and higher piglet survival rates (Davoudi et al., 2022). The adoption of GS for disease resistance traits continues to grow as these traits present complex polygenic challenges that traditional selection methods have struggled to address. The development of more disease-resistant swine breeds is possible when breeders identify genetic markers linked to resistance against common diseases, such as porcine reproductive and respiratory syndrome (Davoudi et al., 2022).

GS in poultry breeding programs primarily targets enhancements in egg production rates, meat output, and disease resistance capabilities. The poultry industry is an optimal setting for the implementation of genomic technology because of its high individual throughput, extensive pedigree, and phenotypic data availability. GS helps layer breeds improve their egg output and shell quality along with increasing laying persistence, whereas broilers gain better growth rates and feed efficiency through improved breast muscle development (Liu et al., 2014). Genomic methods have demonstrated effectiveness in selecting poultry resistant to diseases, such as avian influenza, Newcastle disease, and coccidiosis (Liu et al., 2014). Poultry production systems have achieved superior production traits and strengthened sustainability along with biosecurity through genomic integration, allowing birds to adapt to diverse environmental conditions (Bist et al., 2024).

GS has proven effective in cattle, swine, and poultry to speed up genetic advancement, while also advancing animal health and welfare and boosting production efficiency. The accessibility and refinement of genomic tools will broaden their impact on livestock breeding and provide sustainable ways to ethically satisfy the increasing global demand for animal-derived foods (Yanez et al., 2022).

Emerging trends in genomic selection

The combination of AI and big-data analytics represents a significant breakthrough in GS in livestock genetics. Modern technologies have transformed traditional breeding approaches through their ability to examine large datasets and reveal patterns that conventional statistical methods cannot reveal (Garcia-Ruiz et al., 2016). AI assumes a vital function in extracting valuable insights as livestock data expand in both quantity and diversity across genomics, phenomics, environmental sensors, and management practices (Hickey et al., 2017).

Deep learning, which belongs to the AI domain, has become an exceptionally effective approach for

genomic prediction because it can model complex nonlinear relationships and high-dimensional interactions between genetic markers (Montesinos-Lopez et al., 2018). Deep-learning methods, such as convolutional and recurrent neural networks, surpass traditional models by learning complex data dependencies and hierarchical structures without relying on linearity or additive genetic assumptions (Abdollahi-Arpanahi et al., 2020). These models excel at accurately predicting complex traits when combined with multi-omics data and environmental factors according to Gonzalez-Recio et al. (2015). Deep-learning automation of feature extraction minimizes the need for domain-specific expertise, while improving genomic evaluation strength across various populations and conditions (Ahmed et al., 2023).

Precision livestock farming has transformed phenotyping owing to its capacity for real-time detailed tracking of animal health, behaviour, and productivity metrics (Berckmans, 2014). A continuous flow of phenotypic data from automated phenotyping tools, such as image analysis systems and Internet of Things-enabled devices, can be integrated with genomic data to improve breeding value prediction (Rutten et al., 2013). The transition to detailed phenotyping methodologies has increased selection precision, while allowing breeders to incorporate new traits, such as welfare benchmarks, feed consumption behaviours, and environmental adaptation capabilities, into breeding goals. The uniform collection and merging of phenotypic information from various farms and systems provide big-data resources that enable genomic prediction models to achieve broader applications (Pszczola et al., 2012). The implementation of big-data techniques improves genetic evaluation by allowing longitudinal and multi-environmental data along with the incorporation of genotype-by-environment interactions and environmental sustainability metrics (Crossa et al., 2017). AI-driven models exhibit adaptability to changing datasets because they constantly learn and refine their performance through new data inputs (Olawumi and Oladapo, 2025). The ability to dynamically respond to environmental changes is beneficial for managing climate change and emerging diseases through rapid response and adaptive breeding approaches (Hayes and Daetwyler, 2019). Precision breeding of livestock is entering a new phase through the combined power of AI technology and big data with GS methods. The use of sophisticated computational methods combined with real-time phenotypic data enables breeders to achieve faster and more precise decision-making processes (Bishop and Woolliams, 2014).

The maturation and increased accessibility of these technologies will enable them to transform genetic improvement programs, while supporting sustainable and resilient livestock production worldwide (Georges et al., 2019).

Climate adaptation and resilience genomics

Modern breeding programs have shifted their focus to livestock adaptation capabilities because global climate change poses significant risks to agricultural productivity through environmental stressors such as heat and drought (Rojas-Downing et al., 2017). Climate adaptation and resilience genomics research focus on discovering genetic factors that help animals survive and prosper despite challenging environmental conditions (Hayes and Daetwyler, 2019). Using GS techniques, researchers and breeders have identified essential genes and pathways responsible for thermotolerance and immune function, alongside metabolic regulation, which are vital for environmental resilience (Bishop-Williams et al., 2015).

Researchers have focused heavily on identifying the genes that enable organisms to resist heat stress. Heat stress negatively affects animal feed consumption, fertility, and milk output, while adversely affecting general animal welfare (Carabano et al., 2016). Genomic studies have identified alleles and haplotypes associated with superior thermoregulation, including genes affecting sweat gland function (ATP1A1), skin pigmentation (MC1R), and heat shock protein expression (HSP70) (Kim et al., 2016; Nguyen et al., 2016). The integration of genetic markers into selection indices supports the creation of heat-tolerant livestock breeds, while maintaining productivity (Taye et al., 2017). Researchers have discovered adaptive traits faster because high-throughput genotyping and phenotyping platforms enable precise breeding strategies (Brito et al., 2020).

In addition to specific alleles and heat-response genes, transcription factors play a pivotal role in mediating livestock responses to environmental stressors, such as drought and heat (Figure 3). Several families of transcription factors, including NAC, bZIP, MYB, WRKY, AP2/ERF, C2H2, and bHLH, have been identified as key regulators of gene networks involved in abiotic stress tolerance in plants and are under investigation in animal models (Wang et al., 2025).

These transcription factors control the downstream expression of stress-responsive genes, thereby enhancing the physiological adaptation to challenging conditions (Nakashima et al., 2009).

Advanced breeding strategies that enhance livestock system sustainability under development, along

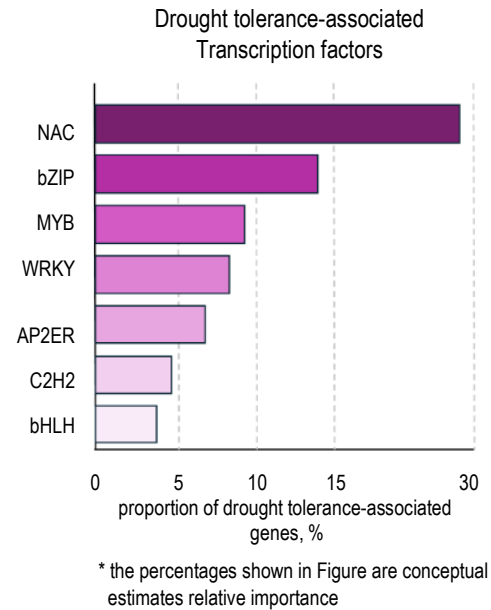


Figure 3. Drought tolerance-associated transcription factors

Bar chart depicting the relative involvement of transcription factor families implicated in livestock adaptation to abiotic stresses such as drought and heat. The chart ranks NAM, ATAF1/2, and CUC2 (NAC), Basic Leucine Zipper (bZIP), Myeloblastosis (MYB), WRKY domain (WRKY), APETALA2/Ethylene-Responsive Factor (AP2/ERF), Cys2-His2 zinc finger (C2H2), and Basic Helix-Loop-Helix transcription factors (bHLH) according to their known regulatory influences on stress-responsive gene expression. These transcription factors modulate downstream pathways involved in thermoregulation, metabolic balance, and cellular protection mechanisms, making them critical targets for climate-resilient breeding strategies.

with the discovery of genes associated with resilience (Garnett et al., 2013). These strategies include the combined use of GS and adaptive management practices, such as modifying breeding schedules to match seasonal changes or selecting animals that thrive under low-input conditions represent these strategies (van Marle-Koster et al., 2021). Researchers are adapting genomic prediction models to incorporate genotype-by-environment interactions which facilitate tailored selection decisions based on specific climatic and production conditions in animal rearing environments (Mollinari et al., 2020).

The combination of resilience genomics with epigenomic and microbiome datasets provides a more comprehensive view of animal responses to environmental stressors across both the molecular and systemic dimensions (Feder and Mitchell-Olds, 2003). Developing livestock populations that maintain productivity, while being strong and adaptable to changing climatic conditions requires a holistic understanding (Silva Neto et al., 2024).

Recent studies have enriched our understanding of heat adaptation in livestock. A 2025 review outlined simplified yet effective adaptation strategies

such as breed selection, shade provision, and feed interventions across scales from herd to national policy levels (Bashiru and Oseni, 2025). A complementary bibliometric analysis mapping the research landscape (1994–2023) emphasizes the growing trends in integrating genetics, management, and sustainability in adaptation studies (Manyike et al., 2025). Molecular insights are also advancing: one review highlights the role of epigenetic mechanisms such as DNA methylation in heat stress responses (Aravindh et al., 2025), and recent proteomic work in tropically adapted cattle identified candidate biomarkers linked to thermotolerance (de Freitas et al., 2024).

Resilience genomics functions as a forward-thinking method to secure livestock production against future challenges. The livestock industry can strengthen its response to environmental challenges and secure food and animal welfare through genetic diversity adoption and adaptive trait promotion alongside technological advancements (Thornton et al., 2022; Papadopoulos et al., 2025).

Genome editing and selection integration

Building on resilience genomics, which identifies naturally occurring adaptive traits, genome editing offers a complementary strategy by allowing the precise modification or introduction of these traits. This transition reflects a shift from understanding and selecting adaptive variation to actively engineering it and accelerating genetic improvement. Merging genome editing methods with GS represents a revolutionary advancement in livestock breeding (Van Eenennaam, 2017). CRISPR-Cas systems have become the foremost method for precise genetic editing because of their cost-effectiveness and efficiency, which allow direct modification of DNA sequences linked to important economic and environmental traits (Jinek et al., 2012). This combination enables researchers to precisely increase or decrease specific alleles chosen by GS, leading to faster genetic improvement outcomes (Mueller and Van Eenennaam, 2022).

The combination of CRISPR-based gene editing and GS transforms genetic improvement strategies from discovering natural variations to purposefully creating better genotypes (Tan et al., 2012). Traits with limited genetic variation in breeding populations or those that conventional selection struggles to improve demonstrate significant power in this approach (Burkard et al., 2017). Gene editing enhances disease resistance (Gao et al., 2017), improves feed

efficiency (Crispo et al., 2015), and reduces the environmental impacts of livestock production, such as methane emissions (Shi et al., 2022). Animal welfare benefits from gene editing by removing harmful mutations and adding alleles that enhance animal health and resilience (Tait-Burkard et al., 2018).

The introduction of genome editing into breeding programs requires a thorough analysis of ethical concerns alongside social implications and regulatory standards (Thompson, 1999). Animal welfare issues, biodiversity protection, and potential unintended genetic impacts require investigation through strict scientific evaluation processes and open communication with stakeholders (McFadden and Lusk, 2016). Different countries have demonstrated diverse regulatory approaches to genome editing, with some jurisdictions allowing more freedom, whereas others enforce strict controls or complete prohibitions (Ishii, 2015). The lack of uniform regulations across countries presents difficulties for the worldwide implementation of genetically edited animals and highlights the importance of creating unified global standards and policies (Smyth, 2020).

Public perception is of significant importance in determining how genome-edited animals are accepted by society (Frewer et al., 2013). The development of communication strategies that describe the advantages of gene editing and its risks and safety measures is vital for building knowledgeable public discussions (McFadden and Lusk, 2016). To responsibly and fairly implement genome editing in livestock breeding, aligning its applications with sustainability, food security, and animal welfare principles is critical (Singh and Ali, 2021).

Genetic improvement has reached new heights in precision and efficiency through the combination of genome editing and GS (Woolliams et al., 2015). The combination of genome editing and GS is a potent approach to solve complicated livestock production issues when operated under strong scientific evidence, ethical standards, and comprehensive governance systems (Lim and Choi, 2023).

Conclusions

Genomic selection (GS) has emerged as a cornerstone of modern livestock breeding, offering new opportunities to improve accuracy, efficiency, and the ability to evaluate complex traits. The integration of multi-omics data provides a deeper understanding of biological pathways and host–microbe interactions, enhancing predictive power for breeding strategies. Artificial intelligence and machine learning add further value by enabling the analysis

of vast datasets, identifying hidden patterns, and simulating breeding outcomes under diverse conditions. At the same time, genome editing expands the scope of genetic improvement but requires careful attention to ethical considerations, transparent governance, and public trust. As climate change, population growth, and resource limitations intensify, GS offers powerful tools to enhance productivity, sustainability, and resilience in animal agriculture. Realizing this potential will depend on interdisciplinary collaboration and responsible communication, ensuring that innovations translate into practical, socially responsible, and globally beneficial breeding solutions.

Funding

This research was supported by the 2024 Chung-Ang University Research Grant, the Korean Fund for Regenerative Medicine (KFRM) grant funded the Ministry of Science and ICT, the Ministry of Health & Welfare (25A0203L1) and the Bio&Medical Technology Development Program of the National Research Foundation (NRF) (RS-2023-00220207) of the Korea Grant-Funded (MSIT, Republic of Korea).

Conflict of interest

The Authors declare that there is no conflict of interest.

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