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Genomic Selection in Livestock Breeding: Opportunities for Improving Productivity and Disease Resistance

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ABSTRACT

Genomic selection has emerged as a transformative approach in livestock breeding, enabling the rapid and precise improvement of productivity and disease resistance traits. By leveraging high-density genomic markers and advanced statistical models, breeders can predict the genetic potential of animals with unprecedented accuracy, reducing generation intervals and accelerating genetic gains. This study reviews current methodologies, including single-step genomic best linear unbiased prediction (ssGBLUP) and machine learning–enhanced models, highlighting their application across major livestock species such as cattle, sheep, pigs, and poultry. Evidence indicates that genomic selection not only enhances growth, milk, and reproductive performance but also contributes significantly to resistance against prevalent diseases, thereby improving herd health and sustainability. Despite these benefits, challenges remain, including high genotyping costs, the need for robust reference populations, and ethical considerations related to genetic diversity. The study underscores the potential of integrating genomic selection with conventional breeding programs and emerging biotechnologies to achieve resilient, high-performing livestock populations. Future research should focus on optimizing genomic prediction models, exploring multi-trait selection strategies, and assessing long-term impacts on genetic diversity and animal welfare.

1. Introduction

Livestock production plays a critical role in global food security, rural livelihoods, and economic development. With the increasing demand for animal protein driven by population growth and rising incomes, enhancing livestock productivity while maintaining animal health has become a central goal for the agricultural sector. Traditional breeding approaches, primarily based on phenotypic selection, have achieved substantial genetic gains over decades (Kasimanickam, 2025). However, these methods are often time-consuming, less precise, and constrained by the need for extensive performance records, particularly for traits with low heritability or those expressed later in life.

The advent of genomic technologies has transformed animal breeding by enabling the direct assessment of genetic potential at the DNA level. Genomic selection (GS) refers to the use of genome-wide markers to predict the breeding value of individuals, allowing for the selection of animals based on their genetic merit rather than solely on observed performance (Jinya, 2024). This approach offers unprecedented accuracy in identifying superior animals and accelerates genetic progress across multiple traits simultaneously, including production traits such as growth rate, milk yield, and carcass quality, as well as functional traits like fertility, disease resistance, and feed efficiency.

One of the most promising applications of genomic selection is the enhancement of disease resistance in livestock populations. Infectious diseases are a major constraint in animal agriculture, leading to reduced productivity, increased production costs, and significant economic losses (Das, 2021). By incorporating genomic information into breeding programs, it is possible to identify animals with favorable alleles associated with disease resilience, thus reducing the reliance on antibiotics and other interventions while promoting sustainable production practices.

Despite its potential, the implementation of genomic selection in livestock breeding faces several challenges, including the high costs of genotyping, the need for large and accurately phenotyped reference populations, and the complexity of integrating genomic data into conventional breeding schemes (Hayes, 2013). Nevertheless, ongoing advancements in sequencing technologies, bioinformatics tools, and statistical models are rapidly overcoming these barriers, making genomic selection an increasingly feasible and cost-effective strategy for improving livestock productivity and health.

This study aims to review the current state of genomic selection in livestock breeding, highlighting its opportunities for enhancing productivity and disease resistance. The paper explores recent advancements, practical applications, and future prospects, providing a comprehensive overview for researchers, breeders, and policymakers seeking to optimize genetic improvement programs in livestock populations (Gutierrez-Reinoso, 2021).

2. Methodology

2.1 Literature Search Strategy

This review employed a systematic and comprehensive literature search to identify studies relevant to genomic selection in livestock breeding, with a particular focus on improving productivity and disease resistance. Scientific databases including PubMed, Web of Science, Scopus, and AGRICOLA were queried using combinations of keywords such as “genomic selection,” “livestock breeding,” “disease resistance,” “genomic prediction,” and “productive traits.” The search was restricted to articles published in English between 2000 and 2025 to capture both foundational research and recent advances. Reference lists of selected studies were further screened to identify additional relevant publications, ensuring a thorough coverage of the topic.

2.2 Inclusion and Exclusion Criteria

Studies were included if they reported on the use of genomic selection, genomic prediction models, or marker-assisted selection in livestock species, including cattle, sheep, goats, pigs, and poultry. Both experimental and observational studies were considered, provided they included measurable outcomes related to productivity traits such as growth rate, milk yield, feed efficiency, and reproductive performance, or disease resistance traits. Studies focusing solely on conventional breeding methods without genomic data, reviews lacking original data, or studies not peer-reviewed were excluded to maintain the quality and relevance of the evidence base.

2.3 Data Extraction and Organization

From each included study, relevant information was systematically extracted, including livestock species, sample size, genotyping platform, statistical models employed for genomic prediction, trait heritability, selection accuracy, and observed outcomes in productivity or disease resistance. Data were organized into thematic categories reflecting the core objectives of the review: advancements in genomic selection methodologies, improvement of production traits, and enhancement of disease resistance. This approach enabled comparison across studies and identification of trends, challenges, and knowledge gaps in the field.

2.4 Analytical Framework

The methodological analysis focused on evaluating the efficacy and applicability of genomic selection in livestock breeding. Studies were critically assessed for the type of genomic prediction models used, such as genomic best linear unbiased prediction (GBLUP), single-step GBLUP, Bayesian approaches, or machine learning models, and their relative accuracy in predicting breeding values. The review also examined the integration of genomic data with phenotypic records and environmental factors, assessing how this combination influences the accuracy of selection for both productivity and disease resistance traits. Furthermore, attention was given to the economic and practical feasibility of implementing genomic selection programs in different livestock production systems.

2.5 Synthesis and Interpretation

Findings from the selected studies were synthesized qualitatively to provide a comprehensive overview of current knowledge and emerging trends in genomic selection. Patterns were identified regarding species-specific effectiveness, trait heritability, and the impact of population structure on selection outcomes. The synthesis also highlighted technological advancements, such as high-density SNP arrays and whole-genome sequencing, that have enhanced the precision of genomic prediction. Potential limitations, such as small reference populations, high genotyping costs, and variable prediction accuracies across traits and environments, were critically analyzed to contextualize the results and guide recommendations for future research.

3. Findings and Discussion

3.1 Genetic Basis of Livestock Traits

Understanding the genetic architecture of economically important traits is foundational for implementing genomic selection in livestock breeding. Traits such as growth rate, reproductive performance, milk yield, and disease resistance are influenced by multiple genetic loci, environmental factors, and their interactions (Poland, 2016). Genomic selection leverages information on these genetic determinants to predict breeding values more accurately and accelerate genetic improvement.

3.1.1 Heritability Estimates

Heritability, which measures the proportion of phenotypic variance attributable to genetic factors, provides insight into the potential efficiency of selection programs. High heritability indicates that selection can effectively drive genetic progress, whereas low heritability suggests stronger environmental influence, limiting selection response. Studies have shown that growth traits in cattle, such as weaning and yearling weight, generally exhibit moderate to high heritability, ranging from 0.30 to 0.50 (Tade, 2024). Similarly, milk yield in dairy cattle shows heritability estimates between 0.25 and 0.35, reflecting moderate genetic control that allows effective selection over successive generations (Bora, 2023). In pigs, litter size traits tend to have lower heritability (~0.10–0.15), whereas backfat thickness and growth rate are moderately heritable (~0.25–0.40), highlighting species- and trait-specific differences (Xu, 2020). Comparatively, disease resistance traits often exhibit low to moderate heritability (0.05–0.30), reflecting complex polygenic control and significant environmental effects, as observed in mastitis resistance in dairy cows and PRRS resistance in pigs (Meuwissen, 2016). These variations underscore the need to tailor genomic selection strategies according to trait-specific heritability to maximize genetic gain.

3.1.2 Genetic Correlations

Genetic correlations describe the relationship between traits at the genetic level and are crucial in multi-trait selection programs. Positive correlations suggest that selection for one trait may improve another, while negative correlations indicate potential trade-offs. For instance, in dairy cattle, a positive genetic correlation between milk yield and udder health traits has been observed in some populations, suggesting simultaneous improvement is feasible (Burrow, 2021). Conversely, a negative correlation between growth rate and fertility in beef cattle indicates that rapid growth selection could inadvertently reduce reproductive efficiency, necessitating balanced selection indices (Stock, 2013). In pigs, genetic correlations between backfat thickness and growth rate are typically negative, meaning selection for leaner carcasses may slightly compromise growth (Plastow, 2016). Understanding these correlations is critical for optimizing selection strategies to avoid unintended consequences and to exploit synergistic relationships between traits for overall productivity and resilience.

3.1.3 Identification of Quantitative Trait Loci (QTL) and Candidate Genes

Genomic studies have identified numerous QTLs and candidate genes associated with productivity and disease resistance in livestock. In cattle, significant QTLs for milk yield and composition have been consistently mapped to chromosomes BTA14 and BTA20, with the DGAT1 and GHR genes frequently highlighted as key determinants (Arya, 2024). Growth traits are influenced by QTLs in regions containing genes such as MSTN and IGF1, which regulate muscle development and growth rates. In pigs, the IGF2 and MC4R genes have been repeatedly associated with growth performance and carcass traits (Jones, 2022). For disease resistance, candidate genes such as BoLA-DRB3 in cattle and RELA in pigs have been linked with immune response traits, reflecting potential for selective breeding to enhance resistance (Dube-Takaza, 2021). While many QTLs show consistency across studies, some are population- or breed-specific, emphasizing the importance of validating findings in target breeding populations before widespread application. These insights have facilitated the development of genomic selection models that integrate QTL information to improve prediction accuracy for complex traits, ultimately enabling faster and more precise genetic improvement.

3.2 Genomic Prediction Accuracy and Tools

The effectiveness of genomic selection (GS) in livestock breeding largely depends on the accuracy of predicting breeding values using genomic information. Our review of recent studies indicates that the predictive ability of GS varies across species, traits, and the genomic tools employed. High-density genomic data, combined with robust computational models, has significantly enhanced selection for complex traits such as milk yield in dairy cattle, growth rate in pigs, and disease resistance in poultry. For instance, studies in Holstein cattle have demonstrated that genomic estimated breeding values (GEBVs) can achieve prediction accuracies exceeding 0.7 for milk production traits, substantially outperforming traditional pedigree-based selection (Rotimi, 2025). Similarly, in pigs, genomic selection has improved accuracy for growth and carcass quality by 15–20% compared to conventional selection methods.

3.2.1 SNP Panels and Genotyping Technologies

Single nucleotide polymorphism (SNP) arrays remain the most widely used genotyping platform in livestock GS. Commercially available SNP panels, such as the Illumina BovineSNP50 and PorcineSNP60, provide dense coverage across the genome and enable high-resolution detection of quantitative trait loci (QTL). Low-density SNP panels have been explored as a cost-effective alternative, particularly in large-scale breeding programs, with imputation to higher density achieving near-equivalent prediction accuracy. Next-generation sequencing (NGS) approaches, including whole-genome sequencing (WGS), offer comprehensive coverage and allow the identification of rare and structural variants, although they remain more expensive and computationally intensive. Studies in dairy cattle show that WGS can improve the prediction of traits with low heritability, such as fertility, by capturing rare alleles not present on standard SNP arrays (ASLAM, 2024). Overall, the choice of genotyping technology reflects a trade-off between cost, coverage, and prediction performance.

3.2.2 Statistical Models and Algorithms

The predictive power of genomic selection also depends on the statistical and computational models applied. Genomic Best Linear Unbiased Prediction (GBLUP) remains the benchmark approach due to its simplicity and strong performance for traits controlled by many small-effect loci. Bayesian models, including BayesA, BayesB, and BayesR, account for variable marker effects and have shown superior prediction accuracy for traits influenced by a few major genes. More recently, machine learning algorithms, such as random forests and deep learning networks, have been explored for capturing non-additive genetic effects and complex interactions. For example, machine learning models have enhanced prediction for disease resistance in chickens and growth traits in beef cattle when compared to linear models (Hu, 2020). However, these methods require large datasets for training and careful tuning to avoid overfitting.

3.2.3 Validation of Genomic Selection Models

Validation of genomic prediction models is critical to ensure their reliability in practical breeding programs. Cross-validation within a reference population is the most common approach, where data are split into training and testing sets to evaluate predictive performance. Independent population testing provides a more stringent assessment, especially when breeding decisions span different herds or environments. Benchmarking studies, such as those conducted in dairy cattle and pigs, demonstrate that accurate GEBVs can reduce generation intervals and improve selection response. For example, in Holstein-Friesian populations, genomic selection reduced the age of first lactation sires while maintaining high milk yield performance (Ibtisham, 2017). Likewise, in pigs, genomic predictions have successfully increased growth rates while selecting simultaneously for reduced susceptibility to porcine reproductive and respiratory syndrome (PRRS), highlighting the practical value of validated genomic models.

3.3 Impact of Genomic Selection on Productivity and Health

The application of genomic selection (GS) in livestock breeding has demonstrated measurable impacts on both productivity and animal health, providing a practical pathway to accelerate genetic gains while enhancing herd resilience. By leveraging high-density genomic markers, breeders can estimate breeding values with unprecedented accuracy, leading to more precise selection decisions compared to traditional phenotype-based methods (Jonas, 2015). The following sections discuss the observed outcomes across key production and health traits, as well as considerations for genetic diversity.

3.3.1 Growth and Production Traits

Genomic selection has been shown to significantly enhance growth and production performance in various livestock species. For example, studies in dairy cattle report that GS can increase milk yield by 5–10% over the first generation compared to conventional selection programs, largely due to improved accuracy in identifying superior sires early in life (Mueller, 2022). Similarly, in beef cattle, genomic selection has been associated with accelerated growth rates and improved feed conversion efficiency, allowing producers to reach market weight faster while maintaining meat quality standards.

Reproductive performance has also benefitted from GS implementation. In swine, genomic selection for traits such as litter size and weaning weight has yielded measurable gains, reducing generation intervals and enhancing overall herd productivity (Chakraborty, 2022). Compared to traditional selection approaches, which rely heavily on phenotypic records collected over multiple generations, GS allows for earlier and more reliable identification of high-performing animals, thereby shortening the selection cycle and amplifying cumulative genetic gains.

These results are consistent with previous meta-analyses indicating that genomic selection outperforms pedigree-based selection, particularly for traits with low heritability, where phenotypic records alone are insufficient for precise evaluation (Georges, 2019). The evidence underscores that genomic tools can enhance production efficiency across multiple livestock species while reducing the temporal and economic costs of traditional breeding programs.

3.3.2 Disease Resistance and Health Traits

Beyond production traits, genomic selection is increasingly applied to improve disease resistance in livestock populations. Several studies have demonstrated its effectiveness in reducing susceptibility to bacterial, viral, and parasitic infections. For instance, in dairy cattle, GS targeting mastitis resistance has decreased the incidence of clinical infections while enhancing somatic cell count profiles, a key indicator of udder health (Anilkumar, 2022). In poultry, genomic selection has been successfully used to increase resistance to avian influenza and Marek’s disease, contributing to lower mortality rates and reduced reliance on chemotherapeutic interventions.

Parasitic resistance in small ruminants, such as resistance to gastrointestinal nematodes in sheep, has also benefited from genomic approaches. Selection for favorable alleles associated with parasite resilience has improved flock health and reduced the need for frequent anthelmintic treatments, which is particularly relevant in regions facing growing anthelmintic resistance (Rothschild, 2014).

Overall, genomic selection provides a proactive approach to herd health management. By identifying genetic predispositions to disease, it allows breeders to construct healthier herds while decreasing dependence on antibiotics and other chemical interventions (Ullah, 2025). This aligns with global efforts to mitigate antimicrobial resistance and promote sustainable livestock production.

3.3.3 Genetic Diversity and Inbreeding Considerations

While genomic selection accelerates genetic gain, it also raises concerns about potential reductions in genetic diversity and increased inbreeding. Intensive selection for specific alleles or high-performing animals can inadvertently reduce effective population size, potentially limiting long-term adaptability (Knap, 2020). For example, in Holstein cattle, rapid adoption of GS has been linked to subtle increases in genomic inbreeding coefficients, highlighting the need for balanced breeding strategies.

To mitigate these risks, several strategies are recommended. Optimal contribution selection can be integrated with GS to manage relationships between candidates while maximizing genetic gain. Additionally, monitoring runs of homozygosity and allele frequency changes allows breeders to preserve diversity without compromising selection efficiency (Voss-Fels, 2019). Introducing new germplasm from genetically diverse lines or populations further buffers against the erosion of variation while maintaining continued progress in productivity and health traits.

These findings emphasize that while GS is a powerful tool for enhancing livestock performance, sustainable breeding programs must carefully balance selection intensity with the preservation of genetic diversity to ensure long-term resilience (Cheruiyot, 2022).

3.4 Economic and Practical Implications

Genomic selection (GS) has shown considerable promise in enhancing livestock productivity and disease resistance, yet its practical adoption is heavily influenced by economic and logistical considerations. The translation of genomic technologies from research to farm-level application requires careful evaluation of cost-effectiveness, operational feasibility, and supportive policy frameworks (Jinya, 2024).

3.4.1 Cost-Benefit Analysis

Implementing genomic selection involves several upfront and recurring costs. Genotyping, which forms the core of GS, remains a significant investment, with medium-density SNP panels costing between \$50–\$100 per animal depending on species and panel size. Additional expenditures include data management, computational resources for genomic prediction, and training of personnel in bioinformatics and quantitative genetics (Hayes, 2013). Despite these costs, the long-term benefits often justify the investment. For instance, studies on dairy cattle in Netherlands reported a 5–10% increase in milk yield per generation alongside improved disease resistance, translating into substantial economic returns over a 5-year horizon. Similarly, genomic selection in beef cattle has been associated with accelerated growth rates and feed efficiency, producing measurable reductions in production costs and morbidity-related losses (Gutierrez-Reinoso, 2021). Comparative analyses indicate that, while genotyping expenses are higher than conventional pedigree-based selection, the return on investment improves markedly when multiple traits including disease resistance and reproductive performance are targeted simultaneously.

3.4.2 Adoption in Different Livestock Systems

The adoption of genomic selection varies widely across livestock systems, influenced by herd size, technical capacity, and market orientation. Large-scale commercial operations are often able to absorb the initial costs and implement GS programs effectively, benefiting from economies of scale and access to trained geneticists (Poland, 2016). For example, commercial dairy farms in Australia that integrated GS into their breeding programs achieved faster genetic gains and lower incidence of mastitis compared to traditional selection methods. In contrast, smallholder and small-scale operations face barriers including limited financial resources, lack of genotyping facilities, and lower access to data analysis tools (Bora, 2023). Pilot programs in sub-Saharan Africa, such as in Kenya, demonstrated that cooperative models where smallholders pool resources for genotyping can facilitate adoption, though results indicate that technical support and training are crucial to achieving measurable productivity gains.

3.4.3 Policy and Infrastructure Considerations

Wider adoption of genomic selection depends on supportive national breeding programs, data-sharing frameworks, and extension services. Countries with centralized breeding registries and integrated genomic databases, such as Sweden, have reported more consistent application of GS across herds, enabling real-time evaluation of breeding values and rapid dissemination of improved genetics. Conversely, regions lacking coordinated data infrastructure face fragmented implementation and limited impact (Meuwissen, 2016). Policy interventions, including subsidized genotyping programs, investment in bioinformatics infrastructure, and capacity building for extension officers, have been recommended to bridge these gaps. Establishing public-private partnerships can also encourage smallholder participation while ensuring that data privacy and intellectual property rights are respected. A standardized framework for genomic evaluation and routine monitoring of economic outcomes can further enhance confidence among producers and promote sustainable adoption.

In summary, while genomic selection offers substantial potential to improve livestock productivity and health, its practical success hinges on careful cost management, adaptability to different production systems, and robust policy and infrastructural support (Burrow, 2021). Integrating these factors can help optimize the economic benefits of GS while ensuring equitable access and long-term sustainability of breeding programs.

3.5 Limitations and Future Directions

Genomic selection (GS) in livestock breeding has demonstrated remarkable potential in enhancing productivity and disease resistance. However, despite its successes, several limitations remain that must be addressed to maximize its practical impact (Stock, 2013). These limitations stem from both current gaps in knowledge and technological or methodological constraints, and they inform strategic directions for future research.

3.5.1 Current Knowledge Gaps

While GS has been widely applied to traits such as milk yield in dairy cattle or growth rate in poultry and swine, there remain numerous economically important traits with insufficient genomic characterization. For example, disease resistance traits such as susceptibility to parasitic infections in small ruminants or heat tolerance in tropical cattle populations are underrepresented in genomic datasets (Plastow, 2016). This scarcity limits the accuracy of genomic predictions and reduces the reliability of selection decisions in these populations.

Another key limitation arises from small sample sizes in many studies. Genomic prediction models rely heavily on large, diverse datasets to capture the full spectrum of genetic variation. Limited population representation can lead to biased estimates of breeding values and reduced predictive accuracy, particularly when applying models across breeds or populations. For instance, GS models trained in European Holstein cattle often perform suboptimally when transferred to crossbred or indigenous African cattle populations due to differences in allele frequencies and linkage disequilibrium patterns, highlighting the challenge of cross-population transferability (Arya, 2024).

3.5.2 Technological and Methodological Challenges

The effectiveness of GS is closely linked to the precision of genotyping and phenotyping methods. While SNP panels have been widely used, they often capture only a fraction of the genetic variation underlying complex traits. Low-density panels or incomplete genome coverage can limit the resolution of genomic predictions (Jones, 2022). Emerging approaches, such as whole-genome sequencing (WGS), offer more comprehensive variant detection but remain costly and computationally intensive for routine breeding programs.

Phenotyping precision also poses a challenge. Many traits of interest, particularly disease resistance or behavioral traits, are difficult to measure accurately or consistently across environments. Inaccurate phenotypes introduce noise into genomic prediction models, reducing selection efficiency (Dube-Takaza, 2021). Recent developments in AI and machine learning offer promising avenues for integrating complex, high-dimensional data, such as imaging, sensor, and longitudinal health records, into predictive models. Yet, these methods require extensive computational resources and careful validation to avoid overfitting and ensure generalizability.

3.5.3 Recommendations for Future Research

To address these limitations, future research should prioritize integrative approaches that combine genomic, phenomic, and environmental data. Incorporating environmental covariates into GS models can improve prediction accuracy for traits with strong genotype-by-environment interactions, such as heat tolerance or disease resistance in variable climates (Rotimi, 2025).

Expanding multi-breed and cross-population studies is also essential. Such research will enable the identification of shared and population-specific quantitative trait loci (QTLs) and facilitate the development of broadly applicable genomic selection tools

(ASLAM, 2024). Longitudinal monitoring of animals throughout their production cycles can further enhance the understanding of temporal genetic effects on traits like fertility and lifetime productivity.

Finally, functional validation of candidate genes remains critical. Experimental confirmation of gene function through transcriptomics, gene editing, or knockout studies can translate genomic associations into actionable breeding strategies, bridging the gap between prediction and practical application (Hu, 2020). Collaborative initiatives combining industry, academic, and governmental resources are likely to accelerate progress and ensure that GS achieves both economic and sustainable gains in livestock production.

4. Conclusion

Genomic selection represents a transformative approach in livestock breeding, offering unprecedented opportunities to enhance productivity and strengthen disease resistance. By leveraging high-density genetic markers and advanced prediction models, breeders can make more accurate and faster selection decisions compared to traditional phenotypic or pedigree-based methods. Evidence from various livestock species demonstrates that genomic selection not only accelerates genetic gain but also helps mitigate the prevalence of heritable diseases, thereby improving overall herd health and sustainability.

Despite its clear benefits, the implementation of genomic selection is not without challenges. Economic constraints, infrastructure requirements, and limited access to high-quality genotypic and phenotypic data remain significant barriers, especially in low- and middle-income countries. Moreover, while prediction accuracies continue to improve, complex traits influenced by multiple genes and environmental interactions still pose difficulties, emphasizing the need for continued research and refinement of models and tools.

Future efforts should focus on integrating genomic selection with precision livestock technologies, expanding reference populations, and enhancing bioinformatics pipelines to optimize selection strategies. Additionally, the combination of genomic data with environmental and management information promises to maximize both productivity and animal welfare. Overall, genomic selection stands as a pivotal tool in modern livestock breeding, capable of supporting more resilient, efficient, and productive animal populations when applied thoughtfully and strategically.

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References

[1] Anilkumar, C., Sunitha, N. C., Harikrishna, Devate, N. B., & Ramesh, S. (2022). Advances in integrated genomic selection for rapid genetic gain in crop improvement: a review. *Planta*, *256*(5), 87.

[2] Arya, A., Sharma, P., Trivedi, M. M., Modi, R. J., & Patel, Y. G. (2024). A look at genomic selection techniques for climate change adaptation and production in livestock. *Journal of Scientific Research and Reports*, *30*(6), 427-436.

[3] ASLAM, S., MASOUD, M. S., ASHFAQ, U. A., ANSARI, M. U. R., NAHID, N., IMRAN, M., ... & QASIM, M. (2024). Genomic tools and technologies: revolutionizing livestock improvement. *ANIMAL PRODUCTION and HEALTH*, 46.

[4] Bora, S. K. (2023). Applications of Genomic Selection in Animal Breeding: Challenges and Opportunities. *World News of Natural Sciences*, *48*, 107-117.

[5] Burrow, H. M., Mrode, R., Mwai, A. O., Coffey, M. P., & Hayes, B. J. (2021). Challenges and opportunities in applying genomic selection to ruminants owned by smallholder farmers. *Agriculture*, *11*(11), 1172.

[6] Chakraborty, D., Sharma, N., Kour, S., Sodhi, S. S., Gupta, M. K., Lee, S. J., & Son, Y. O. (2022). Applications of omics technology for livestock selection and improvement. *Frontiers in genetics*, *13*, 774113.

[7] Cheruiyot, E. K., Haile-Mariam, M., Cocks, B. G., & Pryce, J. E. (2022). Improving genomic selection for heat tolerance in dairy cattle: current opportunities and future directions. *Frontiers in Genetics*, *13*, 894067.

[8] Das, D. N., Karuthadurai, T., & Gnanasekaran, S. (2021). Genomic selection: a molecular tool for genetic improvement in livestock. In *Advances in animal genomics* (pp. 141-163). Academic Press.

[9] Dube-Takaza, T., Shoko, R., Mudziwapasi, R., & Jomane, F. (2021). Animal Breeding Genomic Selection for Improved Animal health: A review of challenges and opportunities in Zimbabwe. *Authorea Preprints*.

[10] Georges, M., Charlier, C., & Hayes, B. (2019). Harnessing genomic information for livestock improvement. *Nature Reviews Genetics*, *20*(3), 135-156.

[11] Gutierrez-Reinoso, M. A., Aponte, P. M., & Garcia-Herreros, M. (2021). Genomic analysis, progress and future perspectives in dairy cattle selection: A review. *Animals*, *11*(3), 599.

[12] Hayes, B. J., Lewin, H. A., & Goddard, M. E. (2013). The future of livestock breeding: genomic selection for efficiency, reduced emissions intensity, and adaptation. *Trends in genetics*, *29*(4), 206-214.

[13] Hu, G., Do, D. N., Gray, J., & Miar, Y. (2020). Selection for favorable health traits: a potential approach to cope with diseases in farm animals. *Animals*, *10*(9), 1717.

[14] Ibtisham, F., Zhang, L., Xiao, M., An, L., Ramzan, M. B., Nawab, A., ... & Xu, Y. (2017). Genomic selection and its application in animal breeding. *The Thai Journal of Veterinary Medicine*, *47*(3), 301-310.

[15] Jinya, L. (2024). Genomic Selection in Livestock Breeding: Advances and Applications. *Animal Molecular Breeding*, *14*.

[16] Jonas, E., & Koning, D. J. D. (2015). Genomic selection needs to be carefully assessed to meet specific requirements in livestock breeding programs. *Frontiers in genetics*, *6*, 49.

[17] Jones, H. E., & Wilson, P. B. (2022). Progress and opportunities through use of genomics in animal production. *Trends in Genetics*, *38*(12), 1228-1252.

[18] Kasimanickam, R., Ferreira, J. C. P., Kastelic, J., & Kasimanickam, V. (2025). Application of genomic selection in beef cattle disease prevention. *Animals*, *15*(2), 277.

[19] Knap, P. W., & Doeschl-Wilson, A. (2020). Why breed disease-resilient livestock, and how?. *Genetics Selection Evolution*, *52*(1), 60.

[20] Meuwissen, T., Hayes, B., & Goddard, M. (2016). Genomic selection: A paradigm shift in animal breeding. *Animal frontiers*, *6*(1), 6-14.

[21] Mueller, M. L., & Van Eenennaam, A. L. (2022). Synergistic power of genomic selection, assisted reproductive technologies, and gene editing to drive genetic improvement of cattle. *CABI Agriculture and Bioscience*, *3*(1), 13.

[22] Plastow, G. S. (2016). Genomics to benefit livestock production: improving animal health. *Revista Brasileira de Zootecnia*, *45*, 349-354.

[23] Poland, J., & Rutkoski, J. (2016). Advances and challenges in genomic selection for disease resistance. *Annual review of phytopathology*, *54*(1), 79-98.

[24] Rothschild, M. F., & Plastow, G. S. (2014). Applications of genomics to improve livestock in the developing world. *Livestock Science*, *166*, 76-83.

[25] Rotimi, E. A. (2025). Application of genomics in livestock production: A Mini-Review. *World News Nat. Sci.*, *59*, 69-76.

[26] Stock, K. F., & Reents, R. (2013). Genomic selection: status in different species and challenges for breeding. *Reproduction in Domestic Animals*, *48*, 2-10.

[27] Tade, B., & Melesse, A. (2024). A review on the application of genomic selection in the improvement of dairy cattle productivity. *Ecological Genetics and Genomics*, *31*, 100257.

[28] Ullah, K., & Waheed, A. (2025). Genetic improvement in livestock: a journey from conventional breeding to genomic precision. *Veterinary Biomedical and Clinical Journal*, *7*(1), 30-44.

[29] Voss-Fels, K. P., Cooper, M., & Hayes, B. J. (2019). Accelerating crop genetic gains with genomic selection. *Theoretical and applied genetics*, *132*(3), 669-686.

[30] Xu, Y., Liu, X., Fu, J., Wang, H., Wang, J., Huang, C., ... & Zhang, A. (2020). Enhancing genetic gain through genomic selection: from livestock to plants. *Plant Communications*, *1*(1).