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Observation Analysis of Embryonic Development Genes in High Fertility Goat Breeds

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Abstract This study explores the key embryonic development genes in high fertility goat breeds, identifying major genes and their regulatory mechanisms. We conducted a comparative genomic analysis of selected breeds to assess genetic diversity and its correlation with fertility rates. Additionally, we examined gene expression patterns and the effects of environmental factors, such as nutrition and housing conditions, on gene activity. A case study of a specific high fertility goat breed provided insights into relevant genes and their implications for breeding strategies. The findings highlight the potential for enhancing fertility through genetic selection and integration of these insights into breeding programs, ultimately benefiting livestock production. Future research directions include exploring additional embryonic development genes and expanding studies to other livestock species.

Keywords Goat reproduction; Embryonic development; Genetic variation; Gene expression; Breeding strategies

1 Introduction

Goat reproduction is a complex biological process that significantly impacts the agricultural economy, particularly in regions where goats are a primary livestock resource. High fertility in goat breeds is a desirable trait that enhances productivity and economic returns. The reproductive performance of goats, such as the Dazu black goats, is influenced by various genetic and environmental factors. These goats are known for their adaptability and high fertility, making them an excellent model for studying reproductive traits (Zhao et al., 2023). Understanding the genetic basis of fertility can help in breeding programs aimed at improving reproductive efficiency in goats (Wang et al., 2020; Ghafouri et al., 2023).

Embryonic development is a critical phase in the reproductive cycle of livestock, determining the success of pregnancy and the overall fecundity of the species. In goats, as in other livestock, the process of embryo implantation is crucial for establishing pregnancy. However, the genetic mechanisms underlying this process are not fully understood (Zhao et al., 2023). Research into the genes involved in embryonic development and implantation can provide insights into improving fertility rates and reducing pregnancy loss, which is a significant issue affecting livestock productivity (Du et al., 2023). Identifying key regulatory genes and pathways can lead to targeted interventions to enhance reproductive success in high-fertility breeds (Fonseca et al., 2020).

This study attempts to explore the genes associated with embryonic development in high fertility goat breeds, discuss the genetic factors that contribute to successful embryo implantation and development, and provide an overview of the expression profiles of mRNAs, lncRNAs, and miRNAs in the uterine tissues of these breeds. By leveraging advanced genomic techniques, this research aims to provide a comprehensive understanding of the molecular mechanisms underpinning high fecundity. The findings are expected to contribute to the development of genetic strategies for enhancing fertility in livestock, thereby supporting sustainable agricultural practices.

2 Key Embryonic Development Genes

2.1 Identification of major genes

In the study of embryonic development genes in high fertility goat breeds, several key genes have been identified. Notably, the genes HOXA10 and HOXA11 have been highlighted for their roles in embryo implantation in Dazu black goats, a breed known for its high fertility (Zhao et al., 2023). Additionally, the *DNMT3B* gene has been identified as a candidate gene for goat fertility, with specific mutations associated with litter size (Hui et al., 2020). These genes are crucial for understanding the genetic basis of reproductive success in goats (Mason, 2024).

2.2 Functions and regulatory mechanisms

The *HOXA10* and *HOXA11* genes are involved in the regulation of uterine receptivity and embryo implantation, which are critical processes for successful pregnancy (Zhao et al., 2023). These genes are part of the homeobox gene family, which plays a significant role in the development and differentiation of tissues during embryogenesis. On the other hand, DNMT3B is responsible for DNA methylation, a key epigenetic modification that regulates gene expression during embryonic development. The expression of DNMT3B is notably higher in the ovaries of goats with higher litter sizes, suggesting its role in enhancing reproductive capacity (Hui et al., 2020).

2.3 Impact of gene expression on developmental processes

The expression of HOXA10 and HOXA11 is crucial for the proper development of the uterine environment, facilitating successful embryo implantation and subsequent development (Zhao et al., 2023). Disruptions in the expression of these genes can lead to implantation failures and reduced fertility. Similarly, the DNMT3B gene, through its role in DNA methylation, influences the expression of various genes involved in embryonic development. Variations in DNMT3B expression have been linked to differences in litter size, indicating its impact on the reproductive efficiency of goats (Hui et al., 2020). Understanding these gene expressions provides insights into the molecular mechanisms that underpin high fertility in goat breeds (Kropp et al., 2017; Ghafouri et al., 2023; Hou et al., 2023).

In summary, the identification and understanding of key embryonic development genes such as *HOXA10*, *HOXA11*, and *DNMT3B* are essential for advancing reproductive genetics in goats. These genes play pivotal roles in regulating processes critical for successful reproduction and offer potential targets for genetic improvement in high fertility goat breeds.

3 Genetic Variation in High Fertility Goat Breeds

Genetic variation plays a crucial role in determining the fertility rates of goat breeds. Understanding the genetic differences among high fertility breeds can provide insights into the mechanisms that enhance reproductive performance.

3.1 Comparative genomics of selected breeds

Comparative genomics involves analyzing the genetic sequences and expression levels of genes related to reproductive traits across different goat breeds. In a study comparing prolific Jintang black goats and nonprolific Tibetan goats, variations in nucleotide sequences and expression levels of genes related to follicular development were observed. Notably, differences in the *FSHR*, *LHCGR*, and *B4GANT2* genes were identified, which may contribute to the higher fertility observed in Jintang black goats (Zi et al., 2019). Additionally, the study of Dazu black goats (DBGs) revealed differentially expressed genes during embryo implantation, highlighting the genetic basis for their high fertility (Zhao et al., 2023).

3.2 Assessment of genetic diversity

Genetic diversity within goat breeds is assessed by examining variations in gene sequences and expression levels. The study on Spanish goat breeds using a random regression model demonstrated that reproductive efficiency, a trait linked to fertility, is moderately heritable and varies with age. This suggests that genetic diversity plays a significant role in reproductive traits, and selecting for these traits can enhance fertility (Ziadi et al., 2021). Furthermore, the genetic analysis of DBGs identified numerous differentially expressed genes and pathways, such as oxidative phosphorylation and immune response, which are crucial for successful embryo implantation and may reflect genetic diversity contributing to fertility (Martínez-Castillero et al., 2020; Zhao et al., 2023).

3.3 Correlation between genetic variation and fertility rates

The correlation between genetic variation and fertility rates is evident in the differences observed in gene expression and sequence variations among goat breeds. For instance, the lower plasma concentrations of LH, P4, and E2 in prolific Jintang black goats compared to nonprolific Tibetan goats suggest a genetic basis for their higher fertility rates (Zi et al., 2019). Similarly, the identification of candidate genes and enriched pathways in DBGs provides a genetic framework for understanding their high fertility, as these genes are involved in critical reproductive processes (Zhao et al., 2023). The genetic analysis of Spanish goat breeds further supports the notion that reproductive efficiency, influenced by genetic variation, is a key determinant of fertility (Ziadi et al., 2021; Porto-Neto et al., 2023).

In summary, genetic variation among high fertility goat breeds is closely linked to differences in reproductive traits and efficiency. Comparative genomics and genetic diversity assessments provide valuable insights into the genetic mechanisms underlying fertility, which can be leveraged to improve breeding strategies and enhance reproductive performance in goats.

4 Gene Expression Patterns in High Fertility Breeds

4.1 Techniques for measuring gene expression

In the study of gene expression patterns in high fertility goat breeds, various advanced techniques are employed. RNA sequencing (RNA-seq) is a prominent method used to measure mRNA and long non-coding RNA (lncRNA) expression levels, providing insights into the molecular mechanisms underlying reproductive traits (Figure 1) (Sun et al., 2022). Single-cell RNA sequencing (scRNA-seq) is another powerful tool that allows for the detailed profiling of gene expression in specific cell types, such as granulosa cells, which are crucial for fertility (Ghafouri et al., 2023). Additionally, quantitative real-time PCR (qPCR) is used to determine the expression profiles of specific genes, such as the PRNT gene, across different tissues (Bi et al., 2021).

4.2 Variability of expression across breeds

Gene expression variability across different goat breeds is significant and can be linked to differences in reproductive performance. For instance, in Dazu black goats, transcriptome analysis revealed numerous differentially expressed mRNAs during embryo implantation, highlighting breed-specific gene expression patterns (Zhao et al., 2023). Similarly, in Chuanzhong black goats, whole-genome sequencing identified distinct genetic variations associated with high and low litter sizes, indicating variability in gene expression related to fecundity (Guo et al., 2024). These differences underscore the importance of breed-specific studies to understand the genetic basis of fertility.

4.3 Relationship between gene expression and reproductive performance

The relationship between gene expression and reproductive performance is complex and involves multiple pathways and regulatory networks. In high-fertility goats, differentially expressed genes are often enriched in pathways related to reproductive processes, such as the AMPK, PI3K-Akt, and ECM-receptor interaction pathways, which directly or indirectly affect reproduction (Sun et al., 2022). Additionally, genes like DNMT3B and PRNT have been associated with litter size, with specific genetic variants influencing reproductive traits (Hui et al., 2020; Bi et al., 2021). These findings suggest that gene expression patterns are closely linked to reproductive efficiency and can serve as potential markers for breeding programs aimed at enhancing fertility (Tobolski et al., 2021).

In summary, the study of gene expression patterns in high fertility goat breeds involves advanced techniques like RNA-seq and scRNA-seq, reveals significant variability across breeds, and highlights the intricate relationship between gene expression and reproductive performance. These insights are crucial for developing strategies to improve fertility in goat breeding programs.

5 Environmental Factors Influencing Gene Expression

5.1 Effects of nutrition on gene activity

Nutrition plays a crucial role in regulating gene activity related to embryonic development in goats. The oviduct, which provides nutrition and a location for early embryonic development, is directly involved in the reproductive process. Studies have shown that the expression of mRNAs and long non-coding RNAs (lncRNAs) in the oviduct is associated with prolificacy, indicating that nutritional factors may influence gene expression and, consequently, fertility outcomes in goats (Sun et al., 2022). Additionally, the expression of genes related to energy metabolism, such as those involved in glucolipid metabolism, suggests that nutritional status can impact gene activity and reproductive success.

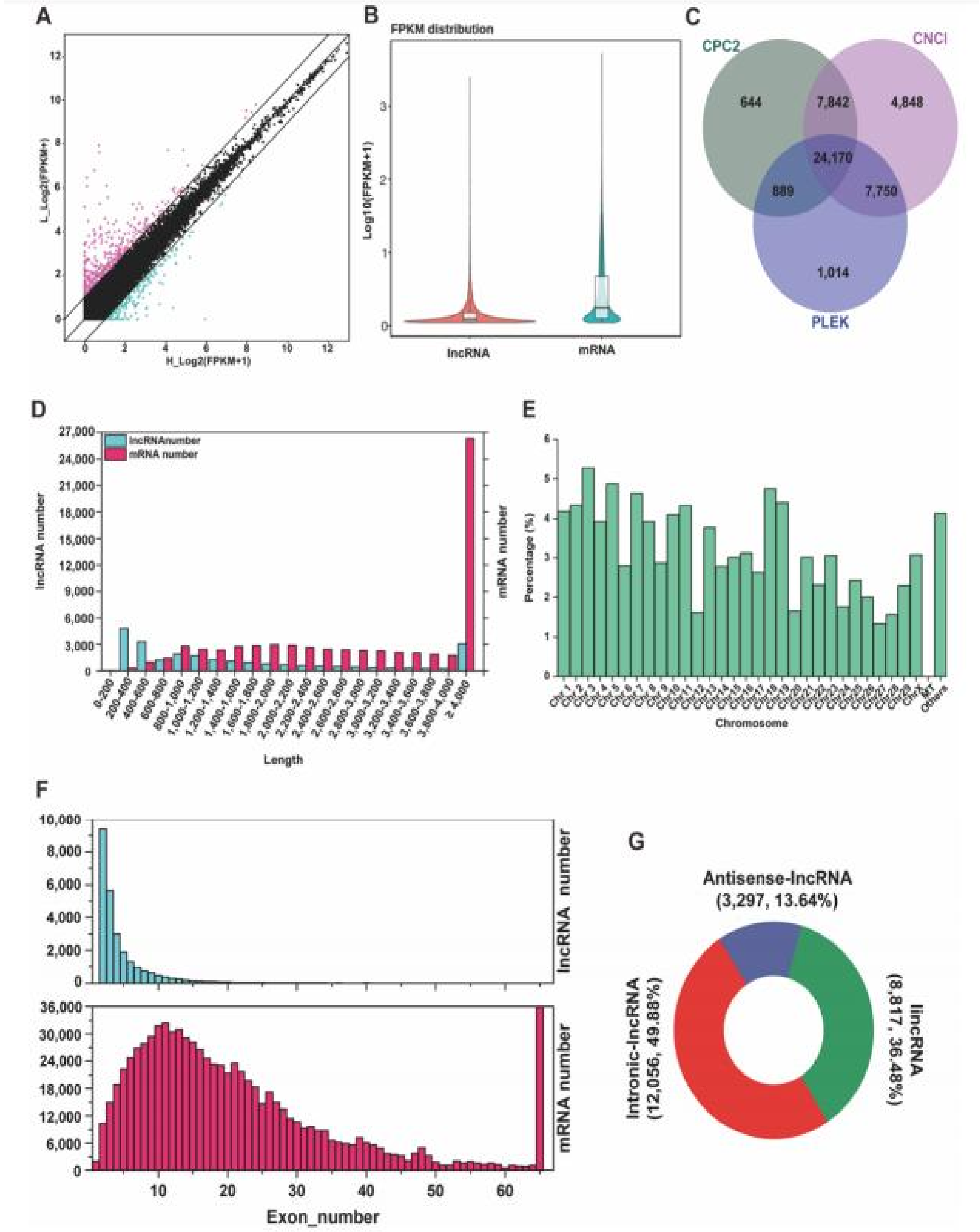

Figure 1 Expression profiles of lncRNA and mRNA in the oviduct (Adopted from Sun et al., 2022)

Image caption: (A) The scatter plot presents the mRNA expression variations between FL and FH groups. The values of the X and Y axes represent the normalized mRNA signal values (log, scaled), and the mRNAs above the top black line and below the bottom black line displayed greater than a two-fold change of up- and downregulation. (B) The expression level of lncRNA transcripts and mRNA transcripts. (C) Venn diagram showing the common and unique number of novel lncRNAs by CNCI, CPC2, and PLEK methods. (D) The length statistics of lncRNA and mRNA. (E) The distribution of lncRNAs in different chromosomes. (F) The statistics of lncRNA and mRNA exon number. (G) Classification of novel lncRNAs, including lincRNAs, intronic-lncRNAs, and antisense-lncRNAs (Adopted from Sun et al., 2022)

5.2 Impact of housing conditions on development

Housing conditions, particularly those affecting oxygen levels, can significantly impact embryonic development in goats. Research indicates that hypoxic environments are more suitable for the in vitro development of mammalian embryos, including goats. Under hypoxic conditions, differentially expressed genes (DEGs) related to biological processes and function regulation are observed, suggesting that housing conditions that mimic these environments could enhance embryonic development by modulating gene expression. The expression levels of zygotic genes and transcription factors are notably affected by oxidative stress, which is influenced by housing conditions, further highlighting the importance of environmental control in goat breeding (Wan et al., 2021; Yang et al., 2022).

5.3 Role of seasonal variations in fertility

Seasonal variations can influence fertility in goats by affecting gene expression related to reproductive processes. The hypothalamus, which coordinates the neuroendocrine system, plays a pivotal role in regulating reproductive hormones and processes. Seasonal changes can alter the expression of lncRNAs and mRNAs in the hypothalamus, impacting pathways such as the estrogen and oxytocin signaling pathways, which are crucial for ovarian development and hormone synthesis. These seasonal effects on gene expression can lead to variations in fertility rates, emphasizing the need to consider seasonal factors in goat breeding programs (Fernandes et al., 2018; Hou et al., 2023).

In summary, environmental factors such as nutrition, housing conditions, and seasonal variations significantly influence gene expression related to embryonic development and fertility in goats. Understanding these influences can help optimize breeding strategies and improve reproductive outcomes in high fertility goat breeds.

6 Case Study: Analysis of a Specific High Fertility Goat Breed

6.1 Selection criteria and overview of the breed

The Dazu black goat (DBG) was selected for this study due to its high fertility and adaptability, making it an ideal model for examining reproductive performance in goats. This breed is popular in southwest China and is known for its robust reproductive traits, which are crucial for understanding the genetic basis of fertility in goats (Zhao et al., 2023).

6.2 Detailed analysis of relevant genes

In the study of the Dazu black goat, transcriptome analysis identified several differentially expressed genes (DEGs) during embryo implantation. Key genes such as *CSF1, C1S, CST6, SLC24A4, HOXA10, HOXA11, MMP9*, and *ITGA11* were highlighted for their roles in processes like oxidative phosphorylation and immune response, which are critical during early pregnancy (Zhao et al., 2023). Additionally, the study of the Jintang black goat (JTG) revealed significant DEGs like SRD5A2, MSMB, STAR, and 3BHSD, which are associated with high fecundity and ovulation rate (Zi et al., 2018). The DNMT3B gene, with its 11-bp indel mutation, was also found to be significantly associated with litter size, indicating its potential as a marker for breeding high-fertility goats (Hui et al., 2020).

6.3 Implications for breeding strategies and genetic improvement

The identification of these genes provides valuable insights for breeding strategies aimed at enhancing fertility in goats. The DEGs and pathways identified, such as the Hippo signaling pathway and ECM-receptor interaction, offer targets for genetic improvement programs (Guo et al., 2024). Marker-assisted selection (MAS) using genes like DNMT3B could be employed to select for goats with higher litter sizes, thereby improving breeding efficiency and economic returns (Hui et al., 2020). Furthermore, understanding the role of miRNAs, such as miR-21-5p, in follicular development can aid in developing strategies to enhance ovulation rates in prolific breeds like the Jintang black goat (Zi et al., 2017).

In summary, the analysis of high fertility goat breeds like the Dazu black goat provides critical insights into the genetic mechanisms underlying reproductive performance. These findings can inform breeding strategies and genetic improvement efforts to enhance fertility traits in goats.

7 Implications for Goat Breeding Practices

7.1 Strategies for enhancing fertility through genetics

To enhance fertility in goat breeds, a focus on genetic markers and pathways associated with reproductive traits is essential. Studies have identified several genes and pathways that play crucial roles in fertility. For instance, the *DNMT3B* gene has been linked to litter size, with specific indel mutations associated with higher fertility rates in goats (Hui et al., 2020). Additionally, the identification of differentially expressed genes (DEGs) and pathways such as the *AMPK*, *PI3K-Akt*, and *ECM*-receptor interaction pathways can provide targets for genetic selection aimed at improving fertility (Figure 2) (Sun et al., 2022; Ghafouri et al., 2023). By selecting for these genetic markers, breeders can potentially increase the reproductive success of their herds.

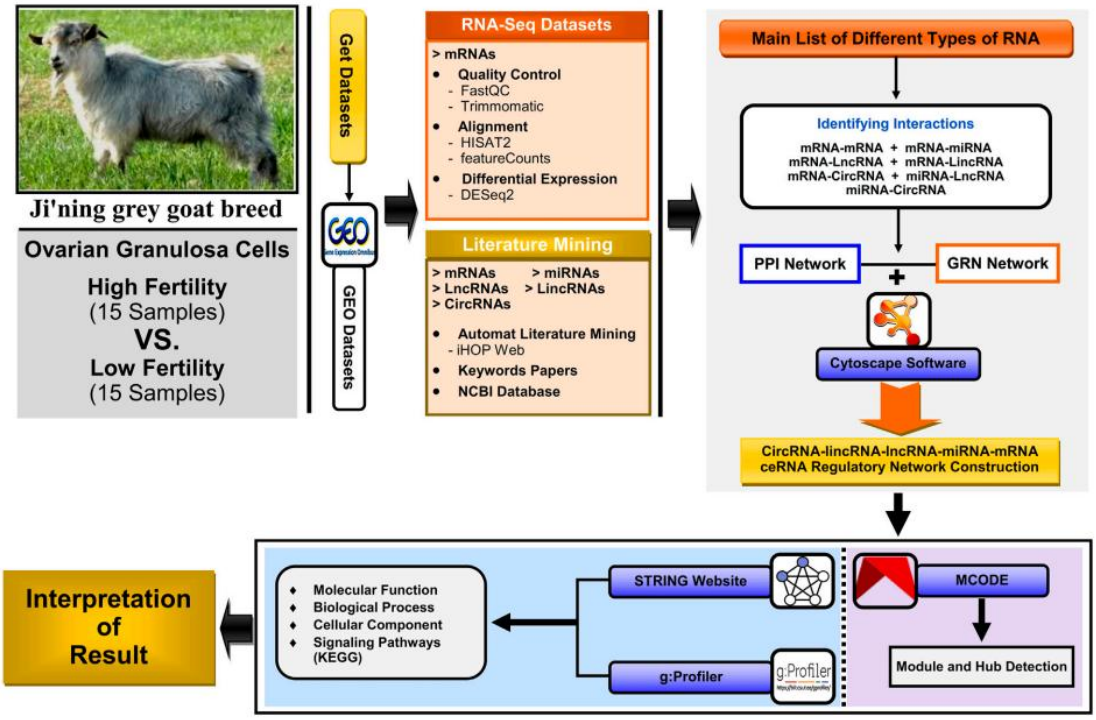

Figure 2 Workflow for analyzing the scRNA-seq dataset, literature mining, protein–protein interaction (PPI) network, gene regulatory network (GRN), and downstream ontology functions (Adopted from Ghafouri et al., 2023)

Image caption: Constructing the circRNA-incRNA-lncRNA-miRNA-mRNA ceRNA regulatory network; module analyses were constructed and visualized using Cytoscape software v3.9.1 (Adopted from Ghafouri et al., 2023)

7.2 Integration of genetic findings into breeding programs

Integrating genetic findings into breeding programs involves using marker-assisted selection (MAS) to identify and propagate desirable traits. The use of genetic parameters and selection indices, as demonstrated in Spanish goat breeds, can optimize genetic responses for fertility traits. By incorporating genetic markers such as those identified in the *DNMT3B* gene and other fertility-related genes, breeding programs can be tailored to enhance reproductive performance. This approach not only improves fertility but also ensures the sustainability and profitability of goat farming operations (Hui et al., 2020; Ziadi et al., 2021).

7.3 Long-term benefits for livestock production

The long-term benefits of integrating genetic insights into goat breeding practices are substantial. Enhanced fertility leads to increased kidding rates, which can improve the overall productivity and economic viability of goat farming. Moreover, understanding the genetic basis of fertility allows for more precise and efficient breeding strategies, reducing the time and resources needed to achieve desired traits (Sun et al., 2022; Ghafouri et al., 2023; Zhao et al., 2023). This genetic approach also contributes to the conservation of high-fertility breeds, ensuring their continued contribution to livestock production and genetic diversity. By focusing on genetic improvements, the goat industry can achieve sustainable growth and meet the increasing demand for goat products.

8 Future Research Directions

8.1 Exploration of additional embryonic development genes

Future research should focus on identifying and characterizing additional genes involved in embryonic development in high fertility goat breeds. Current studies have highlighted several candidate genes, such as *CSF1, C1S, CST6, SLC24A4, HOXA10, HOXA11, MMP9,* and *ITGA11*, which are associated with embryo implantation in goats (Zhao et al., 2023). Expanding this research to include a broader range of genes could provide deeper insights into the molecular mechanisms that underpin high fertility in goats.

8.2 Expansion to other livestock species

The methodologies and findings from studies on high fertility goat breeds can be extended to other livestock species to enhance reproductive performance across the board. For instance, the comparative analysis of ovarian transcriptomes and the identification of differentially expressed genes in goats can serve as a model for similar studies in other species (Zi et al., 2018). This cross-species research could lead to the discovery of universal genetic markers for fertility, thereby improving breeding strategies in various livestock.

8.3 Development of advanced breeding technologies

The integration of genomic and transcriptomic data can lead to the development of advanced breeding technologies, such as marker-assisted selection (MAS) and genomic selection. For example, the identification of specific genetic variants, like the 11-bp indel in the *DNMT3B* gene associated with litter size, can be utilized in breeding programs to select for high fertility traits (Hui et al., 2020). Additionally, constructing comprehensive ceRNA networks and understanding the interactions between different types of RNAs can further refine these technologies, offering more precise and efficient breeding strategies (Ghafouri et al., 2023).

In summary, future research should aim to explore additional embryonic development genes, expand findings to other livestock species, and develop advanced breeding technologies to enhance fertility in goats and potentially other livestock. These efforts will contribute to more efficient and productive breeding programs, ultimately benefiting agricultural practices and economic returns.

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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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