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International Journal of Molecular Zoology 2024, Vol.14, No.5, 265-272
http://animalscipublisher.com/index.php/ijmz

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Impact of Genomic Selection on Fertility Traits in Beef Cattle

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International Journal of Molecular Zoology, 2024, Vol.14, No.5 doi: 10.5376/ijmz.2024.14.0024
Received: 11 Jul., 2024
Accepted: 22 Aug., 2024
Published: 13 Sep., 2024

Preferred citation for this article:
Li J., 2024, Impact of genomic selection on fertility traits in beef cattle, International Journal of Molecular Zoology, 14(5): 265-272 (doi: 10.5376/ijmz.2024.14.0024)

Abstract Fertility traits play a critical role in the overall productivity and profitability of beef cattle production. This study examines the impact of genomic selection on improving fertility traits in beef cattle, highlighting its advantages over traditional breeding methods. Genomic selection, leveraging advances in genomic technologies, allows for more precise identification and selection of key fertility-related genes, leading to significant genetic gains in reproductive efficiency. Through a case study focusing on a specific beef cattle breed, applying genomic selection techniques to enhance fertility traits and analyzed the improvements in reproductive performance. Findings suggest that genomic selection not only accelerates genetic progress but also has considerable implications for the beef industry in terms of profitability and sustainability. Looking forward, integrating genomic selection with other breeding strategies and advancing genomic technologies may further revolutionize cattle breeding. Continued research and ethical considerations are essential for maximizing the potential of genomic selection in enhancing fertility traits in beef cattle.

Keywords Genomic selection; Beef cattle; Fertility traits; Reproductive efficiency; Genetic improvement

1 Introduction

Fertility is a critical component of beef cattle production, directly influencing the efficiency and profitability of the industry. Reproductive performance in beef cattle encompasses a range of traits, including age at puberty, age at first calving, and pregnancy status, which are essential for maintaining a productive herd (Toghiani et al., 2017). Historically, the heritability of these traits has been low, making genetic improvement challenging through traditional selection methods (Berry et al., 2014).

Fertility traits are paramount in beef production as they determine the reproductive efficiency and overall productivity of the herd. Efficient reproduction leads to more calves per cow over her lifetime, reducing the cost per calf and increasing the overall profitability of beef operations (Miglior et al., 2017). Traits such as pregnancy rate, calving interval, and age at first calving are directly linked to the economic viability of beef production systems (Keogh et al., 2020). Moreover, improved fertility can mitigate the economic losses associated with subfertility and reproductive failures (Fonseca et al., 2020).

Genomic selection (GS) is a revolutionary approach that leverages high-density single nucleotide polymorphism (SNP) data to predict the genetic potential of animals for various traits, including fertility (Xu et al., 2015). This method enhances the accuracy of selection by incorporating genomic information, thereby accelerating genetic gain, especially for low heritability traits (García-Ruiz et al., 2016). GS has been successfully implemented in dairy cattle, leading to significant improvements in fertility, longevity, and health traits. In beef cattle, GS holds promise for similar advancements, although its application has been less widespread compared to dairy cattle.

This study evaluates the impact of genomic selection on fertility traits in beef cattle, using genomic data to assess the heritability of key reproductive traits, comparing the accuracy of genomic predictions with traditional pedigree-based methods, and identifying potential genetic markers associated with improved reproductive performance, aiming to provide insights into the effectiveness of genomic selection for enhancing fertility traits and contributing to the development of more efficient beef cattle breeding programs.

2 Genomic Selection in Livestock

2.1 Definition and principles of genomic selection

Genomic selection (GS) is a form of marker-assisted selection that utilizes genetic markers covering the entire genome to predict the breeding values of individuals. Unlike traditional marker-assisted selection, which focuses on a few significant markers, GS assumes that all markers might be linked to genes affecting the trait and estimates their effects collectively. This approach allows for the inclusion of thousands of genes with small effects on the phenotype, which are often ignored in traditional methods due to their statistical insignificance (Meuwissen et al., 2016).

2.2 Advances in genomic technologies

The widespread adoption of GS in livestock breeding has been facilitated by several technological advancements. The development of high-throughput genotyping technologies has made it possible to genotype animals for hundreds of thousands of single nucleotide polymorphisms (SNPs) cost-effectively (Moravčíková et al., 2019). Additionally, the availability of whole-genome sequence data has further enhanced the accuracy of genomic predictions (Nadri and Bagheri, 2022). These advancements have enabled the implementation of GS in various livestock species, including dairy and beef cattle, pigs, and poultry (Wiggans et al., 2017).

2.3 Comparison of genomic selection vs. traditional breeding methods

Genomic selection offers several advantages over traditional breeding methods. Traditional methods rely heavily on phenotypic selection and pedigree information, which can be less accurate and slower due to longer generation intervals. In contrast, GS increases the accuracy of selection by incorporating genomic information, which allows for the prediction of breeding values at an early age (Figure 1). This results in shorter generation intervals and faster genetic progress (García-Ruiz et al., 2016; Randhawa et al., 2016).

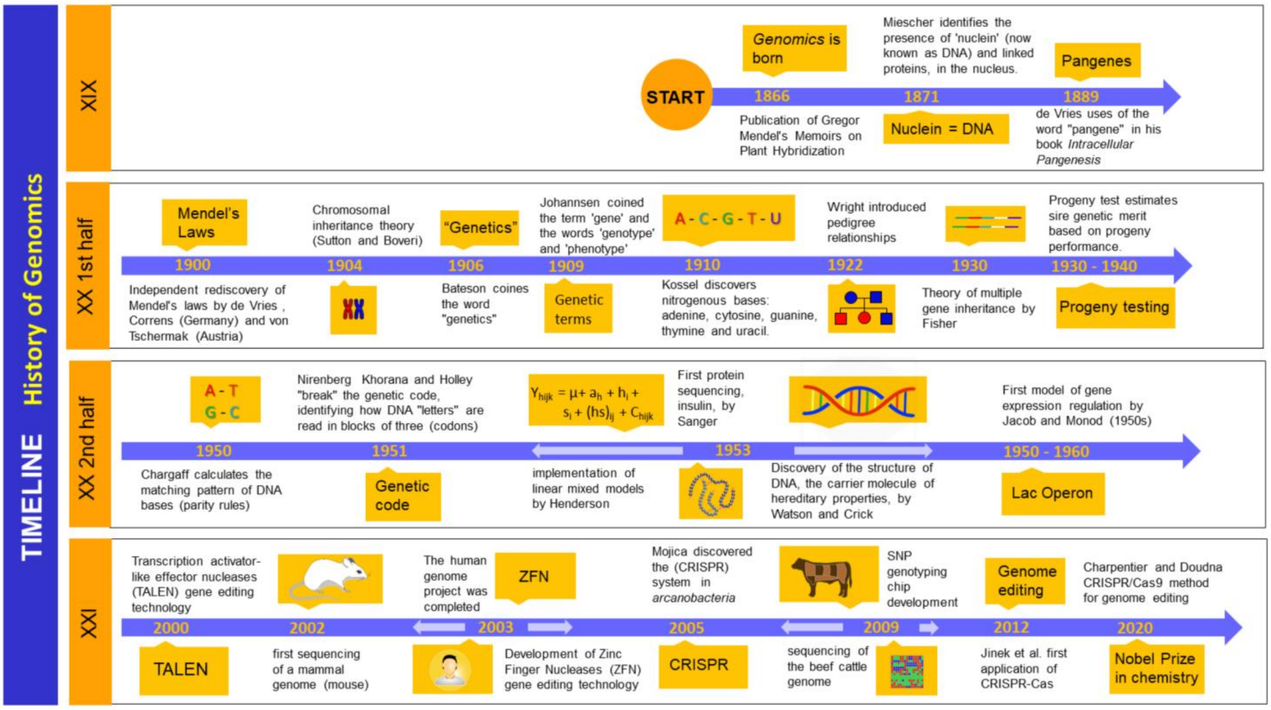

Figure 1 Brief historical evolution of genomics. Origins of classic genetic knowledge are undoubtedly based on Mendel's discoveries on the inheritance of characters in plants in the XIX century. During the early XX century concepts of genes and chromosome theory became consolidated. Later, during the XX century advances on the chemical basis of inheritance, the breaking of the genetic code and gene regulation discoveries marked the development of genomics and the development of genomic tools in animal science. An impacting development in genomics was the sequencing of the whole human genome in the early XXI century, followed by the ultimate application of this knowledge, the discovery of the gene-editing tools. This led to the awarding of the Nobel Prize to women researchers Charpentier and Doudna in 2020 (Adopted from Gutierrez-Reinoso et al., 2021)

In dairy cattle, the implementation of GS has led to significant improvements in traits of economic importance, such as milk production, fertility, and longevity. The rate of genetic gain has doubled, and the costs associated with progeny testing have been reduced (Guinan et al., 2022). In beef cattle, although the adoption of GS has been slower due to different breeding structures, studies have shown that selective genotyping can improve prediction accuracy even with a limited number of genotyped animals (Mohammaddiyeh et al., 2023).

3 Fertility Traits in Beef Cattle

3.1 Key fertility traits affecting beef production

Key fertility traits that significantly impact beef production include age at first calving (AFC), calving interval (CI), and heifer pregnancy status (HPS). Age at first calving is crucial as it determines the onset of a cow's reproductive life and influences lifetime productivity. Calving interval, the period between successive calvings, affects the number of calves a cow can produce over her lifetime. Heifer pregnancy status, which indicates whether a heifer becomes pregnant during the breeding season, is essential for ensuring that heifers contribute to the herd's productivity (Toghiani et al., 2017; Brzáková et al., 2020).

3.2 Genetic basis of fertility traits

The genetic basis of fertility traits in beef cattle is complex and involves multiple genes. Heritability estimates for these traits are generally low to moderate, indicating that while genetic selection can improve these traits, environmental factors also play a significant role. For instance, heritability for age at first calving ranges from 0.03 to 0.31, and for calving interval, it is similarly low (Berry and Evans, 2014). Genomic selection has shown promise in improving the accuracy of predicting these traits, with studies identifying specific single nucleotide polymorphisms (SNPs) associated with reproductive efficiency (Melo et al., 2018; Keogh et al., 2020; Jiménez et al., 2023). However, the genetic correlations between fertility traits and other performance traits, such as growth and carcass traits, can be antagonistic, complicating selection strategies (Pardo et al., 2020).

3.3 Challenges in measuring fertility traits

Measuring fertility traits in beef cattle presents several challenges. One major issue is the low heritability of these traits, which makes genetic improvement slow and difficult. Additionally, the collection of accurate phenotypic data is labor-intensive and time-consuming, often requiring long-term monitoring of individual animals (Zhang et al., 2014). Environmental factors, such as nutrition, management practices, and climate, also significantly influence fertility traits, adding variability that can obscure genetic effects. Furthermore, the complexity of reproductive physiology means that multiple traits must be considered simultaneously, complicating the analysis and interpretation of data (Berry et al., 2014; Meier et al., 2021).

4 Impact of Genomic Selection on Fertility Traits

4.1 Genetic gain in fertility traits through genomic selection

Genomic selection (GS) has shown significant potential in enhancing genetic gain for fertility traits in beef cattle. Studies have demonstrated that GS can improve the predictive accuracy and genetic gain of various fertility traits, such as age of puberty (AOP), age at first calving (AOC), and heifer pregnancy status (HPS). The heritability estimates for these traits were found to be higher when using genomic approaches compared to traditional pedigree-based methods, indicating a more effective selection process (Toghiani et al., 2017). Additionally, the introduction of GS in dairy cattle has led to increased genetic trends for fertility, lifespan, and udder health, suggesting similar potential benefits for beef cattle (Figure 2) (García-Ruiz et al., 2016).

4.2 Impacts on reproductive efficiency and profitability

The implementation of GS has positively impacted reproductive efficiency and profitability in beef cattle production. Improved reproductive efficiency, particularly in traits with low heritability, can lead to significant economic benefits (Berry et al., 2014). For instance, the use of GS has been associated with increased rates of genetic gain and inbreeding in the Australian national herd, which has implications for long-term productivity and profitability (Scott et al., 2021). Furthermore, advancements in genomic technologies have enabled more accurate selection for reproductive traits, thereby enhancing overall herd fertility and reducing economic losses associated with subfertility (Thundathil et al., 2016; Fonseca et al., 2020).

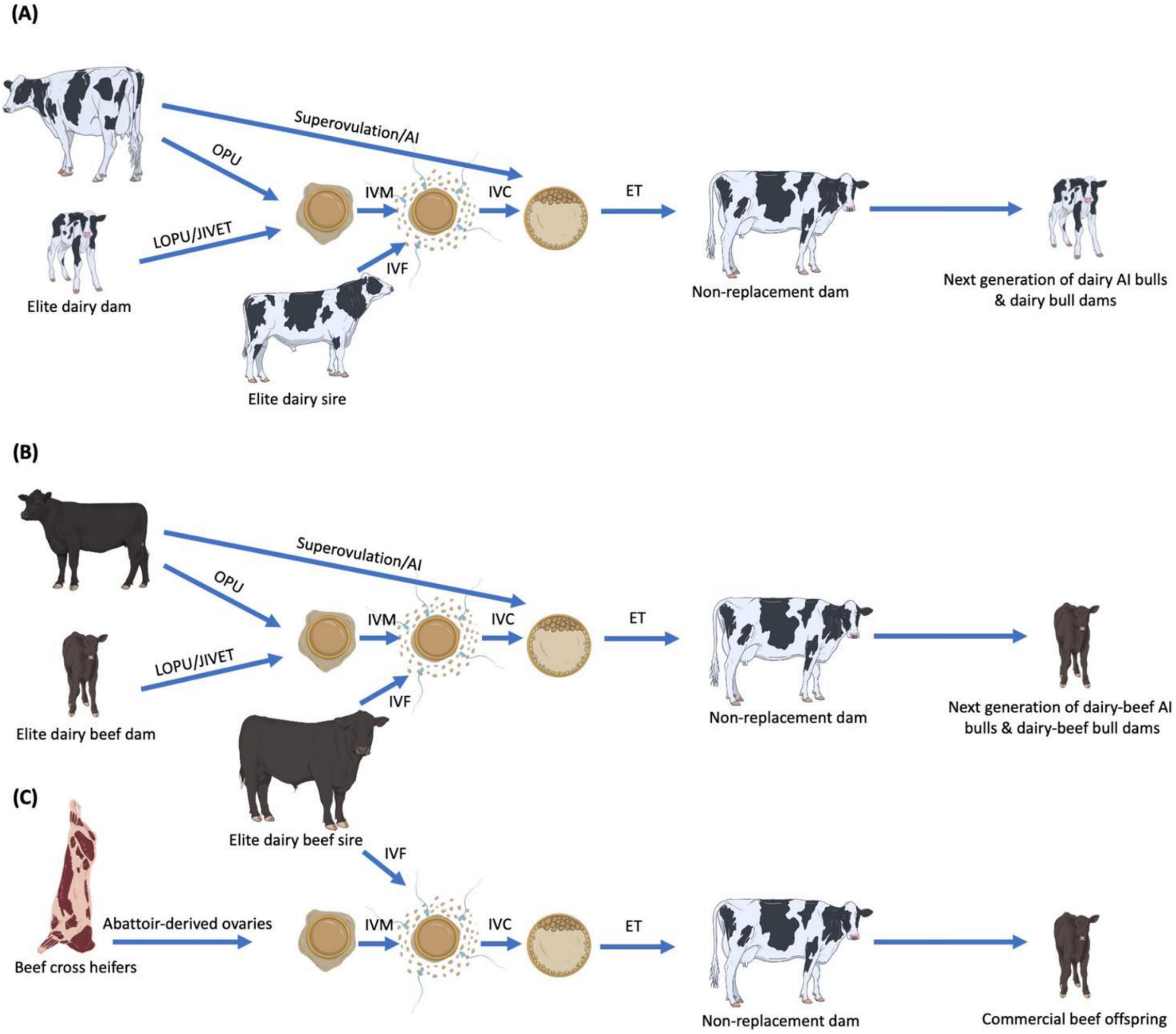

Figure 2 Use of assisted reproductive technologies to generate the next generation of elite dairy, elite dairy-beef, and commercial beef calves. (A) To create the next generation of dairy AI bulls and dairy bull dams, embryos are generated from elite dairy dams by superovulation and AI or by using ovum pick-up (OPU) or laparoscopic OPU (LOPU) or juvenile in vitro fertilization and embryo transfer (JIVET) to collect oocytes followed by in vitro maturation (IVM), fertilization (IVF) with semen from elite dairy bulls, and culture (IVC) to produce embryos for transfer (ET) to recipient dairy dams not required to generate replacement females (either surplus to requirements or genetically inferior). (B) To create the next generation of dairy-beef AI bulls and dairy-beef bull dams, superovulation and AI or OPU and LOPU followed by IVF with semen from elite dairy-beef bulls (e.g., Angus) is conducted on elite dairy-beef dams to generate embryos for transfer to recipient dairy dams. (C) To produce commercial beef animals, ovaries collected postslaughter from beef-cross heifers are used as a source of low-cost oocytes. These oocytes are fertilized with semen from elite dairy-beef bulls (different breed to maximize heterosis), resulting in embryos suitable for transfer to recipient dairy dams. The male and female offspring are all commercial beef animals, with female offspring also being a potential source of oocytes after slaughter (Adopted from Crowe et al., 2021)

4.3 Case studies demonstrating genomic selection effects

Several case studies highlight the effectiveness of GS in improving fertility traits in beef cattle. For example, a study on composite gene combination (CGC) beef cattle demonstrated that genomic prediction accuracy was higher for AOP compared to AOC, likely due to the higher heritability of AOP. Another study on Charolais and Limousin beef cows identified significant single nucleotide polymorphisms (SNPs) associated with reproductive and productive traits, suggesting the potential for incorporating these genetic markers into breeding programs (Keogh et al., 2020). Additionally, research on Retinta beef cattle revealed high heritability estimates for reproductive efficiency, indicating that GS could be effectively used to select more fertile cows in extensive production systems (Jiménez et al., 2023).

5 Case Study

5.1 Overview of a specific beef cattle breed or population

This case study focuses on the composite gene combination (CGC) breed, which is a composite of 50% Red Angus, 25% Charolais, and 25% Tarentaise. The CGC breed was selected for its unique genetic makeup, combining traits from these three breeds to enhance overall performance, including fertility traits. The study population consisted of 1 365 first parity females born between 2002 and 2011, with a pedigree file including 5 374 animals (Toghiani et al., 2017).

5.2 Methodology of genomic selection applied

Genomic selection (GS) was applied to improve fertility traits in the CGC breed using a combination of univariate and multivariate classical quantitative models and univariate genomic approaches. The study utilized different density SNP chips (3 K to 50 K SNP) for genotyping 3 902 animals, with low-density arrays imputed to higher density using FImpute. Three Bayesian methods (BayesA, BayesB, and BayesCπ) were implemented to estimate heritabilities and genetic correlations for traits such as age of puberty (AOP), age at first calving (AOC), and heifer pregnancy status (HPS).

5.3 Results and analysis of fertility trait improvements

The heritability estimates for the fertility traits varied, with AOP showing higher heritability (0.2) compared to AOC (0.03). The heritability of pregnancy status was 0.15 using univariate analysis and 0.09 using multivariate analysis. Genetic correlations between pregnancy status and other traits were low, with 0.08 for AOP and -0.10 for AOC. The accuracy of genomic prediction was higher for AOP than AOC, likely due to the higher heritability of AOP. The prediction accuracy for binary pregnancy status, measured using the area under the curve, increased by 27%-29% compared to a random classifier.

5.4 Implications for the beef industry

The application of genomic selection in the CGC breed demonstrated significant potential for improving fertility traits, which are crucial for the profitability of the beef industry. The increased accuracy of genomic predictions and the identification of key genetic variants associated with fertility traits can lead to more efficient breeding programs (Porto-Neto et al., 2023). This, in turn, can enhance reproductive efficiency, reduce economic losses due to subfertility, and improve overall productivity in beef cattle herds (Fonseca et al., 2020; Keogh et al., 2020). The findings underscore the importance of incorporating genomic tools in breeding strategies to achieve sustainable genetic gains in fertility traits, ultimately benefiting the beef industry at large.

6 Future Perspectives

6.1 Potential advancements in genomic technologies

The future of genomic selection in beef cattle fertility traits is promising, with several potential advancements on the horizon. One significant area of development is the use of whole-genome sequencing, which can provide a more comprehensive understanding of the genetic architecture underlying fertility traits. This approach allows for the identification of rare variants and the fine-mapping of quantitative trait loci (QTL) that are crucial for reproductive performance (Meuwissen et al., 2016). Additionally, advancements in high-throughput genotyping technologies will enable the cost-effective analysis of large populations, thereby increasing the accuracy of genomic predictions. The integration of multi-omics data, including transcriptomics and proteomics, can further elucidate the biological pathways involved in fertility, leading to more targeted breeding strategies (Tahir et al., 2021).

6.2 Integration of genomic selection with other breeding strategies

Integrating genomic selection with traditional breeding methods and other advanced technologies can enhance the overall effectiveness of breeding programs (Yang, 2024). For instance, combining genomic selection with marker-assisted selection (MAS) can improve the accuracy of selecting animals with desirable fertility traits (Ma et al., 2024). Moreover, the use of reproductive technologies such as artificial insemination (AI) and embryo transfer (ET) can be optimized through genomic selection, ensuring that only the best genetic material is propagated. The adoption of sexed semen in AI programs can also facilitate the selection of heifers with superior fertility traits, thereby accelerating genetic gain (García-Ruiz et al., 2016). Additionally, the implementation of fixed-time AI in commercial beef operations can capture valuable phenotypic data, which can be used to refine genomic predictions for both male and female fertility (Keogh et al., 2020).

6.3 Ethical considerations and public perception

As genomic technologies continue to advance, ethical considerations and public perception will play a crucial role in their adoption and implementation. One major concern is the potential for increased inbreeding and reduced genetic diversity, which can negatively impact animal health and welfare (Lozada-Soto et al., 2021). It is essential to monitor and manage inbreeding levels to ensure the long-term sustainability of breeding programs. Public perception of genomic selection and genetic modification in livestock can also influence the acceptance of these technologies. Transparent communication about the benefits and risks associated with genomic selection, as well as the implementation of ethical guidelines, will be necessary to gain public trust and support. Additionally, addressing concerns related to animal welfare and ensuring that breeding practices do not compromise the well-being of the animals will be critical for the ethical advancement of genomic selection in beef cattle (Taylor et al., 2018).

7 Concluding Remarks

The research on genomic selection and its impact on fertility traits in beef cattle has yielded several important insights. Firstly, reproductive traits in beef cattle, particularly in females, tend to have low heritability, which poses challenges for traditional selection methods. However, genomic selection (GS) has shown promise in improving the accuracy and genetic gain for these traits. Studies have identified specific genomic regions and candidate genes associated with fertility traits, such as those involved in embryonic development, germ cell proliferation, and ovarian hormone regulation. Additionally, the integration of high-density SNP chips and advanced statistical models has enhanced the prediction accuracy for fertility traits, even in small datasets.

Continued research in genomic selection is crucial for several reasons. Firstly, the identification of functional candidate genes and genomic regions associated with fertility traits can lead to more targeted and effective breeding programs. This is particularly important for traits with low heritability, where traditional selection methods are less effective. Moreover, advancements in genomic technologies, such as whole-genome sequencing and high-throughput genotyping, can further improve the accuracy of genomic predictions and facilitate the discovery of causative mutations. Understanding the genetic mechanisms underlying fertility traits can also help resolve genetic antagonisms and improve overall reproductive performance in beef cattle.

The future of beef cattle breeding lies in the integration of genomic selection with traditional breeding methods. The ability to identify and select for fertility traits at an early age can significantly enhance the genetic improvement of beef herds, leading to increased productivity and economic benefits. As genomic technologies continue to advance, the accuracy and efficiency of selection for complex traits like fertility will improve, making it possible to achieve simultaneous genetic gains in both reproductive and production traits. Ultimately, the successful implementation of genomic selection strategies will depend on the development of large, diverse reference populations and the continuous refinement of statistical models to account for breed differences and environmental factors.

Acknowledgments

I would like to thank Professor Feng for his invaluable guidance, insightful suggestions, and continuous support throughout the development of this study.

Conflict of Interest Disclosure

The author affirms 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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