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Analyzing the Impact of Marker-Assisted Selection on Livestock Productivity and Genetic Diversity

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Abstract Marker-assisted selection (MAS) has emerged as a pivotal tool in enhancing livestock productivity and maintaining genetic diversity. This study analyzes the impact of MAS on livestock by integrating molecular markers with traditional breeding methods. This study highlights the efficiency of MAS in improving quantitative traits, disease resistance, and overall genetic diversity in livestock populations. The integration of genomic selection (GS) with MAS has further revolutionized animal breeding by enabling the identification and selection of superior traits with higher precision. Despite the challenges associated with complex traits and the need for large reference populations, MAS has shown significant promise in accelerating genetic gains and improving livestock productivity. Future directions include the adoption of high-throughput genotyping technologies and the development of more robust selection indices to enhance the efficiency of MAS in livestock breeding programs.

Keywords Marker-assisted selection; Livestock productivity; Genetic diversity; Genomic selection; Quantitative traits

Marker-Assisted Selection (MAS) has emerged as a revolutionary tool in the field of livestock breeding, significantly enhancing the precision and efficiency of selecting desirable traits. Initially developed for plant breeding, MAS leverages molecular markers linked to specific genetic traits, allowing breeders to identify and select individuals with favorable genetic profiles more accurately and rapidly than traditional methods (Boopathi, 2020; Kumawat et al., 2020; Hasan et al., 2021). This technique has been adapted and refined for use in livestock, where it holds the potential to transform breeding programs by improving productivity and maintaining genetic diversity.

The evolution of MAS in livestock breeding has been marked by significant advancements in molecular genetics and genomics. Early applications focused on identifying markers associated with economically important traits such as disease resistance, growth rate, and reproductive performance (Raina et al., 2020; Shepelev et al., 2023). With the advent of high-throughput sequencing technologies and genome-wide association studies (GWAS), the scope of MAS has expanded, enabling the identification of a broader range of genetic markers and their integration into breeding programs (Degen and Müller, 2023; Song et al., 2023). This evolution has not only accelerated the breeding process but also increased the accuracy of selection, leading to more robust and productive livestock populations.

The dual significance of MAS lies in its ability to enhance livestock productivity while also impacting genetic diversity. On one hand, MAS can significantly improve traits such as milk yield, meat quality, and disease resistance, thereby boosting overall productivity and economic returns for farmers (Singh et al., 2022; Shepelev et al., 2023). On the other hand, the focus on specific genetic markers can lead to a reduction in genetic diversity if not managed carefully. This potential impact on genetic diversity is a critical consideration, as it can affect the long-term sustainability and resilience of livestock populations (Degen and Müller, 2023).

The primary goals of this study are to conduct a systematic review of the existing literature on MAS and to analyze its effects on livestock productivity and genetic diversity. Through a detailed examination of both literature reviews and case studies, this study aims to provide a comprehensive understanding of the benefits and potential drawbacks of MAS in livestock breeding. By synthesizing findings from multiple studies, this study will offer insights into the practical applications of MAS and its implications for the future of livestock breeding. This comprehensive analysis will inform future breeding strategies to optimize both productivity and genetic diversity.

1 Theoretical Framework

1.1 Genetic principles of MAS

Marker-Assisted Selection (MAS) leverages genetic markers to enhance the selection process in breeding programs. Genetic markers are specific DNA sequences that are associated with particular traits, such as disease resistance or productivity. The fundamental principle behind MAS is the identification of quantitative trait loci (QTLs) that are linked to these markers. Once these associations are established, the markers can be used to predict the presence of desirable traits in breeding populations, thereby facilitating the selection of superior individuals (Osei et al., 2018; Eze, 2019).

The genetic mechanisms underlying MAS involve the use of polymorphic DNA markers, such as restriction fragment length polymorphisms (RFLPs), microsatellites, and single nucleotide polymorphisms (SNPs). These markers are used in linkage analysis and association studies to identify QTLs that influence traits of interest. The efficiency of MAS depends on the strength of the linkage between the marker and the QTL, as well as the heritability of the trait (Feng et al., 2020; Shepelev et al., 2023). By integrating molecular genetic information with traditional phenotypic selection, MAS can significantly improve the accuracy and efficiency of breeding programs (Kumawat et al., 2020; Tiwari et al., 2022).

1.2 Technological advancements

Recent technological innovations have greatly enhanced the effectiveness of MAS. Advances in genotyping technologies, such as high-throughput DNA sequencing and microarray analysis, have made it possible to screen large numbers of markers quickly and cost-effectively. These technologies have enabled the development of highly saturated genetic maps for various livestock species, providing a robust framework for MAS programs (Raina et al., 2020; Shepelev et al., 2023).

The completion of genome sequencing projects for key livestock species has also been a major milestone. For example, the sequencing of the cattle, swine, and sheep genomes has facilitated the precise identification and mapping of genes associated with economically important traits. This genomic information is crucial for the detection, evaluation, and implementation phases of MAS, allowing for more accurate prediction of genetic merit and improved selection outcomes (Boopathi, 2020; Raina et al., 2020).

Furthermore, the integration of MAS with other genomic selection techniques, such as genomic selection (GS) and genome editing, has opened new avenues for enhancing livestock productivity and genetic diversity. These combined approaches can accelerate the breeding process and enable the introduction of desirable traits with greater precision (Singh et al., 2022; Tiwari et al., 2022).

1.3 Comparison with other breeding techniques

MAS offers several advantages over traditional selective breeding and genomic selection. Traditional selective breeding relies solely on phenotypic selection, which can be time-consuming and less accurate due to the influence of environmental factors and the complexity of genetic traits. In contrast, MAS uses genetic markers to directly target specific traits, thereby increasing the accuracy and speed of selection (Eze, 2019; Hasan et al., 2021).

Compared to genomic selection, which uses genome-wide marker information to predict the genetic value of individuals, MAS focuses on specific markers linked to QTLs. While genomic selection can capture the effects of many small-effect loci across the genome, MAS is particularly effective for traits controlled by a few major QTLs. This makes MAS a valuable tool for improving traits that are difficult to measure, have low heritability, or are controlled by recessive alleles (Eze, 2019; Kumawat et al., 2020).

However, the success of MAS depends on several factors, including the genetic architecture of the trait, the accuracy of QTL detection, and the genetic background of the breeding population. Empirical applications have shown that MAS can be highly effective for simply inherited traits, such as disease resistance, but may face limitations for more complex traits like yield and stress tolerance (Feng et al., 2020; Tiwari et al., 2022). Despite these challenges, the integration of MAS with other breeding techniques continues to offer promising opportunities for enhancing livestock productivity and genetic diversity (Osei et al., 2018; Boopathi, 2020).

2 Impact of MAS on Livestock Productivity

2.1 Introduction to productivity impacts

Improving productivity in commercial livestock operations is crucial for meeting the growing global demand for animal products. Marker-Assisted Selection (MAS) offers a promising approach to enhance productivity by enabling the selection of animals with superior genetic traits. This method leverages molecular markers linked to desirable traits, allowing for more precise and accelerated breeding compared to traditional methods. By improving traits such as growth rate, feed efficiency, and disease resistance, MAS can significantly boost the overall productivity of livestock operations, ensuring a more sustainable and profitable industry (Eze, 2019; Raina et al., 2020).

2.2 Advances in specific traits

MAS has been successfully applied to enhance various productivity traits across different livestock species. For instance, in fish, MAS has been used to improve economically important traits such as body growth, disease resistance, and meat quality, leading to faster and more accurate selection of superior breeding individuals (Eze, 2019). In dairy cattle, MAS has been employed to improve bull fertility, a critical trait for farm economics, by identifying genetic markers associated with successful conception rates and seminal parameters (Raina et al., 2020). These advancements demonstrate the potential of MAS to address specific productivity challenges in diverse livestock species, thereby enhancing overall performance and efficiency.

2.3 Technological contributions

The role of advanced genetic technologies in facilitating MAS cannot be overstated. The advent of genome-wide data and high-throughput genotyping platforms has significantly increased the number of markers identified and the accuracy of selection. For example, the use of Single Nucleotide Polymorphism (SNP) markers has enabled more precise identification of genetic variations associated with desirable traits, thereby improving the reliability of MAS in breeding programs (Figure 1) (Shepelev et al., 2023). Additionally, the integration of phenotyping and genotyping in early generations has been shown to reduce the number of genotypes needed to be carried forward, resulting in significant cost and time savings (Kumar et al., 2018). These technological advancements have revolutionized the MAS process, making it a more efficient and effective tool for improving livestock productivity.

Figure 1 identifies genes near significant SNPs in Lori-Bakhtiari sheep using the BioMart tool. Five genes were found: *PKP2* on chromosome 3, *ENSOARG00000017510* on chromosome 7, and *IGF2R*, *SLC22A1*, and *SLC22A2* on chromosome 8, with no genes near the SNP on chromosome 4. The study shows these gene locations. Although no QTLs for blood serum proteins were found near the SNPs, QTLs for immunoglobulins were identified. These findings can inform genomic selection strategies to enhance desirable traits in sheep.

3 Impact of MAS on Genetic Diversity

3.1 Introduction to genetic diversity

Genetic diversity is crucial for the health and sustainability of livestock populations. It provides the necessary variability for populations to adapt to changing environmental conditions and resist diseases, thereby ensuring long-term viability and productivity. High genetic diversity within a population enhances its ability to survive and thrive under various stressors, such as climate change, disease outbreaks, and fluctuating market demands (Makanjuola et al., 2020). Without sufficient genetic diversity, livestock populations may face increased risks of inbreeding, which can lead to reduced fitness, lower productivity, and higher susceptibility to diseases (Raina et al., 2020).

Figure 1 The genes found within 50 kbp distances from the significant SNPs on chromosomes 3 (A), 4 (B), 7 (C) and 8 (D), based on BioMart tool of Ensembl (Adopted from Zamani et al., 2021)

3.2 Risks and benefits

Marker-Assisted Selection (MAS) offers both positive and negative effects on genetic diversity. On the positive side, MAS can accelerate the breeding process by precisely selecting for desirable traits, thereby improving productivity, disease resistance, and other economically important traits in a shorter time frame (Eze, 2019; Kumawat et al., 2020; Hasan et al., 2021). For instance, MAS has been shown to improve traits such as drought resistance in alfalfa and disease resistance in wheat (Singh et al., 2022; Shepelev et al., 2023).

However, the intensive selection for specific traits using MAS can also lead to a reduction in genetic diversity. This is because the focus on a limited number of traits may result in the exclusion of other valuable genetic variations within the population (Makanjuola et al., 2020). Studies have shown that the implementation of genomic selection, a form of MAS, has led to increased rates of inbreeding and reduced effective population sizes in dairy cattle populations, highlighting the potential risks to genetic diversity (Makanjuola et al., 2020; Raina et al., 2020). Additionally, the use of MAS in tree breeding has been found to increase inbreeding and reduce genetic diversity more strongly compared to traditional breeding methods (Degen and Müller, 2023).

3.3 Strategies for maintaining diversity

To mitigate the risks associated with MAS and preserve genetic diversity, several strategies can be employed. One approach is to use a broader selection of genetic markers that encompass a wider range of traits, thereby maintaining a more diverse genetic pool (Moriguchi et al., 2020). Another strategy is to implement rotational breeding schemes that periodically introduce new genetic material into the breeding population, reducing the risk of inbreeding and maintaining genetic variability (Makanjuola et al., 2020).

Additionally, combining MAS with traditional breeding methods can help balance the benefits of rapid trait improvement with the need to preserve genetic diversity. For example, integrating MAS with progeny testing and genomic selection can optimize genetic gain while minimizing the loss of genetic diversity (Degen and Müller, 2023). Furthermore, monitoring genetic diversity through regular assessments of inbreeding coefficients and effective population sizes can help identify and address potential issues before they become critical (Makanjuola et al., 2020; Raina et al., 2020).

In conclusion, while MAS offers significant benefits for improving livestock productivity and resilience, careful management and strategic planning are essential to ensure that genetic diversity is maintained, thereby safeguarding the long-term health and sustainability of livestock populations.

4 Case Studies in MAS Applications

4.1 Case study on livestock productivity

Marker-Assisted Selection (MAS) has been effectively utilized to enhance livestock productivity, particularly in cattle. One notable application is in improving thermotolerance traits, which are crucial for maintaining productivity under thermal stress conditions. Thermal stress can significantly reduce feed intake, milk yield, growth rate, and reproductive efficiency in cattle. Recent advances in molecular genetics have enabled the identification of single-nucleotide polymorphisms (SNPs) associated with thermotolerance traits. These SNPs, found in genes such as *HSP70*, *HSP90*, and *HSF1*, play key roles in cellular activities during thermal stress and protect cells against damage. By selecting cattle with favorable SNPs, breeders can develop thermotolerant cattle that maintain high productivity even under extreme temperature conditions (Figure 2) (Hariyono and Prihandini, 2022).

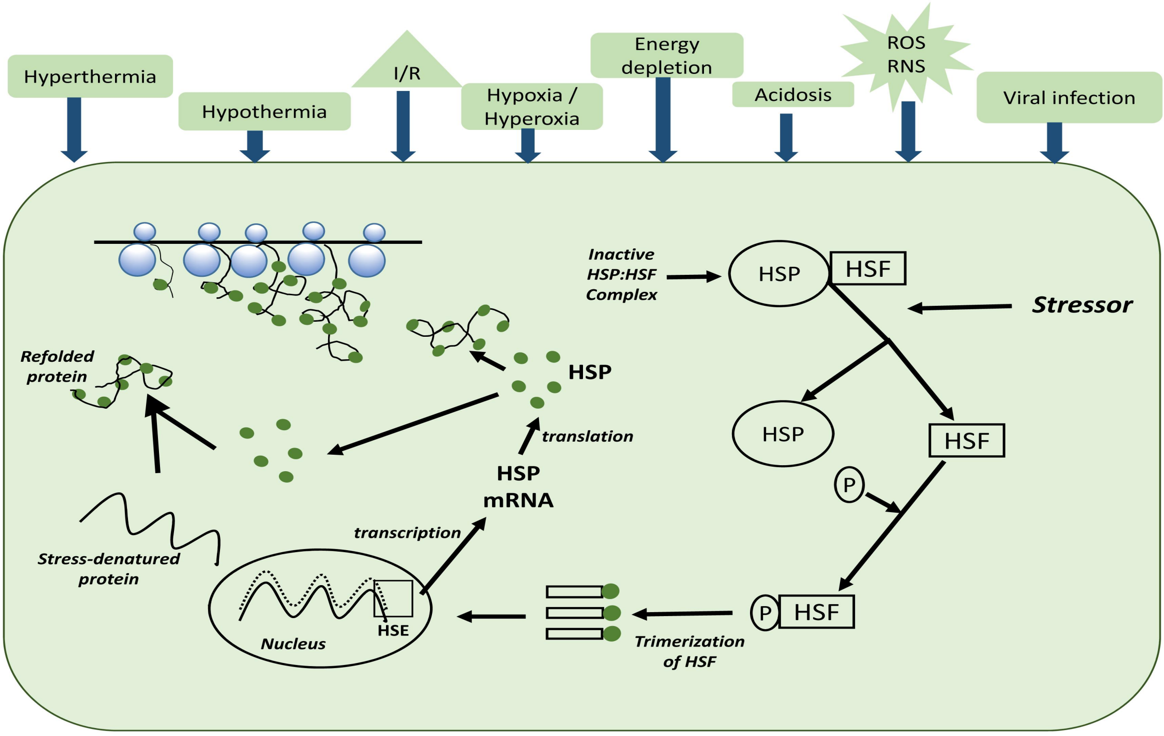

Figure 2 Molecular mechanism for the expression of *HSP70* within a cell (Adapted from Hariyono and Prihandini, 2022)

Image caption: The HSP70 gene family in cattle, consisting of four genes located on different chromosomes, shares homologous relationships with human *HSP70* genes, indicating conserved stress response mechanisms across species. The molecular mechanism involves the activation of heat shock factors (HSFs) under stress, leading to their dissociation from HSPs, phosphorylation, trimer formation, and nuclear translocation. HSF trimers then bind to heat shock elements (HSE) in the *HSP70* gene promoter, initiating transcription. The transcribed HSP70 mRNA is translated into proteins that function in protein assembly, transport, and repair. Understanding these mechanisms is essential for enhancing thermotolerance in livestock through marker-assisted selection (MAS), ultimately boosting productivity and resilience (Adapted from Hariyono and Prihandini, 2022)

4.2 Case study on genetic diversity

Marker-Assisted Selection (MAS) has been instrumental in enhancing genetic diversity within sheep breeding programs (Figure 3). A notable study investigated the genetic diversity and selection signals in 14 indigenous sheep breeds from the Middle East and South Asia, including breeds from Iran, Afghanistan, India, and Bangladesh (Eydivandi et al., 2021). The study utilized SNP genotype data to detect genetic diversity and population structure through various analyses such as principal component analysis (PCA), admixture, phylogenetic analyses, and Runs of Homozygosity. The results revealed significant genetic diversity among the breeds, with several genomic regions identified as candidates for selective sweeps. These regions were associated with economically important traits such as disease resistance and climate adaptation, highlighting the potential of MAS to enhance genetic diversity and improve breed resilience (Eydivandi et al., 2021).

Li et al. (2020) provided offers a comprehensive genetic analysis of sheep horn number variation, combining genome-wide association studies and selective sweep analyses to identify key genetic markers. By analyzing phenotypes across different sheep breeds, the study highlights the significance of specific genes, such as *HOXD1* on chromosome 2 and *RXFP2* on chromosome 10, which are associated with horn development and polled (hornless) traits. The findings are visualized through detailed Manhattan plots, which clearly illustrate significant genetic loci. Furthermore, the study expands beyond horn traits to explore genetic associations with other economically important traits like reproduction and milk yield, utilizing a large dataset of CNVs and SNPs. This integrated approach not only pinpoints genetic variants influencing phenotypic diversity but also offers potential targets for breeding programs focused on specific traits, demonstrating the power of genetic technologies in agricultural improvements.

4.3 Comparative case studies

Marker-Assisted Selection (MAS) has been applied in various pig breeding programs across different regions, yielding diverse outcomes. For instance, in a study conducted in the United States, MAS was employed to enhance growth rate and meat quality in pigs. The results demonstrated significant improvements in these traits, leading to increased productivity and profitability for pig farmers (Singh et al., 2022). Conversely, a similar study in Europe focused on disease resistance, particularly against Porcine Reproductive and Respiratory Syndrome (PRRS). The application of MAS in this context resulted in a notable reduction in disease incidence, although the overall impact on growth performance was less pronounced compared to the U.S. study (Moriguchi et al., 2020). In Asia, MAS has been utilized to improve reproductive traits in pigs, such as litter size and weaning weight. The outcomes of these programs have been mixed, with some studies reporting substantial gains in reproductive efficiency, while others have observed only marginal improvements (Vion et al., 2021). These contrasting results highlight the importance of considering regional differences in genetic backgrounds, environmental conditions, and breeding objectives when implementing MAS in pig breeding programs.

4.4 Innovative applications of MAS

Recent advancements in genomic technologies have enabled the integration of innovative approaches with MAS in dairy and beef cattle breeding. One notable example is the use of genomic selection (GS) to enhance milk production and quality in dairy cattle. A study conducted in the United States demonstrated that combining MAS with GS significantly increased the accuracy of selecting high-yielding dairy cows, leading to substantial improvements in milk yield and composition (Kushanov et al., 2021). Similarly, in beef cattle, the integration of MAS with GS has been employed to improve traits such as feed efficiency and meat quality. In a study conducted in Australia, this combined approach resulted in significant gains in feed conversion ratios and marbling scores, thereby enhancing the overall profitability of beef production (Darmanov et al., 2022). Another innovative application of MAS in cattle breeding involves the use of high-resolution melting (HRM)-based markers to accelerate the development of disease-resistant breeds. For instance, a study in Brazil utilized HRM markers to identify and select cattle with resistance to bovine respiratory disease, leading to a notable reduction in disease prevalence and associated economic losses (Wang et al., 2023). These case studies illustrate the potential of integrating new technologies with MAS to achieve more precise and efficient breeding outcomes in dairy and beef cattle.

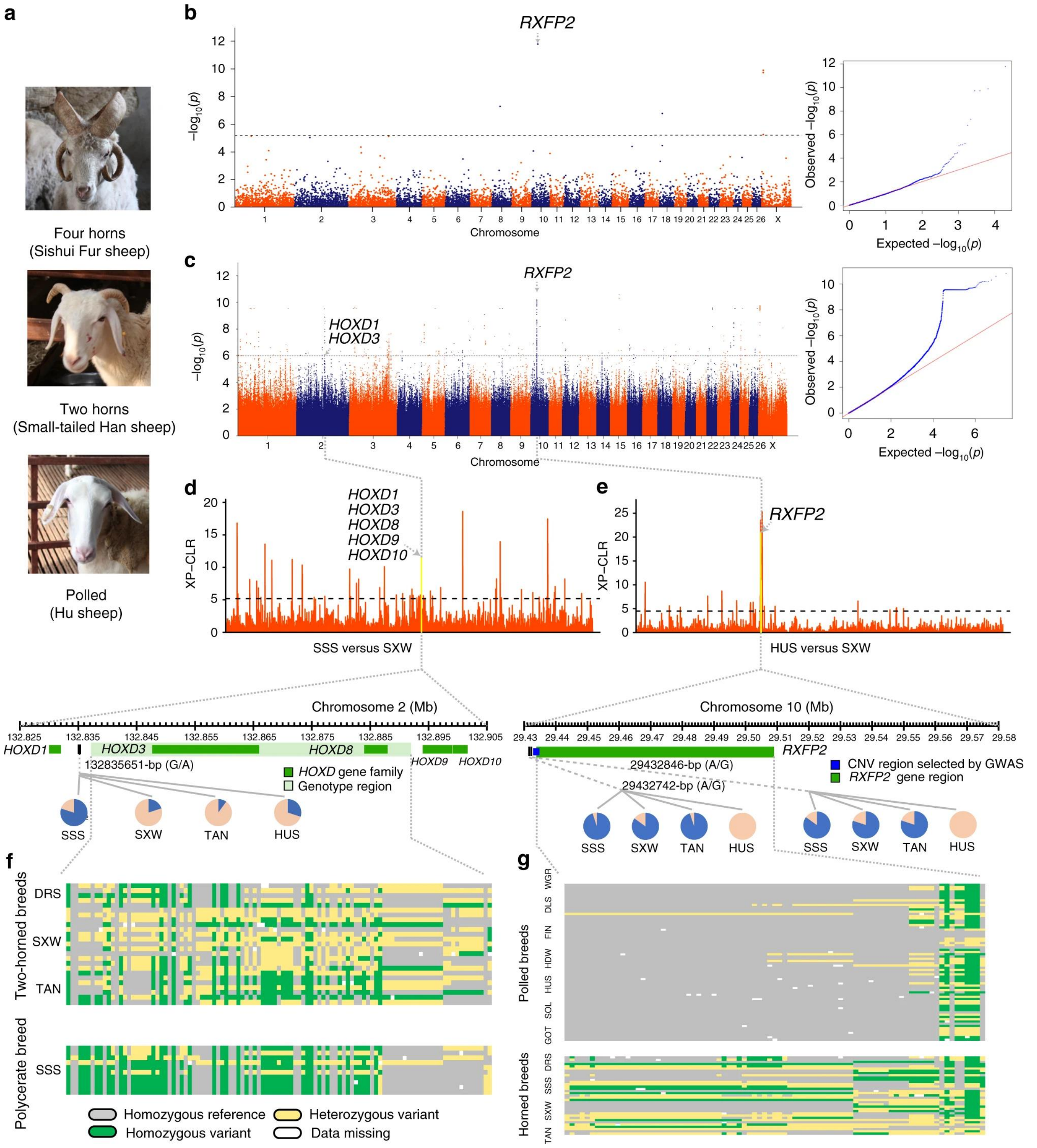

Figure 3 Selective and association signatures for sheep horn number (Adopted from Li et al., 2020)

Image caption: a Different phenotypes of horn types between Sishui Fur sheep (SSS), Small-tailed Han sheep (SXW), and Hu sheep (HUS); b, c Manhattan plot and quantile–quantile plot of association signals for the number of horns based on whole-genome CNV data b and SNPs c. The horizontal dashed lines correspond to the genome-wide significance thresholds (−log10(0.05/Total CNVs) = 5.29 for CNVs and −log10(P value) = 6 for SNPs). d Manhattan plot of selective sweeps for polycerate trait (SSS versus SXW) on chromosome 2. Allele frequency distribution of one non-synonymous SNP at the downstream of *HOXD1* gene in one polycerate breed (SSS), two two-horned breeds (SXW and TAN) and one polled breed (HUS). The horizontal dashed line corresponds to the genome-wide significance threshold (XP-CLR = 5.17). e Manhattan plot of selective sweeps for polled trait (HUS versus SXW) on chromosome 10. Allele frequency distribution of one non-synonymous SNP at the downstream of *RXFP2* gene in one polycerate breed (SSS), two two-horned breeds (SXW and TAN) and one polled breed (HUS). The horizontal dashed line corresponds to the genome-wide significance threshold (XP-CLR = 4.49). In all pie chart figures, the variant allele is indicated in blue, whereas the reference allele is indicated in pink. f Genotype patterns of the genes *HOXD3* and *HOXD8* among one polycerate breed and three two-horned breeds. g Genotype patterns of the gene *RXFP2* among four horned breeds and seven polled breeds (Adopted from Li et al., 2020)

5 Ethical and Social Considerations

5.1 Ethical issues

Marker-Assisted Selection (MAS) in livestock breeding raises several ethical concerns, primarily revolving around genetic manipulation and its implications. One significant ethical issue is the potential for reduced genetic diversity. As MAS focuses on selecting specific traits, there is a risk of narrowing the gene pool, which could make livestock populations more susceptible to diseases and environmental changes (Raina et al., 2020; Singh et al., 2022; Shepelev et al., 2023). Additionally, the manipulation of genetic material in animals raises questions about animal welfare and the naturalness of such interventions. The ethical debate extends to the potential long-term impacts on ecosystems and the balance of natural selection processes (Eze, 2019; Feng et al., 2020).

Another ethical concern is the transparency and consent in the use of genetic technologies. Farmers and consumers may not be fully informed about the genetic modifications involved in MAS, leading to issues of trust and acceptance. The ethical principle of informed consent is crucial, especially when the technology is applied to food-producing animals (Osei et al., 2018; Raina et al., 2020). Furthermore, the ownership and patenting of genetic information and technologies can lead to ethical dilemmas regarding access and control over genetic resources (Vagndorf et al., 2018; Kumawat et al., 2020).

5.2 Social impact

The social implications of MAS are multifaceted, affecting various scales of breeding operations and geographic contexts. On a small scale, MAS can provide significant benefits to individual farmers by improving livestock productivity and disease resistance, thereby enhancing their economic stability and food security (Collins et al., 2018; Singh et al., 2022; Shepelev et al., 2023). However, the high costs associated with MAS technologies may limit their accessibility to larger, more affluent breeding operations, potentially exacerbating inequalities between small-scale and large-scale farmers (Osei et al., 2018; Eze, 2019).

Geographically, the impact of MAS can vary significantly. In developed regions, where technological infrastructure and financial resources are more readily available, MAS can be integrated into existing breeding programs more efficiently. Conversely, in developing regions, the adoption of MAS may face challenges due to limited resources, lack of technical expertise, and infrastructural constraints (Vagndorf et al., 2018; Kumawat et al., 2020). This disparity can lead to a widening gap in agricultural productivity and economic development between different regions (Raina et al., 2020; Feng et al., 2020).

Moreover, the social acceptance of genetically modified organisms (GMOs) plays a crucial role in the implementation of MAS. Public perception and cultural attitudes towards genetic manipulation can influence the adoption and success of MAS technologies. In some cultures, there may be resistance to the use of genetic technologies in livestock breeding, which can hinder the widespread application of MAS (Osei et al., 2018; Hasan et al., 2021). Therefore, it is essential to engage with communities, provide education, and address concerns to ensure the ethical and socially responsible use of MAS in livestock breeding.

6 Discussion

6.1 Synthesis of findings

Marker-assisted selection (MAS) has shown significant potential in improving livestock productivity and genetic diversity. The integration of MAS with traditional breeding methods has led to notable advancements in livestock genetics. For instance, the use of MAS in cattle and sheep has enhanced reproductive efficiency and genetic gain, particularly through the implementation of assisted reproductive technologies (ARTs) such as multiple ovulation and embryo transfer (MOET) and juvenile in vitro fertilization and embryo transfer (JIVET) (Daly et al., 2020). Additionally, genomic selection has been instrumental in identifying and utilizing quantitative trait loci (QTLs) associated with economically important traits, thereby accelerating genetic improvement in livestock (Makanjuola et al., 2020; Raza et al., 2020). The application of genomic tools has also facilitated the conservation of genetic diversity in livestock breeds, ensuring sustainable animal production (Eusebi et al., 2019).

6.2 Challenges and limitations

Despite the promising outcomes, several challenges and limitations hinder the widespread adoption of MAS in livestock breeding. One major limitation is the high cost associated with genomic technologies and the implementation of ARTs, which can be prohibitive for many breeders (Daly et al., 2020). Additionally, the variability in the ability of embryo transfer recipients to maintain pregnancy poses a significant constraint to the efficiency of ARTs (Daly et al., 2020). Another challenge is the potential loss of genetic diversity due to intense selection pressures, which can lead to increased rates of inbreeding and coancestry, as observed in Holstein and Jersey cattle populations (Makanjuola et al., 2020). Furthermore, the complexity of quantitative traits, which are controlled by multiple genes with small effects, limits the effectiveness of MAS in improving these traits (Budhlakoti et al., 2022).

6.3 Potential biases and research gaps

Several potential biases and research gaps need to be addressed to optimize the use of MAS in livestock breeding. One potential bias is the reliance on pedigree data for estimating genetic diversity parameters, which may not be as accurate as genomic data (Eusebi et al., 2019). There is also a need for more comprehensive studies on the long-term impacts of genomic selection on genetic diversity and inbreeding rates (Makanjuola et al., 2020). Additionally, further research is required to develop cost-effective and efficient methods for the selection and management of recipient animals in ARTs (Daly et al., 2020). Another research gap is the limited understanding of the genetic architecture of complex traits under different environmental conditions, which is crucial for the development of stress-resilient livestock breeds (Budhlakoti et al., 2022). Addressing these biases and gaps will be essential for the successful implementation of MAS in livestock breeding programs.

7 Concluding Remarks

Marker-Assisted Selection (MAS) has demonstrated significant potential in enhancing livestock productivity and genetic diversity. The application of MAS has led to improved accuracy and efficiency in breeding programs by enabling the selection of desirable traits at the molecular level. For instance, MAS has been shown to significantly affect forage productivity in alfalfa under drought-stressed environments, indicating its potential to improve crop resilience and yield in challenging conditions. Additionally, MAS has been instrumental in identifying and developing markers for traits such as disease resistance and drought tolerance in various crops, which can be extrapolated to livestock breeding. The integration of MAS with genomic selection and other advanced breeding techniques has further accelerated genetic gains and improved the precision of breeding programs.

For breeders, it is recommended to incorporate MAS into their breeding programs to enhance the selection process's efficiency and accuracy. Utilizing MAS can significantly reduce the time required to develop new varieties with desirable traits, thereby increasing productivity and genetic diversity. Researchers should focus on identifying and validating new molecular markers associated with economically important traits to expand the MAS toolkit. Policymakers should support the adoption of MAS by providing funding for research and development and creating policies that encourage the use of advanced breeding technologies. Additionally, there should be an emphasis on training and capacity-building programs to equip breeders and researchers with the necessary skills to implement MAS effectively.

Future research should focus on the following areas to enhance the understanding and application of MAS in livestock breeding: Continued efforts are needed to identify and validate new molecular markers associated with traits of economic importance, such as disease resistance, drought tolerance, and productivity. Research should explore the integration of MAS with genomic selection and other advanced breeding techniques to maximize genetic gains and improve breeding efficiency. Developing high-throughput phenotyping and genotyping methods will enable the rapid and accurate assessment of large populations, facilitating the implementation of MAS on a broader scale. Investigating the applicability of MAS techniques developed for plants in livestock breeding could provide valuable insights and accelerate the adoption of MAS in animal breeding programs. Developing cost-effective MAS approaches, such as the HRMA-based method for genotyping, will make the technology more accessible to breeders, especially in developing regions.

By addressing these research areas, the potential of MAS in improving livestock productivity and genetic diversity can be fully realized, contributing to sustainable agricultural practices and food security.

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Conflict of Interest Disclosure

The 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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