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Genomic Selection in Livestock Breeding: Advances and Applications

Jinya Li, Mengyue Chen
Animal Science Research Center, Cuixi Academy of Biotechnology, Zhuji, 311800, Zhejiang, China
Corresponding email: mengyue.chen@cuixi.org

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Abstract This study explores the latest advancements and applications of Genomic Selection (GS) in livestock breeding. With the development of high-throughput genomic sequencing technologies, GS has shown tremendous potential in improving breeding efficiency and accelerating genetic progress. This study systematically analyzes the specific applications of GS in dairy cattle, beef cattle, pigs, poultry, small ruminants, and aquaculture species, and discusses the implementation effects of these technologies across different species. It also delves into the challenges faced by GS, including ethical issues, economic barriers, concerns about genetic diversity, and technical and practical difficulties. Furthermore, this study provides insights into the future directions of GS, particularly the integration of emerging technologies such as CRISPR and artificial intelligence, as well as the potential for global collaboration. Through comprehensive research and case studies, this study offers essential scientific foundations and practical guidance for livestock researchers and practitioners to drive the continued progress of global livestock breeding.

Keywords Genomic selection; Livestock breeding; Genetic progress; CRISPR; Artificial intelligence

1 Introduction

The field of livestock breeding has witnessed significant advancements over the past few decades, with genomic selection (GS) emerging as a transformative technology. This chapter will explore the background, evolution, and relevance of livestock breeding, with a particular focus on the introduction and importance of genomic selection in modern practices. We will also outline the purpose and scope of this study to provide a comprehensive understanding of GS and its applications in livestock breeding. Livestock breeding has been a cornerstone of agricultural development for centuries, focusing on improving the genetic quality of farm animals for traits such as productivity, disease resistance, and adaptability. Traditional breeding methods, based on phenotypic selection, have gradually evolved into more sophisticated approaches, integrating genetic information to achieve faster and more accurate results (Meuwissen et al., 2016).

The evolution of breeding techniques has transitioned from basic selective breeding to marker-assisted selection (MAS) and now to genomic selection (GS). While MAS has been somewhat successful, it failed to fully harness the complexity of traits controlled by multiple genes with small effects. GS, however, represents a paradigm shift by using dense genetic markers across the genome, allowing for more accurate selection decisions at earlier stages of animal development (Tan et al., 2017). Genomic selection involves predicting the genetic value of an animal using genome-wide markers, enabling the selection of superior animals at an earlier age. This method contrasts with traditional selection methods by providing high accuracy without the need for direct phenotypic measurements.

The development of high-density SNP chips and advancements in sequencing technologies have facilitated the widespread adoption of GS in species like cattle, pigs, and poultry (Ibtisham et al., 2017). The importance of GS in modern livestock breeding cannot be overstated. It significantly enhances genetic gain by reducing the generation interval and increasing the accuracy of breeding value predictions. The ability to implement GS across various species has led to substantial improvements in economically important traits, ultimately contributing to global food security and agricultural sustainability (Singh et al., 2019).

This study comprehensively analyzes the progress and applications of genomic selection (GS) in livestock breeding, covering its technical foundation, applications across various livestock species, and future prospects, providing insights into how GS can further revolutionize animal breeding to enhance efficiency, productivity, and sustainability in livestock production.

2 Principles of Genomic Selection

2.1 The genetic basis of livestock traits

Genomic selection (GS) is an innovative approach in livestock breeding that leverages the comprehensive analysis of genetic markers across the entire genome to predict an animal's breeding value. This method has revolutionized the field by enabling breeders to make more informed and accurate selection decisions. Unlike traditional methods that focus on observable traits or a limited number of genetic markers, GS utilizes high-density single nucleotide polymorphism (SNP) chips to evaluate thousands of markers simultaneously. This approach allows for the capture of both large and small genetic effects, leading to more precise genetic predictions and faster genetic progress. The principles of GS are rooted in understanding the genetic architecture of traits and applying advanced statistical models to integrate vast amounts of genomic data. As the technology and computational methods continue to evolve, the application of GS is expanding across various livestock species, enhancing the efficiency and effectiveness of breeding programs (Xu et al., 2019).

Livestock traits, particularly those related to productivity, health, and reproduction, are often complex and influenced by multiple genes with varying effects. These traits are typically categorized into two groups: qualitative traits, controlled by a few genes with large effects, and quantitative traits, influenced by many genes each contributing a small effect. For quantitative traits, which include most economically important characteristics such as milk yield, growth rate, and disease resistance, the genetic basis is polygenic. Advances in genomics have enabled the identification of SNPs associated with these traits, providing a deeper understanding of the genetic architecture underlying livestock performance. This knowledge is crucial for implementing GS, as it allows breeders to estimate the cumulative effects of numerous small-effect genes, thereby improving the accuracy of selection. The ability to assess the genetic potential of animals at an early age, without waiting for phenotypic data, represents a significant advancement over traditional breeding methods (Singh et al., 2019).

2.2 Theoretical framework of genomic selection

The theoretical foundation of GS is based on the principle that all loci across the genome contribute to the genetic variance of a trait. In contrast to marker-assisted selection (MAS), which focuses on a few selected markers, GS considers the entire genome, including regions with small effects that might be overlooked in traditional approaches. The effectiveness of GS lies in its ability to use dense genetic marker data to predict breeding values with high accuracy. This is achieved through the use of statistical models that estimate the effects of all SNPs simultaneously, allowing for the capture of additive genetic variation.

The integration of genomic information into breeding programs has led to significant improvements in genetic gain, as it reduces the generation interval and increases the reliability of breeding value predictions. The theoretical framework of GS also accounts for non-additive genetic effects, such as dominance and epistasis, which can further refine the accuracy of predictions. As genomic technologies continue to advance, the framework of GS is expected to evolve, incorporating more sophisticated models and larger datasets to enhance selection accuracy (Meuwissen et al., 2016).

2.3 Genomic prediction models

Genomic prediction models are central to the implementation of GS. These models use genome-wide marker data to estimate the breeding values of animals, allowing breeders to make selection decisions based on genetic potential rather than phenotypic performance alone. Several models are used in GS, each with its strengths and weaknesses. The most common models include Best Linear Unbiased Prediction (BLUP), Bayesian methods (such as BayesA and BayesB), and machine learning approaches. BLUP models are widely used due to their simplicity and effectiveness in predicting additive genetic values (Gutierrez-Reinoso et al., 2021).

Bayesian methods, on the other hand, provide more flexibility by allowing different prior distributions for marker effects, which can be particularly useful when dealing with traits influenced by large-effect loci. More recently, machine learning algorithms have been explored for GS, offering the potential to capture complex interactions between markers that traditional models might miss. The choice of model depends on the specific breeding objectives, the genetic architecture of the traits in question, and the available data. Advances in computational power and statistical methodologies continue to drive the development of more accurate and efficient genomic prediction models, further enhancing the potential of GS in livestock breeding (Ibtisham et al., 2017).

2.4 Marker-assisted selection vs. genomic selection

Marker-assisted selection (MAS) and genomic selection (GS) are both used to enhance the genetic improvement of livestock, but they differ significantly in their approach and effectiveness. MAS relies on a limited number of markers linked to specific traits, making it suitable for traits controlled by a few major genes (Meuwissen et al., 2016). However, its effectiveness diminishes for complex traits governed by many genes with small effects. In contrast, GS uses high-density SNP data covering the entire genome, allowing for the simultaneous consideration of all genetic markers. This comprehensive approach enables GS to capture the total genetic variance, including contributions from small-effect loci that MAS might miss.

As a result, GS provides more accurate predictions of breeding values and can be applied to a broader range of traits. The ability of GS to reduce the generation interval and increase the rate of genetic gain makes it a superior tool for modern livestock breeding programs. The transition from MAS to GS marks a significant evolution in genetic selection strategies, reflecting the advancements in genomic technologies and the growing understanding of complex trait genetics (Priyadarshini et al., 2017).

3 Advances in Genomic Selection

The field of genomic selection (GS) in livestock breeding has evolved significantly over the past decade, driven by technological innovations, the integration of big data and machine learning, improvements in genomic prediction accuracy, and enhanced breeding program efficiency. These advances have not only improved the accuracy of selection but also accelerated the rate of genetic gain, making GS an essential tool in modern livestock breeding.

3.1 Technological innovations in genomic sequencing

Technological advancements in genomic sequencing have played a critical role in the evolution of GS. The development of high-throughput sequencing technologies has enabled the generation of vast amounts of genomic data at a reduced cost, making it feasible to implement GS on a large scale. The introduction of next-generation sequencing (NGS) technologies, such as whole-genome sequencing and genotyping-by-sequencing, has revolutionized the ability to capture genetic variation across the entire genome. These innovations have led to the identification of single nucleotide polymorphisms (SNPs) that serve as the basis for GS, allowing for more accurate predictions of breeding values.

Additionally, advances in sequencing technologies have improved the resolution of genomic data, enabling the detection of rare variants and structural variations that contribute to complex traits in livestock. The combination of these technological improvements has resulted in a more comprehensive understanding of the genetic architecture of economically important traits, thereby enhancing the effectiveness of GS in breeding programs (Meuwissen et al., 2016).

3.2 Integration of big data and machine learning

The integration of big data and machine learning into GS has significantly enhanced the ability to predict complex traits in livestock. The vast amounts of genomic, phenotypic, and environmental data generated through modern breeding programs require advanced analytical tools to extract meaningful insights. Machine learning algorithms, such as random forests, support vector machines, and deep learning models, have been increasingly applied to GS to improve prediction accuracy.

These models are capable of handling large, noisy datasets and capturing non-linear relationships between markers and traits, which are often missed by traditional statistical methods. The use of ensemble learning techniques, such as Adaboost, has further improved the robustness and stability of genomic predictions. Additionally, machine learning models have shown promise in integrating multi-omics data, including transcriptomics, proteomics, and metabolomics, to refine predictions and identify novel genetic markers associated with complex traits. The continued development of these models is expected to further optimize GS and lead to more precise and targeted breeding strategies (Liang et al., 2020; Chafai et al., 2023).

3.3 Advances in Genomic Prediction Accuracy

Improvements in genomic prediction accuracy are central to the success of GS. The accuracy of genomic predictions depends on several factors, including the density and quality of SNP data, the size of the reference population, and the statistical models used. Recent advances have focused on optimizing these factors to enhance prediction accuracy. High-density SNP arrays and whole-genome sequencing have increased the resolution of genetic data, allowing for the capture of more genetic variation and improving the accuracy of estimated breeding values (EBVs).

Additionally, the development of single-step genomic best linear unbiased prediction (ssGBLUP) models has allowed for the simultaneous use of pedigree, phenotypic, and genomic data, resulting in more accurate predictions. The incorporation of non-additive genetic effects, such as dominance and epistasis, into prediction models has also contributed to improved accuracy. As the field continues to evolve, the use of more sophisticated models that account for genotype-by-environment interactions and other complex genetic architectures is expected to further enhance the precision of GS (Wang et al., 2022; Passamonti et al., 2021).

3.4 Improvements in breeding program efficiency

The adoption of GS has led to significant improvements in the efficiency of breeding programs. By enabling the early selection of genetically superior animals, GS has reduced the generation interval and accelerated the rate of genetic gain. The ability to predict breeding values with high accuracy at a young age has also reduced the need for extensive phenotyping, lowering the overall cost and time required for breeding programs.

Additionally, the integration of GS with other breeding tools, such as marker-assisted selection and genome editing, has created more efficient and targeted breeding strategies. The use of digital tools and automation in the selection process has further streamlined breeding programs, allowing for the rapid deployment of new genetic lines. As the technology continues to advance, the efficiency gains achieved through GS are expected to play a crucial role in meeting the growing global demand for animal products while ensuring the sustainability of livestock production systems (Xu et al., 2019; Rosa et al., 2023).

4 Applications of Genomic Selection in Livestock Breeding

Genomic selection (GS) has been a transformative tool in livestock breeding, offering precise and efficient selection methods across various species. Its application spans several key livestock categories, including dairy cattle, beef cattle, swine, poultry, small ruminants, and aquaculture species. This section explores the specific applications of GS in these livestock categories, highlighting the advancements, challenges, and successes in each area.

4.1 Dairy cattle

The dairy cattle industry has been at the forefront of implementing GS, with the technology significantly enhancing genetic gain and breeding efficiency. GS has been widely adopted in dairy cattle due to the economic importance of traits like milk yield, fertility, and longevity. The introduction of GS has reduced generation intervals and increased the accuracy of selecting young animals, leading to accelerated genetic improvement. In the United States, for example, the adoption of GS has doubled the rate of genetic gain since its implementation, with traits such as feed efficiency and health traits benefiting from the enhanced accuracy provided by genomic evaluations (Wiggans et al., 2017; Wiggans and Carrillo, 2022) (Figure 1).

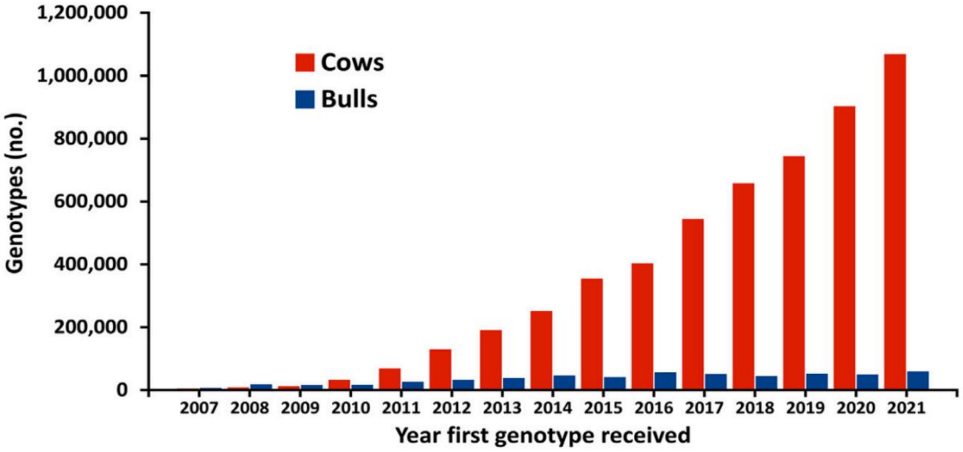

Figure 1 Number of dairy cattle genotypes submitted in the United States by year that first genotype was received (Adopted from Wiggans and Carrillo, 2022)

Wiggans and Carrillo (2022) shows the number of genotyped animals included in the US genomic evaluations for dairy cattle. Since the official evaluations began in January 2009, the number of genotyped Holstein and Jersey cattle has significantly increased. The figure indicates a substantial rise in the number of genotyped female cattle since the implementation of genomic evaluations, with a peak observed between 2015 and 2016. This trend highlights the growing importance of genomic selection in the dairy industry. The success of GS in dairy cattle is also evident in the extensive use of genomic data across various breeds, which has improved the prediction of breeding values and allowed for more precise selection strategies (Cole and Silva, 2016).

4.2 Beef cattle

GS in beef cattle has shown promising results, although its implementation has been more challenging compared to dairy cattle due to differences in breeding structures. The application of GS in beef cattle primarily focuses on improving traits such as growth rate, carcass quality, and feed efficiency. Studies have demonstrated that selective genotyping, combined with GS, can enhance the prediction accuracy of breeding values even with a limited number of genotyped animals (Esrafili Taze Kand Mohammaddiyeh et al., 2023).

Additionally, GS has been used to manage genetic diversity and reduce inbreeding, which are critical for maintaining the long-term viability of beef cattle populations. The integration of GS with traditional breeding programs has resulted in significant genetic gains, although challenges related to cost, genotyping strategies, and the diversity of breeding objectives rem aim (Liang et al., 2020).

4.3 Swine

The swine industry has rapidly adopted GS, benefiting from the technology's ability to improve traits such as growth rate, feed efficiency, and reproductive performance. GS in swine has been facilitated by the development of high-density SNP panels and advances in genome sequencing. The implementation of GS has led to more accurate breeding value predictions, particularly for traits with low heritability, which are traditionally challenging to improve through conventional selection methods.

However, the application of GS in swine faces challenges related to the genetic diversity of crossbred populations and the need for robust reference populations (Samoré and Fontanesi, 2016). Despite these challenges, GS has proven to be a valuable tool in enhancing genetic gain and improving the overall efficiency of swine breeding programs.

4.4 Poultry

The poultry industry has leveraged GS to improve a range of economically important traits, including growth rate, egg production, and disease resistance. Poultry breeding programs already benefit from short generation intervals, but GS has further accelerated genetic progress by increasing the accuracy of selection. The unique breeding structures of poultry, such as the use of overlapping generations in broilers and annual generations in layers, have influenced the implementation of GS.

Studies have shown that GS can improve selection efficiency in poultry by integrating genomic data into breeding programs, leading to faster and more targeted genetic improvement (Wolc et al., 2016). However, the success of GS in poultry also depends on the availability of large, well-characterized reference populations, which are essential for accurate genomic predictions.

4.5 Small ruminants (sheep and goats)

The application of GS in small ruminants, such as sheep and goats, has been more recent but is showing significant potential. GS has primarily been applied to enhance production traits, such as growth, milk yield, and wool quality, as well as functional traits like disease resistance and reproductive performance. The smaller reference populations and the use of multi-breed datasets pose challenges, but they have also driven innovations in genomic prediction models.

For example, the integration of molecular data has improved the accuracy of breeding value predictions and provided valuable insights into parentage verification and QTL identification (Zhao and Zhang, 2019; Mrode et al., 2018). In developing countries, GS offers opportunities to enhance breeding programs for small ruminants, particularly in regions where traditional genetic improvement strategies are limited.

4.6 Aquaculture species

GS has been increasingly applied in aquaculture species, including fish and shellfish, to improve traits such as growth rate, disease resistance, and feed efficiency. The success of GS in aquaculture is attributed to its ability to predict breeding values at an early age, thereby accelerating genetic gain. The use of high-density SNP arrays and advanced genomic tools has facilitated the application of GS in species like salmon, tilapia, and shrimp.

However, challenges related to the diversity of breeding objectives, environmental interactions, and the cost of genotyping remain. Despite these challenges, GS has proven to be a powerful tool in enhancing the efficiency of breeding programs in aquaculture, leading to significant improvements in production traits and overall industry sustainability (Jonas and de Koning, 2015).

5 Case Study: Genomic Selection in Dairy Cattle Breeding

5.1 Background of the case study

Genomic selection (GS) has revolutionized dairy cattle breeding, allowing for significant improvements in genetic gain and breeding program efficiency. This case study examines the implementation of GS in dairy cattle, focusing on the background, outcomes, challenges, and lessons learned from its adoption.

The dairy cattle industry has long sought to improve genetic gain through selective breeding. Traditionally, this was accomplished using progeny testing, a time-consuming and expensive process that involved evaluating the offspring of breeding animals for desirable traits. The introduction of GS in the late 2000s marked a turning point, enabling the use of genomic data to predict the breeding value of animals at a much earlier stage, thus reducing the generation interval and accelerating genetic progress. By 2009, the USDA began releasing official genomic evaluations for Holsteins and Jerseys, marking the widespread adoption of GS in the dairy industry (Wiggans et al., 2017). This case study focuses on the implementation of GS in the U.S. dairy industry, with particular attention to the experiences of Holstein and Jersey breeders.

5.2 Implementation of genomic selection in dairy cattle

The implementation of GS in dairy cattle began with the development and use of high-density SNP chips, which allowed for the genotyping of thousands of genetic markers across the genome. These markers were then used to predict the breeding values of young animals, thereby enabling more accurate and timely selection decisions. The USDA's genomic evaluation program for dairy cattle utilized a combination of pedigree, phenotypic, and genomic data to estimate the genomic estimated breeding values (GEBVs) of animals.

The program significantly reduced the reliance on traditional progeny testing, as young bulls could now be selected based on their genomic profiles, even before they had produced offspring (Wiggans et al., 2017). Additionally, the integration of genomic data into breeding programs has facilitated the identification of deleterious alleles and has improved the management of genetic diversity within the population (Mäntysaari et al., 2020).

5.3 Outcomes and benefits

The outcomes of implementing GS in dairy cattle have been profound. The most significant benefit has been the acceleration of genetic gain. For example, since the adoption of GS, the rate of genetic improvement for traits such as milk yield, fat, and protein content has nearly doubled in some breeds. The reduction in generation intervals-rom over five years to less than three years for bull selection-has also contributed to this increased rate of genetic gain (Guinan et al., 2022).

Moreover, GS has led to cost savings by reducing the need for extensive progeny testing, which was previously a major expense for breeders. The technology has also allowed for more targeted selection, improving the overall health, fertility, and productivity of dairy herds. The ability to screen for and manage inbreeding through genomic data has been another key benefit, helping to maintain genetic diversity while optimizing breeding outcomes (Gutierrez-Reinoso et al., 2021).

5.4 Challenges and lessons learned

Despite the many benefits, the implementation of GS in dairy cattle breeding has not been without challenges. One of the primary issues has been the potential for increased inbreeding, as the use of a limited number of top sires can lead to a reduction in genetic diversity over time. This has raised concerns about the long-term sustainability of breeding programs, particularly in small or isolated populations (Obari et al., 2022).

Additionally, the high costs associated with genotyping, especially in the early stages of GS adoption, have been a barrier for smaller breeding operations. However, as the cost of genotyping continues to decrease, more breeders are expected to adopt GS. Another challenge has been the need for ongoing education and support for breeders to fully understand and utilize GS technologies effectively. Lessons learned from the U.S. experience highlight the importance of developing robust reference populations, investing in infrastructure for data collection and analysis, and ensuring that breeders have access to the necessary tools and knowledge to implement GS successfully (Figure 2) (Wiggans et al., 2017).

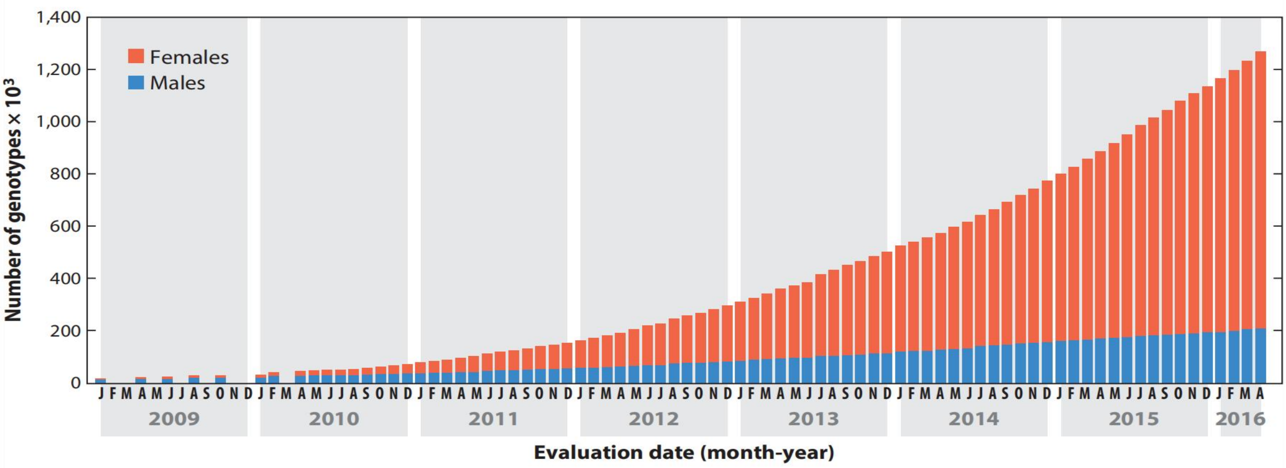

Figure 2 Number of genotyped animals included in US genomic evaluations for dairy cattle since January 2009 (Adopted from Wiggans et al., 2017)

Note: Official US genomic evaluations were first released to the dairy industry in January 2009 for Holsteins and Jerseys, in August 2009 for Brown Swiss, in April 2013 for Ayrshires, and in April 2016 for Guernseys. Data for figure generation were reported by the Council on Dairy Cattle Breeding (27). Months without data represent months in which official evaluations were not released. (Adapted from Wiggans et al., 2017)

6 Challenges and Limitations of Genomic Selection

Despite its transformative potential, the application of genomic selection (GS) in livestock breeding is not without challenges and limitations. These range from ethical considerations to economic barriers, concerns about genetic diversity, and technical and practical challenges. Addressing these issues is essential for the sustainable and equitable use of GS in the livestock industry.

6.1 Ethical considerations

The ethical implications of GS in livestock breeding are a significant concern, particularly regarding animal welfare and the broader societal impact. The use of genomic technologies raises questions about the potential for unintended consequences, such as exacerbating welfare issues by selecting for traits that may compromise the health or well-being of animals. For example, selecting for high milk yield in dairy cattle has been associated with increased incidences of lameness and reproductive disorders, leading to ethical concerns about the balance between productivity and animal welfare (Van Marle-Köster and Visser, 2021).

Additionally, the potential use of gene editing technologies, such as CRISPR, in conjunction with GS, introduces further ethical dilemmas. While these technologies offer the possibility of significant genetic improvements, they also raise questions about the acceptability of such interventions among consumers and the potential long-term impacts on animal populations (Marle-Köster and Visser, 2018).

6.2 Economic barriers

The economic barriers to the widespread adoption of GS are particularly pronounced in developing regions and among smallholder farmers. The high costs associated with genotyping, maintaining reference populations, and implementing advanced genomic technologies are significant hurdles for many breeding programs. In regions like Africa, where resources are limited, the lack of infrastructure and funding poses a major challenge to the implementation of GS (Burrow et al., 2021).

Furthermore, even in developed countries, smaller breeding operations may struggle to afford the upfront costs of GS, limiting their ability to compete with larger, more resource-rich entities. These economic barriers highlight the need for more accessible and cost-effective solutions, as well as supportive policies and funding mechanisms to facilitate the broader adoption of GS (Meuwissen et al., 2016).

6.3 Genetic diversity concerns

One of the primary concerns associated with GS is the potential for reduced genetic diversity within livestock populations. As GS tends to focus on selecting a smaller number of top-performing animals, there is a risk of narrowing the gene pool, which could lead to increased inbreeding and the associated negative consequences, such as reduced fertility and resilience (Eynard et al., 2017).

The long-term sustainability of breeding programs may be compromised if genetic diversity is not carefully managed. Strategies to mitigate these risks include optimizing the composition of reference populations and using breeding strategies that balance genetic gain with the conservation of diversity (Meuwissen et al., 2016). However, implementing these strategies requires careful planning and collaboration across the breeding industry.

6.4 Technical and practical challenges

The technical and practical challenges of GS are multifaceted, involving issues related to data management, model accuracy, and the integration of GS into existing breeding programs. One of the key technical challenges is the need for large, well-phenotyped reference populations to achieve high prediction accuracy. In many breeding programs, particularly those in developing regions, assembling such populations is difficult due to limited resources and the complexity of phenotype recording (Burrow et al., 2021).

Additionally, the accuracy of genomic predictions can be affected by factors such as marker density, genetic architecture, and genotype-by-environment interactions, requiring sophisticated models and substantial computational resources (Zhang et al., 2019). Practical challenges also include the need for continuous education and training for breeders to effectively use GS technologies and the integration of these technologies with traditional selection methods (Tan et al., 2017).

7 Future Directions in Genomic Selection

The future of genomic selection (GS) in livestock breeding is bright, with emerging technologies and new strategies promising to further revolutionize the field. This section explores the role of cutting-edge technologies like CRISPR and artificial intelligence (AI), the expansion of GS to new species, the integration of diverse genomic data, and the potential for global collaboration in livestock breeding.

7.1 Emerging technologies (e.g., CRISPR, AI)

Emerging technologies such as CRISPR and AI are poised to play a transformative role in the future of GS. CRISPR, a powerful tool for genome editing, offers unprecedented precision in modifying specific genes, enabling the enhancement of desirable traits or the elimination of detrimental ones in livestock. CRISPR-based techniques, such as RNA-guided DNA integration, allow for more precise and predictable genetic modifications, making it possible to rapidly improve complex traits that are otherwise difficult to enhance through traditional breeding methods (Park et al., 2021; Cheng et al., 2022).

AI, on the other hand, is being increasingly used to analyze large genomic datasets, identify patterns, and predict breeding outcomes with greater accuracy. AI algorithms, including machine learning models, can integrate genomic, phenotypic, and environmental data to optimize selection decisions, ultimately leading to more efficient and sustainable breeding programs (Manghwar et al., 2020). The combination of CRISPR and AI holds the potential to accelerate the pace of genetic improvement in livestock, making it possible to achieve genetic gains that were previously unimaginable.

7.2 Expanding genomic selection to new species

While GS has been widely adopted in cattle, swine, and poultry, its application in other species, such as aquaculture and small ruminants, is still in its early stages. The expansion of GS to these new species presents both opportunities and challenges. In aquaculture, for instance, GS could significantly improve traits such as growth rate, disease resistance, and feed efficiency, but the development of reliable reference populations and the adaptation of existing models to the specific genetic architectures of these species remain challenging (Figure 3) (Elmore et al., 2023).

Similarly, in species like sheep and goats, GS offers the potential to enhance productivity and health traits, yet the limited availability of genomic resources and the high costs associated with genotyping pose significant barriers (Bhat et al., 2016). As genomic technologies become more affordable and accessible, the expansion of GS to a broader range of species will likely drive significant improvements in global livestock production.

7.3 Enhancing genomic data integration

The integration of diverse genomic data types is critical for enhancing the accuracy and effectiveness of GS. Advances in next-generation sequencing (NGS) and other high-throughput genomic technologies have generated vast amounts of data that can be leveraged to improve the prediction of breeding values. However, integrating these data with traditional phenotypic and pedigree information remains a challenge. Emerging approaches, such as multi-omics data integration and the use of AI for data analysis, offer promising solutions.

By combining genomic, transcriptomic, proteomic, and metabolomic data, researchers can gain a more comprehensive understanding of the genetic basis of complex traits, leading to more accurate predictions and better-informed selection decisions (Nidhi et al., 2021; Arribas et al., 2021). Additionally, the development of new bioinformatics tools and databases that facilitate the seamless integration of these diverse data types will be essential for maximizing the potential of GS.

7.4 Potential for global collaboration in livestock breeding

Global collaboration in livestock breeding is becoming increasingly important as the challenges facing the industry grow more complex. The need for sustainable practices, the impacts of climate change, and the demands of a growing global population all underscore the importance of international cooperation in advancing GS. Collaborative initiatives that share genomic resources, reference populations, and breeding strategies across borders can help to accelerate the development and dissemination of GS technologies.

Moreover, global efforts to establish standardized protocols and data-sharing frameworks will be crucial for ensuring that the benefits of GS are realized worldwide (Policante and Borg, 2023). Such collaboration will not only enhance the effectiveness of breeding programs but also contribute to the equitable distribution of genetic gains, particularly in developing regions where access to genomic technologies has been limited.

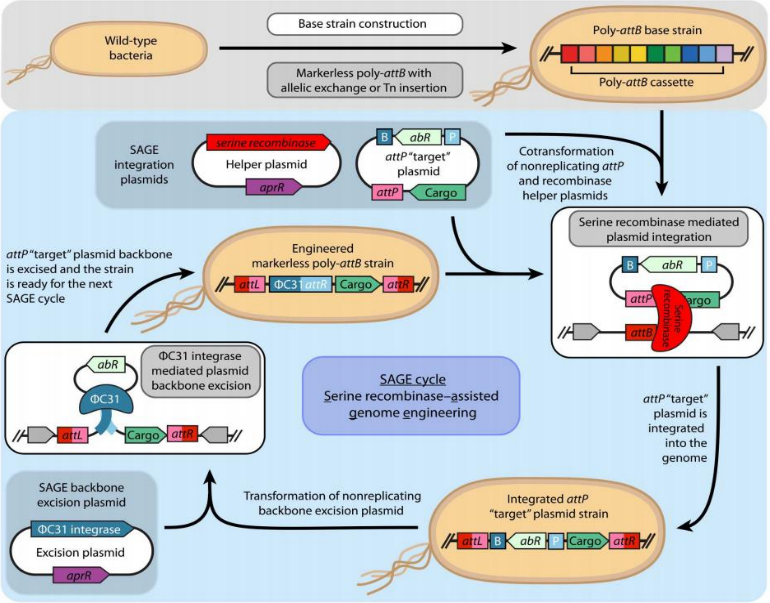

Figure 3 shows the analysis of fluorescent protein expression stability in Pseudomonas fluorescens through flow cytometry (Adopted from Elmore et al., 2023)

Image caption: SAGE is a novel technique under GS (Genome surgery). The experimental results indicate that the strains generated via SAGE (Serine integrase-Assisted Genome Engineering) exhibit more stable fluorescence expression without selective pressure compared to strains generated by plasmid transformation. This demonstrates that the SAGE method effectively reduces plasmid loss, thereby improving the stable expression of exogenous genes (Adapted from Elmore et al., 2023).

8 Concluding Remarks

The exploration of genomic selection (GS) within the context of livestock breeding reveals a transformative shift in how genetic improvement is pursued across various species. GS has provided unprecedented opportunities for enhancing genetic gain, improving breeding efficiency, and addressing complex challenges within the livestock industry. As we look toward the future, the continued advancement and application of GS will play a critical role in shaping the global landscape of livestock production.

The key findings from the analysis of GS in livestock breeding underscore its profound impact on accelerating genetic improvement. GS allows for the early selection of breeding candidates based on genomic data, significantly reducing the generation interval and enhancing the accuracy of breeding decisions. This technology has been widely adopted across various species, including dairy and beef cattle, swine, poultry, and small ruminants, leading to substantial gains in productivity, disease resistance, and other economically important traits. Despite these successes, challenges remain, particularly regarding the integration of GS into traditional breeding programs, managing genetic diversity, and addressing ethical and economic concerns.

The impact of GS on the future of livestock breeding is expected to be far-reaching. The integration of emerging technologies such as CRISPR and AI with GS will enable even more precise and targeted genetic improvements. These advancements will likely lead to the development of livestock that are more resilient to environmental changes, possess enhanced production traits, and contribute to more sustainable farming practices. Additionally, the expansion of GS to new species, including aquaculture and underutilized livestock breeds, holds significant promise for addressing global food security challenges. As GS continues to evolve, it will become an essential tool for breeders, enabling the development of livestock that meet the diverse needs of a growing global population.

The evolution of breeding strategies has been marked by the transition from traditional phenotypic selection to the integration of advanced genomic technologies. GS represents a significant milestone in this evolution, offering a more efficient and accurate approach to genetic improvement. However, the success of GS depends on the careful management of its implementation, particularly concerning genetic diversity, ethical considerations, and the economic viability for breeders. As the technology continues to advance, it will be crucial to address these challenges to ensure that the benefits of GS are realized globally and equitably. The future of livestock breeding will undoubtedly be shaped by GS, but its success will require collaboration, innovation, and a commitment to sustainable practices.

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Conflict of Interest Disclosure

Authors affirm that this research was conducted without any commercial or financial relationships that could be construed as a potential conflict of interest.

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