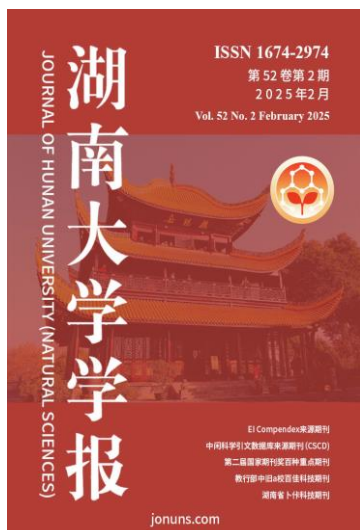




Journal of Hunan University (Natural Sciences)

Vol. 52 No. 2
February 2025

Available online at
<https://jonuns.com>



ELSEVIER
Scopus



Clarivate
WEB OF SCIENCE

Open Access Article

 <https://doi.org/10.55463/issn.1674-2974.52.2.6>

Genetic Influences on Reproductive Traits in Goats of Malaysia: A Review

Armiyas Shibesh Faris¹, Candyline Su Chui Len¹, Mohammad Mijanur Rahman¹, Mohamad Zaihan Bin Zailan¹, Juplikely James Silip¹, Subir Sarker², Md. Safiul Alam Bhuiyan^{1*}

¹Faculty of Sustainable Agriculture, University Malaysia Sabah, Sandakan, Sabah, Malaysia

²Biomedical Sciences & Molecular Biology, College of Public Health, Medical and Veterinary Sciences, James Cook University, Townsville, QLD 4811, Australia

* Corresponding author: md.safiul@ums.edu.my

Article History:

Received: February 3, 2025

Reviewed: February 24, 2025

Revised: March 2, 2025

Accepted: March 11, 2025

Published: March 31, 2025

Abstract: This review investigates the genetic influences on key reproductive traits in Malaysian goats, which are crucial for improving meat production and economic value. Traits such as litter size, kidding interval, age at first service, and gestation length show varying heritability, indicating limited potential for selection improvement in some cases. Significant major genetic markers, including DNAH1, GDF9, BMP15, and BMPRI1B, have been linked to reproductive performance, particularly litter size and fertility. The high levels of inbreeding observed in Malaysian goats could negatively impact these reproductive traits, further complicating traditional selection methods. Seasonal breeding patterns and environmental factors, such as melatonin secretion, significantly impact reproductive outcomes, highlighting the importance of effective herd management. Variability in reproductive traits among breeds like Shaanbei white cashmere goats, Chinese native breeds, and Alpine versus Saanen bucks is noted, with generally low heritability estimates for traits like litter size and age at first kidding. Advanced reproductive technologies, including marker-assisted selection, multiple ovulations, and genomic selection, offer the potential for accelerating genetic gain,



Copyright: © 2025 by the Authors; Journal of Hunan University Natural Sciences.

This is an open-access article distributed under the terms and conditions of the Creative Commons Attribution License (<https://creativecommons.org/licenses/by-nc-sa/4.0/>)

particularly in addressing the challenges posed by inbreeding. Integrating genetic and environmental factors into breeding programs can enhance reproductive efficiency and overall productivity. This study provides a framework for targeted breeding strategies to improve the reproductive performance of goats in Malaysia.

Keywords: Genetic marker, goat, heritability, litter size, reproductive trait.

马来西亚山羊生殖特性的遗传影响：综述

摘要：本综述探讨了遗传因素对马来西亚山羊关键生殖性状的影响，这些性状对于提高肉类产量和经济价值至关重要。产仔数、产羔间隔、首次配种年龄和妊娠期长度等性状表现出不同的遗传性，表明在某些情况下选择改进的潜力有限。重要的主要遗传标记，包括 DNAH1、GDF9、BMP15 和 BMPR1B，与生殖性能有关，特别是产仔数和生育力。马来西亚山羊的近亲繁殖程度高，可能会对这些生殖性状产生负面影响，使传统的选择方法更加复杂。季节性繁殖模式和褪黑激素分泌等环境因素对生殖结果有显著影响，凸显了有效畜群管理的重要性。陕北白绒山羊、中国本土品种、阿尔卑斯山羊和萨能公羊等品种的生殖性状存在差异，产仔数和首次配种年龄等性状的遗传性估计值通常较低。先进的生殖技术，包括标记辅助选择、多次排卵和基因组选择，提供了加速遗传增益的潜力，特别是在应对近亲繁殖带来的挑战方面。将遗传和环境因素整合到育种计划中可以提高生殖效率和整体生产力。这项研究为有针对性的育种策略提供了一个框架，以提高马来西亚山羊的生殖性能。

关键词：遗传标记，山羊，遗传力，产羔数，繁殖性状

1. Introduction

Goats (*Capra hircus*) are one of the earliest domesticated livestock species, with a significant economic role in milk, meat, and fiber production, and they exhibit remarkable adaptability to diverse environmental conditions across all continents [1], [2]. Goats play a multifaceted role in the livestock industry, significantly contributing to the economic and nutritional aspects. They are particularly valued for their adaptability to harsh environmental conditions, making them ideal for landless and marginal farmers. Goats are a major source of milk and meat, with their milk being especially noted for its high calcium, magnesium, and phosphorus content and bioactive compounds that offer various health benefits, including cardiovascular, metabolic, and immunomodulatory properties. Furthermore, goats contribute significantly to the rural economy and well-being by providing a reliable source of high-quality proteins and other essential nutrients, which are particularly beneficial for children, older adults, and individuals recovering from illness [3].

There are approximately one billion goats globally, with the population having more than doubled in the past 40 years. The Food and Agriculture Organization states that over 90% of goats are located in developing countries, with Asia hosting the largest share of the

world’s goat population, followed by Africa [4]. The contribution of goats to global milk production is significant and growing. Goats are versatile livestock, well-adapted to diverse environmental conditions, and are particularly valuable in regions where other dairy animals may not thrive. According to [5], dairy products from sheep and goats make up approximately 20.8% of the world’s dairy production. Specifically, goats alone contribute roughly 1.9% of the total milk production globally. Many people, including infants, have allergic reactions to cow’s milk but tolerate goat and sheep milk and their dairy products well. Consequently, goat and sheep milk offer significant medical benefits for those with cow’s milk allergies [5].

Goats play an important role in Malaysia’s agricultural and economic landscape, serving as a source of income and contributing to the livestock sector. The importance of goats in Malaysia can be understood through several dimensions, including economic, health, and environmental aspects. Economically, goats are a vital part of Malaysia’s livestock sector, which is experiencing increasing demand due to population and economic growth. The sector is dominated by poultry, swine, non-dairy cattle, and goats, with goats contributing to the diversity of livestock products available in the market [6].

2. Literature Review

2.1 Reproductive Traits and Challenges of Goat Production

Reproductive traits in the goat production sector play a vital role in the meat production industry, with genetic analysis being crucial for enhancing their potential. Studies have shown that reproductive traits like age at first service, age at first kidding, gestation length, and litter weight exhibit varying heritability estimates, indicating a limited scope for selection for further improvement and successful genetic gain [7]. In addition, research has explored the association between specific gene polymorphisms and reproductive traits in goats, suggesting potential candidate markers for genetic selection [8].

Following the health problem, reproductive performance is another critical aspect of goat farming in Malaysia. Studies have shown that controlled internal drug release (CIDR) devices can enhance reproductive outcomes, such as estrus synchronization and increased twin rates, particularly in Boer goats. This improvement in reproductive performance can lead to higher productivity and better herd management [9].

Seasonal breeding patterns in goats, influenced by factors like melatonin secretion and environmental conditions, impact the availability of goat products in the market, emphasizing the need for effective reproductive herd management strategies [10]. Furthermore, non-genetic factors such as production systems and breed significantly affect reproductive and litter traits in goats, highlighting the importance of considering both genetic and environmental factors for successful breeding programs [11]. Lastly, environmental factors like aridity and management practices have been shown to influence the reproductive performance of local goat populations, indicating the potential for implementing selection programs to improve fertility traits in these breeds [12]. Reproductive traits in small ruminants play a vital role in determining the genetic potential and economic value of goats.

Key reproductive traits in goats include litter size, kidding interval, age at first kidding, gestation length, age at first service, and prolificacy. Studies on various goat populations such as Dazu Black Goats [13], Alpine x Beetal goats [7], Tunisian local goat population [12], and general goat farming practices [14] emphasize the significance of these traits for genetic improvement and efficient production. Factors influencing reproductive traits include genetic components, environmental conditions, nutritional status, and management practices. Heritability estimates for traits like litter size and kidding interval vary across populations, indicating the need for extensive data for accurate selection and genetic improvement. Understanding and enhancing these key reproductive traits are crucial for maximizing

productivity and profitability in goat farming [15].

2.2 Variation in Reproductive Traits among Different Goat Breeds

Reproductive traits in goats exhibit variability among different breeds. Studies have shown that genetic factors play a significant role in determining reproductive performance. A recent study showed that the DNAH1 gene variation was associated with litter size in Shaanbei white cashmere goats, with specific genotypes being associated with larger litters [16]. In a genome-wide association study conducted on native Chinese goat breeds, significant SNPs were linked to litter size and various morphological traits, which support the finding that genetics contributes to reproductive characteristics [17], [18].

Additionally, RNA sequencing analysis of the goat hypothalamus revealed differentially expressed genes and microRNAs influencing fertility, shedding light on the molecular mechanisms underlying litter size variations in different goat populations [19]. Furthermore, research on semen quality indicated breed-specific differences, with Alpine bucks generally exhibiting higher sperm quality compared to Saanen bucks, emphasizing the impact of breed on reproductive traits [20].

2.3 Role of Reproductive Traits in Goat Breeding Programs

Reproductive traits are crucial in goat breeding programs as they directly impact the efficiency and economic viability of dairy and meat production. Key reproductive traits include age at first kidding, out-of-season kidding ability, pseudopregnancy, and litter size. Age at first kidding is significant as a reduced and can accelerate genetic improvement and reduce the resources needed to raise animals to produce age [21]. Out-of-season kidding ability is essential for achieving consistent year-round dairy production, which is challenging due to the seasonal breeding nature of goats [22]. Pseudopregnancy can delay the breeding and lactation cycles, affecting the overall productivity [23].

Litter size, influenced by genetic factors, is another critical trait, with specific SNPs identified that affect this trait in various goat breeds [17]. The fertility of goats, influenced by semen quality and female characteristics, is also a vital aspect, with studies showing that younger, primiparous goats have higher fertility rates [24]. Reproductive disorders can significantly reduce milk yield, especially in primiparous goats carrying multiple fetuses [25]. Hormonal profiles, such as the LH peak, are also important because they can affect the success of artificial insemination programs [26]. Photo-stimulation of bucks to induce sexual activity can enhance reproductive performance in does, particularly during the anestrus period, thereby improving productivity

and lifetime reproductive performance [27], [28].

Nutritional management, which is closely linked to reproductive health, is another critical factor, as high-yielding goats require nutrient-dense diets to support their reproductive and overall health [22]. Understanding the genetic and endocrine factors influencing puberty and reproductive traits can further enhance breeding programs by selecting traits that improve fertility and productivity. Overall, incorporating these reproductive traits into breeding programs can lead to more efficient and sustainable goat production systems.

2.4 Optimizing Reproductive Traits in Goat Breeding Programs

The reproductive traits in goat breeding programs can be optimized through various strategies. Genetic correlations between reproductive traits and production traits play an important role in selection for successful selection response and genetic gain [21]. The use of female reproductive technologies such as multiple ovulation and embryo transfer and marker-assisted genomic selection (GS) in reproductive systems can lead to accelerated genetic gains through selection intensification and a decrease in the generation intervals for ovulation [29]. Including genomic information in breeding programs can significantly enhance genetic gain, especially in dairy sheep and goat breeding programs, leading to a substantial increase in annual genetic gain when compared to traditional selection methods [30].

Additionally, exposure of does to photostimulated bucks during anestrus can improve reproductive performance, fertility, and productivity, contributing to increased lifetime reproductive performance in goats [25]. Fixing-time artificial insemination programs in goat breeds like the Payoya can also be enhanced with an understanding of periovulatory hormone release patterns and optimizing treatments based on hormone profiles [24].

2.5 Genetic Factors Influencing Reproductive Traits

The genetic factors influencing reproductive traits in goats have been extensively studied. Research has identified significant single nucleotide polymorphisms (SNPs) and genes associated with reproduction traits like litter size, wattle, coat color, black dorsal line, beard length, and hind leg hair in Chinese native goat breeds [16]. Additionally, DNAH1 mutations and copy number variations have been linked to litter size in Shaanbei white cashmere goats, with specific genotypes showing higher litter sizes [8]. Studies on age at puberty have revealed differential gene expression in pubertal goats, indicating the involvement of genes like PRLR and THBS1 in follicular development and lateralization [28].

Furthermore, genetic correlations have been found between reproductive traits like age at first kidding, pseudopregnancy, and milk production traits in UK dairy goats, suggesting the feasibility of selecting for reproductive traits without compromising milk yield [21]. Selective sweep analyses in Laoshan dairy goats have highlighted genes like CCNB2, AR, and ADCY1 associated with high fecundity, providing insights into the genetic variations influencing fecundity traits in dairy goats [31].

2.6 Genetic Markers and Their Roles in Goat Litter Size

The identification of genetic markers associated with goat litter size has been a focal point of recent research, revealing several key genes and their polymorphisms. Notably, the growth differentiation factor 9 (GDF9), bone morphogenetic protein 15 (BMP15), and bone morphogenetic protein receptor type IB (BMPRI1B) genes have been identified as significant markers influencing litter size in Indonesian goats, with single nucleotide polymorphisms (SNPs) in these genes aiding in the selection of favorable genotypes [32]. In Markhoz goats, a genome-wide association study (GWAS) identified SNPs on chromosomes 2, 20, and 21, with genes such as GABRA5 and AKAP13 playing roles in reproductive processes [33].

The Dynein Axonemal Heavy Chain 1 (DNAH1) gene, with its SNPs, insertion/deletion (InDel) mutations, and copy number variations (CNVs), has also been linked to higher litter sizes in Shaanbei white cashmere goats [16]. Additionally, polymorphisms in the PPP2R5C and SLC39A5 genes were found to be significantly associated with litter size in Yunshang black goats, with higher gene expression correlated with increased litter size [34]. The SNX29 gene, which is involved in lipid metabolism, showed significant associations with litter size through its InDel and CNV polymorphisms in Shaanbei white cashmere goats [34]. The IGF2BP2 gene, which is crucial for germ cell development, also demonstrated significant associations with litter size through specific InDel mutations [35].

Furthermore, the Booroola fecundity (FecB) gene, known for its role in sheep fertility, has been linked to litter size and morphometric traits in goats, suggesting its utility in breeding programs [36]. The GDF9 gene, with its various SNPs, has been consistently associated with litter size across multiple goat breeds, highlighting its importance as a high-fertility candidate gene [37]. Studies in sheep have also identified genes such as BMPRI1B, GDF9, and BMP15 as significant markers for litter size, which may provide insights applicable to goats [38], [39]. These findings collectively underscore the potential of using these genetic markers in marker-assisted selection to enhance the reproductive traits of goats.

2.7 Heritability Estimates of the Reproductive Traits

Heritability estimates for reproductive traits in goats vary across different studies and breeds, reflecting the complexity and genetic diversity of these traits. For instance, in UK dairy goats, heritability estimates for reproductive traits such as out-of-season kidding ability, age at first kidding, and pseudopregnancy were found to be low, ranging from 0.08 to 0.11 [21]. Similarly, in Creole goats, heritability estimates for fertility and litter size were also low, at 0.11 and 0.11, respectively [40].

In the Murciano-Granadina breed, heritability for traits like peak yield and persistency were estimated to be 0.13 and 0.08, respectively, indicating a low to moderate genetic influence [41]. For the Damascus breed, heritability estimates for litter size and litter weight were around zero, whereas those for milk production traits were higher, suggesting a stronger genetic component for milk yield than for reproductive traits [42]. In Zaraibi goats, heritability for litter size was very low, at 0.04-0.05, but the genetic correlation between milk yield and litter size was positive, indicating that selection for milk yield could indirectly improve reproductive performance [43].

Additionally, studies on Jamunapari goats showed that maternal heritability for body weight declined from 0.19 at birth to near zero at weaning, highlighting the diminishing maternal genetic influence as the goats' age [44]. Overall, these findings suggest that while heritability estimates for reproductive traits in goats are generally low, there is still potential for genetic improvement through selective breeding, particularly when considering the genetic correlations with other traits such as milk yield and body weight.

2.8 Heritability differences among various goat breeds

Heritability estimates for various traits in goats show differences among different breeds. Studies have indicated that the heritability of linear body measurements in Jamunapari goats ranged from 0.14 to 0.20, suggesting significant genetic variability for selection [40]. In contrast, a study on Alpine and Saanen dairy goats reported low heritabilities for fecal egg counts (FEC) at 0.07 and moderate heritabilities for FAMACHA® eye score and packed cell volume (PCV) at 0.22 each, with unfavorable genetic correlations between FEC and milk yield [45]. Therefore, these differences could play a significant role in affecting the reproductive performance of these goats accordingly.

Likewise, genetic diversity assessments among Brazilian and U.S. goat breeds using microsatellite markers showed expected heterozygosity ranging from 0.55 to 0.72, indicating ample genetic diversity among the evaluated breeds [46]. These findings collectively highlight the variability in heritability estimates across different goat breeds for various traits.

2.9 Influence of Specific Genes on Fertility, Litter Size, and Reproductive Health

The influence of specific genes on fertility, litter size, and reproductive health is multifaceted, involving numerous genetic factors across various species. In humans, genetic studies have identified mutations in genes that regulate reproductive lifespan and fertility, with genome-wide association studies (GWAS) revealing shared biological pathways linking puberty timing, fertility, and reproductive aging [47]. In swine, genes such as P2RX3, NR2F2, OAS1, and PTPN11 have been associated with age at puberty and reproductive longevity, with specific SNPs showing significant correlations with these traits [48]. Similarly, in sheep, genes like ACTL7A, ACTL7B, and ELP1 are linked to litter size, while others like HECW1 and HTR1E are related to the total number of lambs born [39].

In mice, selection for increased litter size has led to the differential expression of genes associated with steroid metabolism and female fecundity, such as GDF9, indicating a genetic basis for reproductive performance [49]. In pigs, regions of the genome affected by selection for litter size traits include the candidate gene P2X3R, which plays a role in implantation and hormone release [50]. In addition, a nonsense mutation in BMP15 has been linked to atypical external genitalia and fertility issues in German Landrace gilts, demonstrating the impact of deleterious mutations on reproductive health [51].

In sheep from Xinjiang, genes like FSHR, GUCY1A1, and COIL have been identified as significantly associated with litter size, providing potential molecular markers for breeding programs [52]. In rabbits, genomic regions on chromosome 17, including genes like BMP4 and PTGER2, have been associated with litter size traits, highlighting the importance of specific genomic regions in reproductive success [53]. Lastly, the OVGP1 gene in rabbits has been linked to improved fertilization and early embryo development, with specific haplotypes positively affecting litter size and embryo survival [54]. These findings collectively underscore the critical role of specific genes in influencing fertility, litter size, and overall reproductive health across different species.

2.10 Molecular and Genomic Approaches in Goat Reproductive Genetics

Molecular and genomic approaches have significantly advanced our understanding of goat reproductive genetics, revealing key genetic markers and mechanisms. Genome-wide association studies (GWAS) have identified significant single nucleotide polymorphisms (SNPs) and candidate genes associated with reproductive traits such as litter size and morphological traits in various goat breeds [17]. For instance, the DNAH1 gene, with its SNPs,

insertion/deletion mutations, and copy number variations, has been linked to higher litter sizes in Shaanbei white cashmere goats [16]. Comparative genomics has also highlighted genes related to adaptation and milk production, such as HSPB6 and ABCG2, which are crucial for breeding programs aimed at enhancing productivity and environmental adaptability [55].

In Boer goats, selection signatures have pinpointed genes like BMP1B and KIT, which are involved in reproduction and growth, underscoring the impact of artificial selection on genetic diversity [56]. In addition, the role of circular RNAs (circRNAs) in the oviduct during different estrus phases has been explored, identifying key regulatory networks that influence prolificacy traits [57]. The development of high-quality reference genomes, such as Saanen_v1, has improved the accuracy of genetic mapping and the identification of SNPs, facilitating more precise breeding strategies [58].

Long non-coding RNAs (lncRNAs) have also been implicated in ovarian function, with specific lncRNAs associated with progesterone synthesis and oocyte maturation during different estrus phases [59]. Genomic selection methods, including GBLUP and Bayesian approaches, have been optimized for traits like live body weight and fiber diameter, enhancing the accuracy of genomic estimated breeding values (GEBVs) [60]. Furthermore, structural variants on chromosome 1 have been linked to the polled phenotype and polled intersex syndrome (PIS) in goats, providing diagnostic tools for the early prediction of horn status [61]. Finally, studies on local goat populations, such as the Mascaruna in Italy, emphasize the importance of genetic diversity and population structure analyses for conservation and breeding programs [62]. These molecular and genomic approaches collectively contribute to a deeper understanding and improved management of goat reproductive genetics.

3. Techniques for Studying Goat Genetics

Various techniques are employed to study goat genetics related to litter size. Genome-wide association Studies (GWAS) are utilized to identify genetic regions associated with litter size, as seen in the research on Markhoz goats [32]. Moreover, Marker-Assisted Selection (MAS) is applied to utilize genetic markers like GATA4 gene polymorphisms to improve litter size in goats, as demonstrated in Shaanbei white cashmere goats (Wang et al. 2023). Additionally, studies on genes like GDF9 and BMP15 have shown the significance of Single Nucleotide Polymorphisms (SNPs) in enhancing fertility traits and litter size in goats, emphasizing the importance of genetic markers in selection processes [33], [63], [64]. These techniques collectively contribute to advancing goat genetics research to improve litter size

through targeted breeding strategies.

4. Results

4.1 Impact of Genomic Tools on Goat Litter Size

Genomic tools have significantly impacted goat breeding for litter size by identifying key genetic markers associated with reproductive traits. Studies have revealed the importance of various genes such as KITLG, KISS1, SNX29, DNAH1, and BMP15 in influencing litter size in different goat breeds [16], [34], [64], [65], [66]. These genes exhibit polymorphisms, insertions/deletions, and copy number variations that are linked to variations in litter size. For instance, SNX29 and DNAH1 gene variations were significantly associated with litter size, indicating their potential as molecular markers for selecting goats with improved reproductive traits. Along with this, the meta-analysis on the BMP15 gene highlighted the impact of specific polymorphisms on litter size, emphasizing the role of genetic markers in enhancing goat breeding programs focused on improving litter size through marker-assisted selection (MAS).

The Indigenous Katjang goat, the only domestic breed in Malaysia, faces the threat of extinction due to low genetic diversity, high inbreeding coefficients, and deviations from Hardy-Weinberg equilibrium, indicating a historical population bottleneck, highlighting the imperative to enhance its genetic pool to safeguard and rejuvenate this breed [67]. Therefore, identifying key genetic markers such as GDF9, BMP15, and Kiss1, which are linked to litter size, is crucial. Harnessing these markers can significantly improve the reproductive performance and breeding gains, ensuring the sustainability and genetic vitality of the Katjang goat and its crossbreeds in Malaysia.

In Malaysia, studies have shown that the goat farm system did not show a significant effect on reproductive performance [68]. On the other hand, the reproduction improvement measure (controlled internal drug release-CIDR) showed a significant effect on reproductive performance, accelerated estrus cycle, and increased twinning rate; therefore, Boer and its strain might help to improve herd production efficiency and overcome the gaps in the self-sufficiency ratio of Mutton demand in the country [9].

The genetic characterization of Malaysian goat breeds, particularly the indigenous Katjang goat, has been extensively studied using microsatellite markers. These studies reveal significant insights into the genetic diversity and structure of these breeds, which are crucial for conservation and breeding strategies. The findings highlight both the genetic markers identified and the challenges these breeds face regarding genetic diversity and inbreeding.

4.2 Genetic Markers and Diversity in Malaysia

Several studies have used microsatellite markers to assess the genetic diversity of Malaysian goat breeds. In the Katjang goat, 25 polymorphic microsatellite markers were identified, indicating low genetic diversity with an observed heterozygosity of 0.29 and an expected heterozygosity of 0.72 [67]. Similarly, 30 microsatellite markers were used to study the Katjang, Jamnapari, Boer, and Savanna breeds, revealing low allelic variation and observed heterozygosity values lower than expected across all breeds [69], [70], [71].

4.2.1 Inbreeding and Genetic Differentiation

The inbreeding coefficient (FIS) was notably high in the Katjang goat at 0.46, indicating significant inbreeding [67]. Across all breeds, the FIS was 0.43, suggesting that inbreeding is a common issue. The FST value of 0.06 indicated a lack of genetic differentiation among the breeds, with genetic identities ranging from 80% to 87% [69].

4.2.2 Conservation and Breeding Implications

•**Conservation Needs:** The Katjang goat, which is at risk of extinction, requires urgent conservation efforts. The low genetic diversity and high inbreeding levels necessitate strategies to maintain genetic variability and prevent further loss of genetic resources [67], [70].

•**Breeding Strategies:** For effective breeding programs, understanding the genetic background of these breeds is essential. The use of microsatellite markers provides a foundation for selecting individuals that can enhance genetic diversity and improve breed characteristics [69], [70].

While the focus has been on microsatellite markers, there is a need to explore other genetic markers such as SNPs for a more comprehensive understanding of genetic diversity. In addition, genome mapping using advanced genotyping platforms could offer better insights and solutions for the conservation and improvement of Malaysian goat breeds [69].

4.3 Interaction between Goat Genetics and Environmental Factors that Affect Reproductive Performance

A complex interplay between genetic and environmental factors influences the reproductive performance of goats. Genetic selection has significantly improved production traits, but it has also highlighted the need to enhance resilience to environmental stressors to maintain high performance across varying conditions [72]. Environmental factors such as temperature, humidity, and photoperiod play crucial roles in reproductive cycles, with heat stress negatively impacting semen quality and fertility [73], [74]. Additionally, environmental pollutants and climate

change can alter gamete environments, affecting fertilization outcomes and offspring fitness [75].

The 2003 European heat wave exemplifies how extreme weather can drastically reduce artificial insemination success in dairy goats [76]. Furthermore, reproductive toxicants and nutritional deficiencies can disrupt the hypothalamic-pituitary-gonadal axis, affecting fetal development and adult reproductive function [27], [77]. Genetic polymorphisms also modulate susceptibility to environmental influences, with certain gene-environment interactions affecting prenatal development and reproductive health [78].

The presence of genotype-by-environment ($G \times E$) interactions necessitates careful consideration in breeding programs to accurately estimate genetic correlations and optimize reproductive performance under different environmental conditions [79]. Long-term studies have shown that reproductive costs, such as reduced future reproduction and offspring survival, are influenced by both intrinsic factors like age and parity and extrinsic factors like population density and severe winters [80]. Therefore, a comprehensive understanding of these interactions is essential for developing sustainable breeding techniques that stabilize production and enhance reproductive success in goats across diverse environments.

5. Discussion

5.1 Future Directions and Applications in Goat Breeding

5.1.1 Prospects for Genetic Engineering and Biotechnology for Livestock Breeding

The prospects for genetic engineering and biotechnology in livestock breeding are highly promising, driven by advancements in genome editing technologies such as CRISPR-Cas9, which offer precise and efficient modifications of animal genomes. These technologies have enabled significant improvements in economically important traits such as growth, disease resistance, and product quality. For instance, gene editing has been used to create pigs resistant to porcine reproductive and respiratory syndrome (PRRS) and cattle resistant to tuberculosis by targeting specific genes like CD163 and NRAMP1, respectively [81].

Additionally, the CRISPR-Cas9 system has facilitated the knockout of genes related to lipid deposition and muscle growth in chickens, enhancing their economic traits [82]. The integration of gene editing with traditional breeding programs can accelerate genetic progress by introducing beneficial alleles and eliminating undesirable ones, thus improving overall productivity and sustainability [83], [84]. Moreover, the combination of genome editing with somatic cell nuclear transfer (SCNT) has revolutionized livestock transgenesis, allowing for precise genetic modifications and reducing the risk of genetic

mosaicism [85]. Despite these advancements, challenges remain, particularly in editing polygenic traits and navigating regulatory landscapes, which vary globally and can impact the deployment of these technologies [86], [87]. Nonetheless, the potential for gene-edited livestock to meet the increasing global demand for food, adapt to climate change, and improve animal welfare is substantial [88], [89].

The development of gene-edited ruminants and other livestock species continues to progress, with applications extending to both agricultural and biomedical fields [90]. As regulatory frameworks evolve and public acceptance grows, the commercialization and global valorization of gene-edited livestock are likely to expand, contributing to a more resilient and sustainable agri-food system.

5.2. Ethical Considerations in Genetic Manipulation

Ethical considerations in genetic manipulation, particularly human germline genome editing (HGGE), encompass a broad spectrum of pragmatic, sociopolitical, and categorical arguments. The advent of precise tools like CRISPR/Cas9 has heightened the urgency of these discussions due to their potential societal impacts and applications in both somatic and heritable genome editing [91].

The National Academies of Sciences and Medicine advocate for research in preconception heritable human genome editing (HHGE) to address monogenic disorders, yet they emphasize the need to consider alternative technologies like fetal gene therapy (FGT), which is less ethically contentious and better researched [92].

Current laws often impose broad prohibitions on germline modifications, which may inadvertently restrict beneficial medical interventions, suggesting a need for more nuanced regulatory frameworks [93]. Ethical debates have been intensified by the first clinical applications of HGGE, which shocked the scientific community and highlighted issues of just distribution, national interest, societal consensus, and scientific trustworthiness [94]. The potential benefits of preventing genetic conditions must be weighed against the risks, including the ethical implications of intergenerational monitoring and the long-term effects on future generations [95].

Community engagement and consent are crucial, as the development and deployment of gene-drive technologies must consider the perspectives of local stakeholders to address concerns of marginalization and inequity [96]. Historical controversies in genetic research, such as those involving recombinant DNA and human cloning, provide valuable lessons for current debates on germline editing [97].

The tension between reactionary and precautionary policies underscores the need for a balanced approach

that prioritizes basic and preclinical research while cautiously advancing clinical applications [98]. Overall, the ethical landscape of genetic manipulation is complex and requires careful consideration of both the potential benefits and the profound societal and moral implications [99].

5.3 Potential for Sustainable and Productive Goat Breeding Programs

Sustainable and productive goat breeding programs hold significant potential, particularly when they are community-based and tailored to local conditions.

Community-based breeding programs (CBBPs) have shown promise in Malawi, Uganda, and Ethiopia by focusing on indigenous breeds and involving farmers in the decision-making process, which enhances genetic improvement and sustainability [26], [100]. These programs empower smallholders through capacity building in pasture production and the conservation of feed resources, leading to improved animal performance and economic benefits [101]. In Senegal, similar initiatives have improved goat-rearing systems by integrating local agricultural resources and strengthening breeding techniques, which are crucial for the sustainable development of family goat farming [102].

The role of women in goat rearing is also vital, as seen in rural areas where they promote economic autonomy and food security, although there is a need for better breed characterization and market linkages [103]. Technological advancements, such as precision livestock farming and genomic tools, can further enhance productivity and sustainability by addressing issues like nutrition, health, and environmental adaptation [104]. For instance, genomic studies have identified genes related to climate adaptation and milk production, which can be leveraged in breeding programs to select more efficient breeds [55].

Moreover, the success of livestock transfer programs in Haiti highlights the importance of targeting beneficiaries based on specific criteria to ensure sustainable herd growth and health [105]. In Brazil, the focus should be on characterizing genetic resources and organizing data collection to support breeding programs [106]. Finally, comparative studies of different goat breeds under semi-intensive management have shown that breeds like Kiko and Spanish goats perform better under limited-input conditions, suggesting their suitability for sustainable meat production [107].

Overall, a combination of community involvement, technological innovation, and strategic policy support is essential for the success of sustainable goat breeding programs.

6. Conclusion

The research findings underscore the potential for

targeted genetic selection, focusing on major genetic markers such as BMP15 and GDF9, to enhance the reproductive performance of Malaysian goats. Comparatively, this aligns with international studies on the successful integration of marker-assisted selection in other breeds, such as the Alpine and Saanen goats. Such strategies can enhance the economic viability of Malaysian goat breeds and improve their genetic diversity by reducing inbreeding effects. This review provides evidence that identifying and selecting genetic markers linked to favorable reproductive traits can improve both genetic health and productivity in Malaysian goats. Addressing inbreeding through crossbreeding or targeted genomic selection could be a sustainable approach for the genetic improvement of local breeds. Future research should focus on evaluating the long-term impacts of marker-assisted selection on reproductive traits under various environmental conditions. It is also essential to conduct polymorphism studies across different breeds to develop a comprehensive genetic management framework. Additionally, exploring advanced technologies like CRISPR gene editing could offer insights into further enhancing reproductive traits. Finally, developing policies to monitor and manage inbreeding in goat populations is recommended to sustain the genetic diversity and resilience of Malaysian goat breeds.

Declarations

Author Contributions

Conceptualization, A.S.F. and C.S.C.L.; methodology, A.S.F., and M.M.R.; software, M.Z.B.Z., and J.J.S.; validation, A.S.F. and S.S.; formal analysis, A.S.F., and S.A.A.B.; investigation, A.S.F. and C.S.C.L.; resources, A.S.F.; data curation, A.S.F.; writing—original draft preparation, all authors contributed equally; writing—review and editing, A.S.F.; supervision, A.S.F. and C.S.C.L.; project administration, A.S.F. All authors have read and agreed to the published version of the manuscript.

Data Availability Statement

The data presented in this study are available on request from the corresponding author.

Funding

Funding information is not available.

Conflicts of Interest

The authors declare no conflicts of interest regarding the publication of this manuscript. In addition, ethical issues, including plagiarism, informed consent, misconduct, data fabrication and/or falsification, double

publication and/or submission, and redundancies, have been completely observed by the authors.

References

- [1] AMILLS M., CAPOTE J., and TOSSER-KLOPP G. Goat domestication and breeding: a jigsaw of historical, biological and molecular data with missing pieces. *Animal Genetics*, 2017, 48(6): 631–644. <https://doi.org/10.1111/age.12598>
- [2] GIANNICO F., MASSARI S., CAPUTI JAMBRENGHI A., SORIANO A., PALA A., LINGUITI G., CICCARESE S., & ANTONACCI R. The expansion of the TRB and TRG genes in domestic goats (*Capra hircus*) is characteristic of the ruminant species. *BMC Genomics*, 2020, 21(1): 623, <https://doi.org/10.1186/s12864-020-07022-x>
- [3] TIWARI G., CHAUHAN A., SHARMA P., and TIWARI R. Nutritional Values and Therapeutic Uses of *Capra hircus* Milk. *International Journal of Pharmaceutical Investigation* 2022, 12(4): 408–417, <https://doi.org/10.5530/ijpi.2022.4.71>
- [4] FAO. FAOSTAT: Food and Agriculture Data. FOOD Agric. Organ, 2018. <http://www.fao.org/faostat/en/#data/QA>
- [5] MAZINANI M., and RUDE B. Population, World Production and Quality of Sheep and Goat Products. *American Journal of Animal and Veterinary Sciences*, 2020, 15(4): 291–299, <https://doi.org/10.3844/ajavsp.2020.291.299>
- [6] ZUBIR M. A., BONG C. P. C., ISHAK S. A., HO W. S., and HASHIM H. The trends and projections of greenhouse gas emission by the livestock sector in Malaysia. *Clean Technologies and Environmental Policy*, 2022, 24(1): 363–377, <https://doi.org/10.1007/s10098-021-02156-2>
- [7] SAHOO S., ALEX R., VOHRA V., MUKHERJEE S., and GOWANE G. R. Estimation of genetic parameters and genetic change of first parity reproductive traits in Alpine × Beetal goats. *Reproduction in Domestic Animals*, 2023, 58(9): 1188–1198, <https://doi.org/10.1111/rda.14418>
- [8] FANG X., YANG S., CHEN M., SUN R., ZHAO L., GU B., ZHANG J., HUANG D., ZHENG T., ZHAO Y., PENG P., & ZHAO Y. Association analysis of polymorphisms at *GLRB*, *GRIA2*, and *GASK1B* genes with reproductive traits in Dazu Black Goats. *Animal Biotechnology*, 2023, 34(9): 4721–4729. <https://doi.org/10.1080/10495398.2023.2187406>
- [9] MOHAMMED MUAYAD TA, HANIZA M.Z.H., & HUSNI I. Reproductive performance of different goat breeds in Malaysia. *Indian Journal of Animal Research*, 2017, 53(1): 24–27. <https://doi.org/10.18805/ijar.v0i0E.7002>
- [10] GRIZELJ J., PELLICER-RUBIO M., ŠPOLJARIĆ B., DÁVILA F., and FRERET S. Nonhormonal Reproductive Management in Goat Breeding. *Corpus Journal of Dairy and Veterinary Science*, 2022, 3(4): 1048, <https://doi.org/10.54026/CJDVS/1048>
- [11] BHATTARAI, N., POUDEL, J., KOLAKSHYAPATI, M. R., SHARMA, M. P., GORKHALI, N. A., SIGDEL, A., ... & SAPKOTA, S. Evaluation of reproductive performance and litter traits of Khari, Jamunapari and Sirohi crossbred goats in Surkhet district of Karnali province, Nepal. *Journal of Agriculture and Forestry University*, 2022, 5(1): 71–80, <https://doi.org/10.3126/jafu.v5i1.48444>
- [12] ATOUI A., CARABAÑO M. J., ABDENNEBI M., & NAJARI S. Modélisation des performances de reproduction de la population caprine locale dans les régions arides tunisiennes. *Journal of Oasis Agriculture and Sustainable Development* 2022, 4(3): 29–37,

<https://doi.org/10.56027/JOASD.132022>

- [13] FANG X., GU B., CHEN M., SUN R., ZHANG J., ZHAO L., & ZHAO Y. Genome-Wide Association Study of the Reproductive Traits of the Dazu Black Goat (*Capra hircus*) Using Whole-Genome Resequencing. *Genes*, 2023, 14(10): 1960, <https://doi.org/10.3390/genes14101960>
- [14] MELLADO M. Goat Management: Reproductive Management. In *Encyclopedia of Dairy Sciences*, Elsevier, 2022: 905–912. <https://doi.org/10.1016/B978-0-08-100596-5.00823-4>
- [15] NAVASARDYAN D. S., GRIGORYAN A. G., MARMARYAN YU. G., & BADALYAN M. V. The influence of selection factors on the fertility of female goats and the live weight of newborn goats of the Saanen breed. *AgriScience and Technology*, 2023, 1(81), 75–80, <https://doi.org/10.52276/25792822-2023.1-75>
- [16] WANG Z., WANG R., PAN C., CHEN H., QU L., WU L., GUO Z., ZHU H., & LAN X. Genetic Variations and mRNA Expression of Goat DNAH1 and their Associations with Litter Size. *Cells*, 2022, 11(8): 1371, <https://doi.org/10.3390/cells11081371>
- [17] SUN X., JIANG J., WANG G., ZHOU P., LI J., CHEN C., LIU L., LI N., XIA Y., & REN H. Genome-wide association analysis of nine reproduction and morphological traits in three goat breeds from Southern China. *Animal Bioscience*, 2023, 36(2): 191–199, <https://doi.org/10.5713/ab.21.0577>
- [18] SUN X., NIU Q., JIANG J., WANG G., ZHOU P., LI J., CHEN C., LIU L., XU L., & REN H. Identifying Candidate Genes for Litter Size and Three Morphological Traits in Youzhou Dark Goats Based on Genome-Wide SNP Markers. *Genes*, 2023, 14(6): 1183, <https://doi.org/10.3390/genes14061183>
- [19] HAN M., LIANG C., LIU Y., HE X., & CHU M. Integrated Transcriptome Analysis Reveals the Crucial mRNAs and miRNAs Related to Fecundity in the Hypothalamus of Yunshang Black Goats during the Luteal Phase. *Animals*, 2022, 12(23): 3397, <https://doi.org/10.3390/ani12233397>
- [20] AMOAH E. A., GELAYE S., GUTHRIE P., & REXROAD C. E. Breeding season and aspects of reproduction of female goats. *Journal of Animal Science*, 1996, 74(4): 723–728, <https://doi.org/10.2527/1996.744723x>
- [21] DESIRE S., MUCHA S., COFFEY M., MRODE R., BROADBENT J., & CONINGTON J. Pseudopregnancy and a seasonal breeding in dairy goats: genetic basis of fertility and impact on lifetime productivity. *Animal*, 2018, 12(9): 1799–1806, <https://doi.org/10.1017/S1751731117003056>
- [22] MOCÉ E., MOCÉ M. L., LOZANO-PALAZÓN S. A., BERNÁCER J., MARTÍNEZ-GRANELL M. M., ESTEVE I. C., BERNAT F., CONTRERAS S. J., VILLALBA I., & GÓMEZ E. A. Fertility prediction in dairy goats from Murciano-Granadina breed: The role of sperm evaluation and female traits. *Animal*, 2022, 16(5): 100525, <https://doi.org/10.1016/j.animal.2022.100525>
- [23] MARGATHO G., RODRÍGUEZ-ESTÉVEZ V., QUINTAS H., & SIMÕES J. The Effects of Reproductive Disorders, Parity and Litter Size on Milk Yield of Serrana Goats. *Animals*, 2019, 9(11): 968, <https://doi.org/10.3390/ani9110968>
- [24] ARREBOLA F. A., TORRES-MARTELL R., GONZÁLEZ-CASQUET O., MEZA-HERRERA C. A., & PÉREZ-MARÍN C. C. Perioovulatory Hormonal Profiles after Estrus Induction and Conception Rate by Fixed-Time AI in Payoya Goats during the Anestrous Season. *Animals*, 2022, 12(20): 2853, <https://doi.org/10.3390/ani12202853>
- [25] ZARAZAGA L., GATICA M. C., & HERNANDEZ H., KELLER M., CHEMINEAU P., DELGADILLO SÁNCHEZ J., & GUZMÁN J. The reproductive response to the male effect of 7- or 10-month-old female goats is improved when photostimulated males are used. *Animal*, 2019, 13(8): 1658–1665, <https://doi.org/10.1017/S1751731118003397>
- [26] SIMÕES J., ABECIA J. A., CANNAS A., DELGADILLO J. A., LACASTA D., VOIGT K., & CHEMINEAU P. Review: Managing sheep and goats for sustainable high yield production. *Animal*, 2021, 15(Suppl. 1): 100293, <https://doi.org/10.1016/j.animal.2021.100293>
- [27] DELGADILLO J. A. Environmental and social cues can be used in combination to develop sustainable breeding techniques for goat reproduction in the subtropics. *Animal*, 2011, 5(1): 74–81, <https://doi.org/10.1017/S1751731110001400>
- [28] ZHU Y., YE J., QIN P., YAN X., GONG X., LI X., LIU Y., ... & FANG F. Analysis of serum reproductive hormones and ovarian genes in pubertal female goats. *Journal of Ovarian Research*, 2023, 16(1): 69, <https://doi.org/10.1186/s13048-023-01150-0>
- [29] GRANLEESE T., CLARK S. A., KINGHORN B. P., & VAN DER WERF J. H. J. Optimizing female allocation to reproductive technologies considering merit, inbreeding and cost in nucleus breeding programmes with genomic selection. *Journal of Animal Breeding and Genetics*, 2019, 136(2): 79–90, <https://doi.org/10.1111/jbg.12374>
- [30] SHUMBUSHO F., RAOUL J., ASTRUC J. M., PALHIÈRE I., and ELSEN J. M. Potential benefits of genomic selection on genetic gain of small ruminant breeding programs. *Journal of Animal Science*, 2013, 91(8): 3644–3657, <https://doi.org/10.2527/jas.2012-6205>
- [31] LAI F.-N., ZHAI H.-L., CHENG M., MA J.-Y., SHUN-FENG CHENG, WEI GE, GUO-LIANG ZHANG, JUN-JIE WANG, ZHANG R.-Q., ... & SHEN W. Whole-genome scanning for the litter size trait associated genes and SNPs under selection in dairy goat (*Capra hircus*). *Scientific Reports*, 2016, 6(1): 38096, <https://doi.org/10.1038/srep38096>
- [32] ABUZAHRHA M., ABU EID L., EFFENDI M. H., MUSTOFA I., LAMID M., and REHMAN S. Polymorphism studies and candidate genes associated with litter size traits in Indonesian goats: a systematic review. *F1000Research*, 2023, 12: 61, <https://doi.org/10.12688/f1000research.129050.1>
- [33] MAHMOUDI P., RASHIDI A., NAZARI-GHADIKOLAEI A., ROSTAMZADEH J., RAZMKABIR M., & HUSON H. J. Genome-wide association study reveals novel candidate genes for litter size in Markhoz goats. *Frontiers in Veterinary Science*, 2022, 9: 1045589, <https://doi.org/10.3389/fvets.2022.1045589>
- [34] WANG P., LI W., LIU Z., H X., LAN, R., LIU Y., & CHU M. Analysis of the Association of Two SNPs in the Promoter Regions of the PPP2R5C and SLC39A5 Genes with Litter Size in Yunshang Black Goats. *Animals*, 2022, 12(20): 2801, <https://doi.org/10.3390/ani12202801>
- [35] XIN D., BAI Y., BI Y., HE L., KANG Y., PAN C., ZHU H., CHEN H., QU L., & LAN X. Insertion/deletion variants within the IGF2BP2 gene identified in reported genome-wide

- selective sweep analysis reveal a correlation with goat litter size. *Journal of Zhejiang University. Science B*, 2021, 22(9): 757–766, <https://doi.org/10.1631/jzus. B2100079>
- [36] BI Y., WANG Z., WANG Q., LIU H., GUO Z., PAN C., CHEN H., ZHU H., WU L., & LAN X. Are Copy Number Variations within the FecB Gene Significantly Associated with Morphometric Traits in Goats? *Animals*, 2022, 12(12): 1547, <https://doi.org/10.3390/ani12121547>
- [37] BI Y., LI J., WANG X., HE L., LAN K., QU L., LAN X., SONG X., & PAN C. Two Novel Rare Strongly Linked Missense SNPs (P27R and A85G) Within the GDF9 Gene Were Significantly Associated with Litter Size in Shaanbei White Cashmere (SBWC) Goats. *Frontiers in Veterinary Science*, 2020, 7: 406, <https://doi.org/10.3389/fvets.2020.00406>
- [38] JI X., CAO Z., HAO Q., HE M., CANG M., YU H., MA Q., LI X., BAO S., WANG J., & TONG B. Effects of New Mutations in BMP1B, GDF9, BMP15, LEPR, and B4GALNT2 Genes on Litter Size in Sheep. *Veterinary Sciences*, 2023, 10(4): 258, <https://doi.org/10.3390/vetsci10040258>
- [39] TAO L., HE X. Y., WANG F. Y., PAN L. X., WANG X. Y., GAN S. Q., DI R., & CHU M. X. Identification of genes associated with litter size combining genomic approaches in Luzhong mutton sheep. *Animal Genetics*, 2021, 52(4): 545–549, <https://doi.org/10.1111/age.13078>
- [40] DIGE M. S., ROUT K., SINGH M. K., BHUSAN S., KAUSHIK R., and GOWANE G. R. Estimates of genetic parameters for linear body measurements and prediction of body weight in goat. *Journal of Animal Breeding and Genetics*, 2022, 139(4): 423–433, <https://doi.org/10.1111/jbg.12677>
- [41] GUNIA M., PHOCAS F., ARQUET R., ALEXANDRE G., and MANDONNET N. Genetic parameters for body weight, reproduction, and parasite resistance traits in the Creole goat. *Journal of Animal Science*, 2011, 89(11): 3443–3451, <https://doi.org/10.2527/jas.2011-3872>
- [42] J. MIRANDA C., LEÓN J. M., PIERAMATI C., GÓMEZ M. M., VALDÉS J., and BARBA C. Estimation of Genetic Parameters for Peak Yield, Yield and Persistency Traits in Murciano-Granadina Goats Using Multi-Traits Models. *Animals*, 2019, 9(7): 411, <https://doi.org/10.3390/ani9070411>
- [43] ROY R., MANDAL A., and NOTTER D. R. Estimates of (co)variance components due to direct and maternal effects for body weights in Jamunapari goats. *Animal*, 2008, 2(3): 354–359, <https://doi.org/10.1017/S1751731107001218>
- [44] SHAAT I., and MÁKI-TANILAA A. Variation in direct and maternal genetic effects for meat production traits in Egyptian Zaraibi goats. *Journal of Animal Breeding and Genetics*, 2009, 126(3): 198–208, <https://doi.org/10.1111/j.1439-0388.2008.00784.x>
- [45] MOAEEN-UD-DIN M., DANISH MUNER R., and KHAN M. S. Genome wide association study identifies novel candidate genes for growth and body conformation traits in goats. *Scientific Reports*, 2022, 12(1): 9891, <https://doi.org/10.1038/s41598-022-14018-y>
- [46] CARVALHO G. M. C., PAIVA S. R., ARAÚJO A. M., MARIANTE A., and BLACKBURN H. D. Genetic structure of goat breeds from Brazil and the United States: Implications for conservation and breeding programs. *Journal of Animal Science*, 2015, 93(10): 4629–4636, <https://doi.org/10.2527/jas.2015-8974>
- [47] GAJBHIYE R., FUNG J. N., and MONTGOMERY G. W. Complex genetics of female fertility. *NPJ Genomic Medicine*, 2018, 3(1): 29, <https://doi.org/10.1038/s41525-018-0068-1>
- [48] WIJESENA H. R., KACHMAN S.D., LENTS C.A., RIETHOVEN J.-J., TRENHAILE-GRANNEMANN M.D., SAFRANSKI T.J., SPANGLER M.L., & CIOBANU D.C. Fine mapping genetic variants associated with age at puberty and sow fertility using SowPro90 genotyping array. *Journal of Animal Science*, 2020, 98(10): skaa293, <https://doi.org/10.1093/jas/skaa293>
- [49] MICHAELIS M., SOBCZAK A., KOCZAN D., LANGHAMMER M., REINSCH N., SCHOEN J., & WEITZEL J. M. Selection for female traits of high fertility affects male reproductive performance and alters the testicular transcriptional profile. *BMC Genomics*, 2017, 18(1): 889, <https://doi.org/10.1186/s12864-017-4288-z>
- [50] TRENHAILE M. D., PETERSEN J. L., KACHMAN S. D., R. K. JOHNSON, and CIOBANU D. C. Long-term selection for litter size in swine results in shifts in allelic frequency in regions involved in reproductive processes. *Animal Genetics*, 2016, 47(5): 534–542, <https://doi.org/10.1111/age.12448>
- [51] FLOSSMANN G., WURMSER C., PAUSCH H., TENGHE A., DODENHOFF J., DAHINTEN G., GÖTZ K. U., RUSS I., & FRIES R. A nonsense mutation of bone morphogenetic protein-15 (BMP15) causes both infertility and increased litter size in pigs. *BMC Genomics*, 2021, 22(1): 38, <https://doi.org/10.1186/s12864-020-07343-x>
- [52] MA X., LI P. H., ZHU M. X., HE L. C., SUI S. P., GAO S., SU G. S., ... & HUANG R. H. Genome-wide association analysis reveals genomic regions on Chromosome 13 affecting litter size and candidate genes for uterine horn length in Erhualian pigs. *Animal*, 2018, 12(12): 2453–2461, <https://doi.org/10.1017/S1751731118000332>
- [53] MCLAREN D. G., and BOVEY M. Genetic Influences on Reproductive Performance. *Veterinary Clinics of North America: Food Animal Practice*, 1992, 8(3): 435–459, [https://doi.org/10.1016/S0749-0720\(15\)30697-6](https://doi.org/10.1016/S0749-0720(15)30697-6)
- [54] SOSA-MADRID B. S., SANTACREU M. A., BLASCO A., FONTANESI L., PENA R. N., and IBÁÑEZ-ESCRICHE N. A genomewide association study in divergently selected lines in rabbits reveals novel genomic regions associated with litter size traits. *Journal of Animal Breeding and Genetics*, 2020, 137(2): 123–138, <https://doi.org/10.1111/jbg.12451>
- [55] AMIRI GHANATSAMAN Z., AYATOLAH MEHRGARDI A., ASADOLLAHPOUR NANAIE H., and ESMAILIZADEH A. Comparative genomic analysis uncovers candidate genes related with milk production and adaptive traits in goat breeds. *Scientific Reports*, 2023, 13(1): 8722, <https://doi.org/10.1038/s41598-023-35973-0>
- [56] YUAN Y., ZHANG W., LIU C., HE Y., ZHANG H., XU L., YANG B., ZHAO Y., MA Y., ... & GUANXIN E. Genome-Wide Selective Analysis of Boer Goat to Investigate the Dynamic Heredity Evolution under Different Stages. *Animals*, 2022, 12(11): 1356, <https://doi.org/10.3390/ani12111356>
- [57] SUN Z., LIU Y., HE X., DI R., WANG X., REN C., ZHANG Z., & CHU M. Integrative Proteomics and Transcriptomics Profiles of the Oviduct Reveal the Prolificacy-Related Candidate Biomarkers of Goats (*Capra hircus*) in Estrous Periods. *International Journal of Molecular*

- Sciences*, 2022, 23(23): 14888, <https://doi.org/10.3390/ijms232314888>
- [58] LI R., YANG P., DAI X., ASADOLLAHPOUR NANA EI H., FANG W., ... & JIANG Y. A near complete genome for goat genetic and genomic research. *Genetics, Selection, Evolution*, 2021, 53(1): 74, <https://doi.org/10.1186/s12711-021-00668-5>
- [59] LIU Y., QI B., XIE J., WU X., LING Y., CAO X., KONG F., XIN J., JIANG X., WU Q., ... & LI W. Filtered reproductive long non-coding RNAs by genome-wide analyses of goat ovary at different estrus periods', *BMC Genomics*, 2018, 19(1): 866, <https://doi.org/10.1186/s12864-018-5268-7>
- [60] YAN X., ZHANG T., LIU L., YU Y., YANG G., HAN Y., GONG G., WANG F., ZHANG L., LIU H., LI W., YAN X., ... and SU R. Accuracy of Genomic Selection for Important Economic Traits of Cashmere and Meat Goats Assessed by Simulation Study. *Frontiers in Veterinary Science*, 2022, 9: 770539, <https://doi.org/10.3389/fvets.2022.770539>
- [61] GUO J., JIANG R., MAO A., LIU G. E., ZHAN S., LI L., ZHONG T., ... & ZHANG H. Genome-wide association study reveals 14 new SNPs and confirms two structural variants highly associated with the horned/polled phenotype in goats. *BMC Genomics*, 2021, 22(1): 769, <https://doi.org/10.1186/s12864-021-08089-w>
- [62] TOLONE M., SARDINA M. T., SENCZUK G., CHESSARI G., CRISCIONE A., MOSCARELLI A., RIGGIO S., ... & MASTRANGELO S. Genomic Tools for the Characterization of Local Animal Genetic Resources: Application in Mascaruna Goat. *Animals*, 2022, 12(20): 2840, <https://doi.org/10.3390/ani12202840>
- [63] HUSSEN ALI O., and AL-AZZAWI S.H. Detection of polymorphism in growth differentiation factor 9 gene (GDF9) Exon1 and its association with litter size in local Iraqi goats. *Bionatura*, 2022, 7(4): 1–5, <https://doi.org/10.21931/RB/2022.07.04.49>
- [64] ZERGANI E., RASHIDI A., ROSTAMZADEH J., RAZMKABIR M., and TETENS J. Meta-analysis of association between c.963A > G single-nucleotide polymorphism on *BMP15* gene and litter size in goats. *Archives Animal Breeding*, 2022, 65(3): 309–318, <https://doi.org/10.5194/aab-65-309-2022>
- [65] FEBRIANA A., SUTOPO S., KURNIANTO E., and WIDIYANTO W. A Novel SNPs of *KISS1* Gene Strongly Associated with Litter Size in Indonesian Goat Breeds. *Tropical Animal Science Journal*, 2022, 45(3): 255–269, <https://doi.org/10.5398/tasj.2022.45.3.255>
- [66] ZHANG S., GAO X., JIANG Y., SHEN Y., XIE H., PAN P., HUANG Y., WEI Y., & JIANG Q. Population validation of reproductive gene mutation loci and association with the litter size in Nubian goat. *Archives Animal Breeding*, 2021, 64(2): 375–386, <https://doi.org/10.5194/aab-64-375-2021>
- [67] ERNIE MUNEERAH M. A., MD TAMRIN N. A., SALISI M. S., ZULKIFLY S., GHAZALI S. S. M., ... & MAMAT-HAMIDI K. Microsatellite-Based Genetic Characterization of the Indigenous Katjang Goat in Peninsular Malaysia. *Animals*, 2021, 11(5): 1328, <https://doi.org/10.3390/ani11051328>
- [68] NORHAZIRAH A.H., NULIT R., SHOHAIMI S. and SHIKH MAIDIN M. Assessment of reproductive performance and abortion occurrence of Boer goats as influenced by farm systems and feeding practices. *Malaysian Journal of Animal Science*, 2016, 19(2): 107–115, [https://mjas.my/mjas-v2/rf/pages/journal/v19i2-11-Nurhazirah%20Mashitah\(Assessment\)_r4.pdf](https://mjas.my/mjas-v2/rf/pages/journal/v19i2-11-Nurhazirah%20Mashitah(Assessment)_r4.pdf)
- [69] BAKAR A., and MARINI A. *Genetic characterisations of four goat breeds in Malaysia assessed using microsatellites*. Master's thesis, Universiti Putra Malaysia, Malaysia, 2014. <http://psasir.upm.edu.my/id/eprint/52528>
- [70] AMIE MARINI A.B., MOHD HIFZAN R., JOHARI J. A., TAN S. G., and PANANDAM J. M. Genetic Variation of Four Goat Breeds in Malaysia Using Microsatellite Polymorphism Markers. *Malaysian Journal of Animal Science*, 2013, 16(2): 1–8, [https://msap.my/mjas16-2/1\(GENETIC-Amieza_1-8\)rev3.pdf](https://msap.my/mjas16-2/1(GENETIC-Amieza_1-8)rev3.pdf)
- [71] AMIE MARINI A.B., MOHD HIFZAN R., JOHARI J. A., TAN S. G., and PANANDAM J. M. Assessment of Genetic Diversity on Goat Breeds in Malaysia Using Microsatellite Markers. *Malays. Journal of Animal Science*, 2014, 17(1): 19–26, https://www.msap.my/pdf/2-Assesment-Amie_rev6.pdf
- [72] CORTE PAUSE F., CROCIATI M., URLI S., MONACI M., DEGENO L., and STRADAIOLI G. Environmental Factors Affecting the Reproductive Efficiency of Italian Simmental Young Bulls. *Animals*, 2022, 12(18): 2476, <https://doi.org/10.3390/ani12182476>
- [73] CREAN A. J., and IMMLER S. Evolutionary consequences of environmental effects on gamete performance. *Philosophical Transactions of the Royal Society B: Biological Sciences*, 2021, 376(1826): 20200122, <https://doi.org/10.1098/rstb.2020.0122>
- [74] FURSTOSS V., DAVID I., FATET A., BOISSARD K., CLÉMENT V., and BODIN L. Genetic and non-genetic factors related to the success of artificial insemination in dairy goats. *Animal*, 2015, 9(12): 1935–1942, <https://doi.org/10.1017/S1751731115001500>
- [75] MUCHA S., TORTEREAU F., DOESCHL-WILSON A., RUPP R., and CONINGTON J. Animal Board Invited Review: Meta-analysis of genetic parameters for resilience and efficiency traits in goats and sheep. *Animal*, 2022, 16(3): 100456, <https://doi.org/10.1016/j.animal.2022.100456>
- [76] EVANS T. J. Diminished Reproductive Performance and Selected Toxicants in Forages and Grains. *Veterinary Clinics of North America: Food Animal Practice*, 2011, 27(2): 345–371, <https://doi.org/10.1016/j.cvfa.2011.03.001>
- [77] RHIND S., RAE M., and BROOKS A. Effects of nutrition and environmental factors on the fetal programming of the reproductive axis. *Reproduction*, 2001, 122(2): 205–214, <https://doi.org/10.1530/rep.0.1220205>
- [78] LOZANO-JARAMILLO M., KOMEN H., WIENTJES Y. C. J., MULDER H. A., and BASTIAANSEN J. W. M. Optimizing design to estimate genetic correlations between environments with common environmental effects. *Journal of Animal Science*, 2020, 98(2): skaa034, <https://doi.org/10.1093/jas/skaa034>
- [79] HAMEL S., CÔTÉ S. D., and FESTA-BIANCHET M. Maternal characteristics and environment affect the costs of reproduction in female mountain goats. *Ecology*, 2010, 91(7): 2034–2043, <https://doi.org/10.1890/09-1311.1>
- [80] CUMMINGS A. M. and KAVLOCK R. J. Gene–Environment Interactions: A Review of Effects on Reproduction and Development. *Critical Reviews in Toxicology*, 2004, 34(6): 461–485, <https://doi.org/10.1080/10408440490519786>

- [81] PARK T. S. Gene-editing techniques and their applications in livestock and beyond. *Animal Bioscience*, 2023, 36(2): 333–338, <https://doi.org/10.5713/ab.22.0383>
- [82] GARCIA A. 50 Gene Editing Applications in Livestock Production. *Journal of Animal Science*, 2023, 101(Supplement_1): 43–44, <https://doi.org/10.1093/jas/skad068.050>
- [83] POLEJAEVA I. Generation of Genetically Engineered Livestock Using Somatic Cell Nuclear Transfer. *Reproduction*, 2021, 162(1): F11–F22, <https://doi.org/10.1530/REP-21-0072>
- [84] YÁÑEZ J. M., XU P, CARVALHEIRO R., and HAYES B. Genomics applied to livestock and aquaculture breeding. *Evolutionary Applications*, 2022, 15(4): 517–522, <https://doi.org/10.1111/eva.13378>
- [85]. BAES C. F, ROCHUS C. M., HOULAHAN K., OLIVEIRA JR G. A., VAN STAAVEREN N., and MIGLIOR F. 22 Sustainable Livestock Breeding: Challenges and Opportunities. *Journal of Animal Science*, 2022, 100(Supplement_3): 13–13, <https://doi.org/10.1093/jas/skac247.023>
- [86] BISHOP T. F., and VAN EENENNAAM A. L. Genome editing approaches to augment livestock breeding programs. *Journal of Experimental Biology*, 2020, 223(Suppl_1): jeb207159, <https://doi.org/10.1242/jeb.207159>
- [87] TU C.-F., CHUANG C., and YANG T.-S. The application of new breeding technology based on gene editing in pig industry — A review. *Animal Bioscience*, 2022, 35(6): 791–803, <https://doi.org/10.5713/ab.21.0390>
- [88] ISLAM R., LIU X., GEBRESELASSIE G., ABIED A., MA Q., and MA Y. Genome-wide association analysis reveals the genetic locus for high reproduction trait in Chinese Arbas Cashmere goat. *Genes Genomics*, 2020, 42(8): 893–899, <https://doi.org/10.1007/s13258-020-00937-5>
- [89] PROUDFOOT C., MCFARLANE G., WHITELAW B., and LILLICO S. Livestock breeding for the 21st century: the promise of the editing revolution. *Frontiers of Agricultural Science and Engineering*, 2020, 7(2): 129, <https://doi.org/10.15302/J-FASE-2019304>
- [90] YUAN M., GAO Y., HAN J., WU T., ZHANG J., WEI Y., & ZHANG Y. The development and application of genome editing technology in ruminants: a review. *Frontiers of Agricultural Science and Engineering*, 2020, 7(2): 171, <https://doi.org/10.15302/J-FASE-2019302>
- [91] ALMEIDA M., and RANISCH R. Beyond safety: mapping the ethical debate on heritable genome editing interventions. *Humanities and Social Sciences Communications*, 2022, 9(1): 139, <https://doi.org/10.1057/s41599-022-01147-y>
- [92] MATTAR C. N. Z., LABUDE M. K., LEE T. N., and LAI P. S. Ethical considerations of preconception and prenatal gene modification in the embryo and fetus. *Human Reproduction*, 2021, 36(12): 3018–3027, <https://doi.org/10.1093/humrep/deab222>
- [93] BRANDT R. The ethical gene. *Bioethics*, 2022, 36(4): 403–410, <https://doi.org/10.1111/bioe.13006>
- [94] XAFIS V., SCHAEFER G. O., LABUDE M. K., ZHU Y., ... & CHADWICK R. Germline genome modification through novel political, ethical, and social lenses. *PLOS Genetics*, 2021, 17(9): e1009741, <https://doi.org/10.1371/journal.pgen.1009741>
- [95] KRISHAN K., KANCHAN T., and SINGH B. Human Genome Editing and Ethical Considerations. *Science and Engineering Ethics*, 2016, 22(2): 597–599, <https://doi.org/10.1007/s11948-015-9675-8>
- [96] YEAGER A. Ethical issues raised by intergenerational monitoring in clinical trials of germline gene modification. *Journal of Medical Ethics*, 2021, 47(4): 267–270, <https://doi.org/10.1136/medethics-2020-106095>
- [97] KORMOS A., LANZARO G. C., BIER E., SANTOS V., NAZARÉ L., PINTO J., AGUIAR DOS SANTOS A., & JAMES A. A. Ethical Considerations for Gene Drive: Challenges of Balancing Inclusion, Power and Perspectives. *Frontiers in Bioengineering and Biotechnology*, 2022, 10: 826727, <https://doi.org/10.3389/fbioe.2022.826727>
- [98] SUGARMAN J. Ethics and germline gene editing. *EMBO Reports*, 2015, 16(8): 879–880, <https://doi.org/10.15252/embr.201540879>
- [99] QIU R. Debating Ethical Issues in Genome Editing Technology. *Asian Bioethics Review*, 2016, 8(4): 307–326, <https://doi.org/10.1353/asb.2016.0026>
- [100] KAUMBATA W., NAKIMBUGWE H., NANDOLO W., BANDA L. J., MÉSZÁROS G., GONDWE T., ... & WURZINGER, M. Experiences from the Implementation of Community-Based Goat Breeding Programs in Malawi and Uganda: A Potential Approach for Conservation and Improvement of Indigenous Small Ruminants in Smallholder Farms. *Sustainability*, 2021, 13(3): 1494, <https://doi.org/10.3390/su13031494>
- [101] HAILE A., GIZAW S., GETACHEW T., MUELLER J. P., AMER P., REKIK M., & RISCHKOWSKY B. ... & WURZINGER M. Community-based breeding programmes are a viable solution for Ethiopian small ruminant genetic improvement but require public and private investments. *Journal of Animal Breeding and Genetics*, 2019, 136(5): 319–328, <https://doi.org/10.1111/jbg.12401>
- [102] SOW F., CAMARA Y., TRAORE E., CABARAUX J.-F., MISSOHO A., ANTOINE-MOUSSIAUX N., HORNICK J.-L., & MOULA N. Characterisation of smallholders' goat production systems in the Fatick area, Senegal. *Pastoralism*, 2021, 11(1): 12, <https://doi.org/10.1186/s13570-021-00195-4>
- [103] MONAU P., RAPHAKA K., ZVINOROVA-CHIMBOZA P., and GONDWE T. Sustainable Utilization of Indigenous Goats in Southern Africa. *Diversity*, 2020, 12(1): 20, <https://doi.org/10.3390/d12010020>
- [104] BRAGA LOBO R. N. Opportunities for investment into small ruminant breeding programmes in Brazil. *Journal of Animal Breeding and Genetics*, 2019, 136(5): 313–318, <https://doi.org/10.1111/jbg.12396>
- [105] SILVA S. R., SACARRÃO-BIRRENTA L., ALMEIDA M., RIBEIRO D. M., GUEDES C., GONZÁLEZ MONTAÑA J. R., ... & DE ALMEIDA, A. M. Extensive Sheep and Goat Production: The Role of Novel Technologies towards Sustainability and Animal Welfare. *Animals*, 2022, 12(7): 885, <https://doi.org/10.3390/ani12070885>
- [106] THOMPSON W. M., and MAGNAN N. Predicting Success in a Productive Asset Transfer Program: A Goat Program in Haiti. *Applied Economic Perspectives and Policy*, 2017, 39(2): 363–385, <https://doi.org/10.1093/aep/ppx021>
- [107] WANG L., NGULUMA A., LEITE-BROWNING M. L., and BROWNING R. Differences among four meat goat breeds for doe fitness indicator traits in the southeastern United States. *Journal of Animal Science*, 2017, 95(4): 1481–

1488, <https://doi.org/10.2527/jas.2016.1283>

参考文献:

- [1] AMILLS M., CAPOTE J. 和 TOSSER-KLOPP G. 山羊驯化和育种: 缺失部分的历史、生物和分子数据拼图。动物遗传学, 2017, 48(6): 631–644. <https://doi.org/10.1111/age.12598>
- [2] GIANNICO F., MASSARI S., CAPUTI JAMBRENGHI A., SORIANO A., PALA A., LINGUITI G., CICCARESE S. 和 ANTONACCI R. 家养山羊 (*Capra hircus*) 中 TRB 和 TRG 基因的扩增是反刍动物的特征。BMC 基因组学, 2020, 21(1): 623, <https://doi.org/10.1186/s12864-020-07022-x>
- [3] TIWARI G., CHAUHAN A., SHARMA P. 和 TIWARI R. 山羊奶的营养价值和医疗用途。国际药物研究杂志 2022, 12(4): 408–417, <https://doi.org/10.5530/ijpi.2022.4.71>
- [4] 粮农组织. FAOSTAT: 食品和农业数据。食品农业组织, 2018. <http://www.fao.org/faostat/en/#data/QA>
- [5] MAZINANI M. 和 RUDE B. 绵羊和山羊产品的人口、世界产量和质量。美国动物和兽医学杂志, 2020, 15(4): 291–299, <https://doi.org/10.3844/ajavsp.2020.291.299>
- [6] ZUBIR M. A., BONG C. P. C., ISHAK S. A., HO W. S. 和 HASHIM H. 马来西亚畜牧业温室气体排放趋势和预测。清洁技术和环境政策, 2022, 24(1): 363–377, <https://doi.org/10.1007/s10098-021-02156-2>
- [7] SAHOO S., ALEX R., VOHRA V., MUKHERJEE S. 和 GOWANE G. R. 阿尔卑斯× Beetal 山羊首胎生殖性状遗传参数和遗传变化的估计。家畜繁殖, 2023, 58(9): 1188–1198, <https://doi.org/10.1111/rda.14418>
- [8] FANG X., YANG S., CHEN M., SUN R., ZHAO L., GU B., ZHANG J., HUANG D., ZHENG T., ZHAO Y., PENG P. 和 ZHAO Y. 大足黑山羊 GLRB、GRIA2、GASK1B 基因多态性与生殖性状的关联分析。动物生物技术, 2023, 34(9): 4721–4729. <https://doi.org/10.1080/10495398.2023.2187406>
- [9] MOHAMMED MUAYAD TA., HANIZA M.Z.H. 和 HUSNI I. 马来西亚不同山羊品种的繁殖性能。印度动物研究杂志, 2017, 53(1): 24–27. <https://doi.org/10.18805/ijar.v0i0F.7002>
- [10] GRIZELJ J., PELLICER-RUBIO M., ŠPOLJARIĆ B., DÁVILA F. 和 FRERET S. 山羊育种中的非激素生殖管理。乳品与兽医学文集, 2022, 3(4): 1048, <https://doi.org/10.54026/CJDVS/1048>
- [11] BHATTARAI, N., POUDEL, J., KOLAKSHYAPATI, M. R., SHARMA, M. P., GORKHALI, N. A., SIGDEL, A., ... 和 SAPKOTA, S. 评估尼泊尔卡纳利省苏尔凯特区 Khari, Jamunapari 和 Sirohi 杂交山羊的繁殖性能和产仔性状。农林大学学报, 2022, 5(1): 71–80, <https://doi.org/10.3126/jafu.v5i1.48444>
- [12] ATOUI A., CARABAÑO M. J., ABDENNEBI M. 和 NAJARI S. 突尼斯地区山羊种群繁殖性能模型。《绿洲农业与可持续发展杂志》2022, 4(3): 29–37, <https://doi.org/10.56027/JOASD.132022>
- [13] FANG X., GU B., CHEN M., SUN R., ZHANG J., ZHAO L., 和 ZHAO Y. 利用全基因组重测序对大足黑山羊 (*Capra hircus*) 生殖性状进行全基因组关联研究。基因, 2023, 14(10): 1960, <https://doi.org/10.3390/genes14101960>
- [14] MELLADO M. 山羊管理: 生殖管理。《乳业科学百科全书》, 爱思唯尔, 2022: 905–912. <https://doi.org/10.1016/B978-0-08-100596-5.00823-4>
- [15] NAVASARDYAN D. S., GRIGORYAN A. G., MARMARYAN YU. G. 和 BADALYAN M. V. 选择因素对萨能品种母山羊生育能力和新生山羊活重的影响。农业科学与技术, 2023, 1 (81), 75–80, <https://doi.org/10.52276/25792822-2023.1-75>
- [16] WANG Z., WANG R., PAN C., CHEN H., QU L., WU L., GUO Z., ZHU H., 和 LAN X. 山羊 DNAH1 的遗传变异和 mRNA 表达及其与产仔数的关系。单元格, 2022, 11(8): 1371, <https://doi.org/10.3390/cells11081371>
- [17] SUN X., JIANG J., WANG G., ZHOU P., LI J., CHEN C., LIU L., LI N., XIA Y., 和 REN H. 中国南方三个山羊品种九个繁殖和形态性状的全基因组关联分析。动物生物科学, 2023, 36 (2): 191–199, <https://doi.org/10.5713/ab.21.0577>
- [18] SUN X., NIU Q., JIANG J., WANG G., ZHOU P., LI J., CHEN C., LIU L., XU L., 和 REN H. 基于全基因组 SNP 标记鉴定幽州黑山羊产仔数和三个形态性状的候选基因。基因, 2023, 14(6): 1183, <https://doi.org/10.3390/genes14061183>
- [19] HAN M., LIANG C., LIU Y., HE X., 和 CHU M. 整合转录组分析揭示了云上黑山羊黄体期下丘脑中与繁殖力相关的关键 mRNA 和 miRNA。动物, 2022, 12(23): 3397, <https://doi.org/10.3390/ani12233397>
- [20] AMOAH E. A., GELAYE S., GUTHRIE P. 和 REXROAD C. E. 母山羊的繁殖季节和繁殖方面。《动物科学杂志》, 1996, 74(4): 723–728, <https://doi.org/10.2527/1996.744723x>
- [21] DESIRE S., MUCHA S., COFFEY M., MRODE R., BROADBENT J. 和 CONINGTON J. 奶山羊的假妊娠和季节性繁殖: 生育力的遗传基础及其对终生生产力的影响。动物, 2018, 12(9): 1799–1806, <https://doi.org/10.1017/S1751731117003056>
- [22] MOCÉ E., MOCÉ M. L., LOZANO-PALAZÓN S. A., BERNÁCER J., MARTÍNEZ-GRANELL M. M., ESTEVE I.C., BERNAT F., CONTRERAS S.J., VILLALBA I. 和 GÓMEZ E.A. Murciano-Granadina 品种奶山羊的生育力预测: 精子评估和女性特征的作用。动物, 2022, 16 (5): 100525, <https://doi.org/10.1016/j.animal.2022.100525>
- [23] MARGATHO G., RODRÍGUEZ-ESTÉVEZ V., QUINTAS H. 和 SIMÕES J. 生殖障碍、胎次和产仔数对塞拉纳山羊产奶量的影响。动物, 2019, 9 (11): 968, <https://doi.org/10.3390/ani9110968>
- [24] ARREBOLA F. A., TORRES-MARTELL R., GONZÁLEZ-CASQUET O., MEZA-HERRERA C. A., 和 PÉREZ-MARÍN C. C. 无发情季节 Payoya 山羊发情诱导后围排卵激素分布和受孕率。动物, 2022, 12(20): 2853, <https://doi.org/10.3390/ani12202853>

- [25] ZARAZAGA L., GATICA M.C., HERNANDEZ H., KELLER M., CHEMINEAU P., DELGADILLO SÁNCHEZ J. 和 GUZMÁN J. 当使用光刺激的雄性山羊时, 7 个月或 10 个月大的母山羊对雄性效应的生殖反应会得到改善。动物, 2019, 13(8): 1658–1665, <https://doi.org/10.1017/S1751731118003397>
- [26] SIMÕES J., ABECIA J. A., CANNAS A., DELGADILLO J. A., LACASTA D., VOIGT K. 和 CHEMINEAU P. 评论: 管理绵羊和山羊以实现可持续高产生产。动物, 2021, 15(Suppl. 1): 100293, <https://doi.org/10.1016/j.animal.2021.100293>
- [27] DELGADILLO J. A. 环境和社会线索可以结合使用, 以开发亚热带山羊繁殖的可持续育种技术。动物, 2011, 5(1): 74–81, <https://doi.org/10.1017/S1751731110001400>
- [28] ZHU Y., YE J., QIN P., YAN X., GONG X., LI X., LIU Y., ... 和 FANG F. 青春期雌性山羊血清生殖激素及卵巢基因分析。卵巢研究杂志, 2023, 16(1): 69, <https://doi.org/10.1186/s13048-023-01150-0>
- [29] GRANLEESE T., CLARK S. A., KINGHORN B. P. 和 VAN DER WERF J. H. J. 在具有基因组选择的核心育种计划中, 考虑优点、近亲繁殖和成本, 优化雌性在生殖技术中的分配。《动物育种与遗传学杂志》, 2019, 136(2): 79–90, <https://doi.org/10.1111/jbg.12374>
- [30] SHUMBUSHO F., RAOUL J., ASTRUC J.M., PALHIÈRE I. 和 ELSEN J. M. 基因组选择对小反刍动物育种计划遗传增益的潜在益处。《动物科学杂志》, 2013, 91(8): 3644–3657, <https://doi.org/10.2527/jas.2012-6205>
- [31] LAI F.-N., ZHAI H.-L., CHENG M., MA J.-Y., SHUN-FENG CHENG, WEI GE, GUO-LIANG ZHANG, JUN-JIE WANG, ZHANG R.-Q., ... 和 SHEN W. 全基因组扫描奶山羊 (*Capra hircus*) 产仔数性状相关基因和 SNPs。科学报告, 2016, 6(1): 38096, <https://doi.org/10.1038/srep38096>
- [32] ABUZAHERA M., ABU EID L., EFFENDI M. H., MUSTOFA I., LAMID M. 和 REHMAN S. 印度尼西亚山羊产仔数特征的多态性研究和候选基因。系统评价。F1000Research, 2023, 12: 61, <https://doi.org/10.12688/f1000research.129050.1>
- [33] MAHMOUDI P., RASHIDI A., NAZARI-GHADIKOLAEI A., ROSTAMZADEH J., RAZMKABIR M. 和 HUSON H. J. 全基因组关联研究揭示了马尔霍兹山羊产仔数的新候选基因。兽医学前沿, 2022, 9: 1045589, <https://doi.org/10.3389/fvets.2022.1045589>
- [34] WANG P., LI W., LIU Z., H X., LAN, R., LIU Y., 和 CHU M. 云上黑山羊PPP2R5C和SLC39A5基因启动子区两个SNP与产仔数的关联分析。动物, 2022, 12(20): 2801, <https://doi.org/10.3390/ani12202801>
- [35] XIN D., BAI Y., BI Y., HE L., KANG Y., PAN C., ZHU H., CHEN H., QU L., 和 LAN X. 在报道的全基因组选择性扫描分析中发现的IGF2BP2基因内的插入/缺失变异揭示了与山羊产仔数的相关性。浙江大学学报。科学B, 2021, 22(9): 757–766, <https://doi.org/10.1631/jzus. B2100079>
- [36] BI Y., WANG Z., WANG Q., LIU H., GUO Z., PAN C., CHEN H., ZHU H., WU L., 和 LAN X. FecB 基因拷贝数变异与山羊形态性状有显著相关性吗? 动物, 2022, 12(12): 1547, <https://doi.org/10.3390/ani12121547>
- [37] BI Y., LI J., WANG X., HE L., LAN K., QU L., LAN X., SONG X., 和 PAN C. GDF9 基因内两个新的稀有强连锁错义 SNP (P27R 和 A85G) 与陕北白绒山羊产仔数显著相关。兽医学前沿, 2020, 7: 406, <https://doi.org/10.3389/fvets.2020.00406>
- [38] JI X., CAO Z., HAO Q., HE M., CANG M., YU H., MA Q., LI X., BAO S., WANG J., 和 TONG B. BMP1B、GDF9、BMP15、LEPR 和 B4GALNT2 基因新突变对绵羊产仔数的影响。兽医科学, 2023, 10(4): 258, <https://doi.org/10.3390/vetsci10040258>
- [39] TAO L., HE X. Y., WANG F. Y., PAN L. X., WANG X. Y., GAN S. Q., DI R. 和 CHU M. X. 结合基因组学方法鉴定与鲁中肉羊产仔数相关的基因。动物遗传学, 2021, 52(4): 545–549, <https://doi.org/10.1111/age.13078>
- [40] DIGE M. S., ROUT K., SINGH M. K., BHUSAN S., KAUSHIK R. 和 GOWANE G. R. 山羊线性身体测量和体重预测的遗传参数估计。动物育种与遗传学杂志, 2022, 139(4): 423–433, <https://doi.org/10.1111/jbg.12677>
- [41] GUNIA M., PHOCAS F., ARQUET R., ALEXANDRE G. 和 MANDONNET N. 克里奥尔山羊体重、繁殖和抗寄生虫性状的遗传参数。动物科学杂志, 2011, 89(11): 3443–3451, <https://doi.org/10.2527/jas.2011-3872>
- [42] J. MIRANDA C., LEÓN J. M., PIERAMATI C., GÓMEZ M. M., VALDÉS J. 和 BARBA C. 使用多性状模型估计 Murciano-Granadina 山羊峰值产量、产量和持久性性状的遗传参数。动物, 2019, 9(7): 411, <https://doi.org/10.3390/ani9070411>
- [43] ROY R., MANDAL A. 和 NOTTER D. R. 贾穆纳帕里山羊体重的直接和母体影响导致的(协)方差成分估计值。动物, 2008, 2(3): 354–359, <https://doi.org/10.1017/S1751731107001218>
- [44] SHAAT I. 和 MÄKI-TANILA A. 埃及扎拉比山羊肉用性状的直接和母体遗传效应差异。动物育种与遗传学杂志, 2009, 126(3): 198–208, <https://doi.org/10.1111/j.1439-0388.2008.00784.x>
- [45] MOAEEN-UD-DIN M., DANISH MUNER R. 和 KHAN M. S. 全基因组关联研究确定了山羊生长和身体构造特征的新候选基因。科学报告, 2022, 12(1): 9891, <https://doi.org/10.1038/s41598-022-14018-y>
- [46] CARVALHO G. M. C., PAIVA S. R., ARAÚJO A. M., MARIANTE A. 和 BLACKBURN H. D. 巴西和美国山羊品种的遗传结构: 对保护和育种计划的影响。动物科学杂志, 2015, 93(10): 4629–4636, <https://doi.org/10.2527/jas.2015-8974>
- [47] GAJBHIYE R., FUNG J. N. 和 MONTGOMERY G. W. 女性生育力的复杂遗传学。NPJ 基因组医学, 2018, 3(1): 29, <https://doi.org/10.1038/s41525-018-0068-1>
- [48] WIJESENA H. R., KACHMAN S.D., LENTS C.A., RIETHOVEN J.-J., TRENHAILE-GRANNEMANN M.D., SAFRANSKI T.J., SPANGLER M.L. 和 CIOBANU D.C. 使用 SowPro90 基因分型阵列精细定位与

- 青春期年龄和母猪生育力相关的遗传变异。动物科学杂志, 2020, 98(10): skaa293, <https://doi.org/10.1093/jas/skaa293>
- [49] MICHAELIS M., SOBCZAK A., KOCZAN D., LANGHAMMER M., REINSCH N., SCHOEN J. 和 WEITZEL J. M. 对高生育力雌性特征的选择会影响雄性生殖能力并改变睾丸转录谱。BMC 基因组学, 2017, 18(1): 889, <https://doi.org/10.1186/s12864-017-4288-z>
- [50] TRENHAILE M. D., PETERSEN J. L., KACHMAN S. D., R. K. JOHNSON 和 CIOBANU D. C. 猪对产仔数的长期选择导致参与生殖过程的区域等位基因频率发生变化。动物遗传学, 2016, 47 (5): 534–542, <https://doi.org/10.1111/age.12448>
- [51] FLOSSMANN G., WURMSER C., PAUSCH H., TENGHE A., DODENHOFF J., DAHINTEN G., GÖTZ K. U., RUSS I., 和 FRIES R. 骨形态发生蛋白 15 (BMP15) 的无义突变导致猪不育和产仔数增加。BMC Genomics, 2021, 22(1): 38, <https://doi.org/10.1186/s12864-020-07343-x>
- [52] MA X., LI P. H., ZHU M. X., HE L. C., SUI S. P., GAO S., SU G. S., ... 和 HUANG R. H. 全基因组关联分析揭示了影响二花脸猪产仔数和子宫角长度候选基因的 13 号染色体上的基因组区域。动物, 2018, 12(12): 2453–2461, <https://doi.org/10.1017/S1751731118000332>
- [53] MCLAREN D. G. 和 BOVEY M. 遗传对生殖性能的影响。北美兽医诊所: 食用动物实践, 1992, 8(3): 435–459, [https://doi.org/10.1016/S0749-0720\(15\)30697-6](https://doi.org/10.1016/S0749-0720(15)30697-6)
- [54] SOSA-MADRID B. S., SANTACREU M. A., BLASCO A., FONTANESI L., PENA R. N. 和 IBÁÑEZ-ESCRICHE N. 对兔子不同选择品系的全基因组关联研究揭示了与产仔数性状相关的新基因组区域。动物育种与遗传学杂志, 2020, 137(2): 123–138, <https://doi.org/10.1111/jbg.12451>
- [55] AMIRI GHANATSAMAN Z., AYATOLAH MEHRGARDI A., ASADOLLAHPOUR NANAEI H. 和 ESMAILIZADEH A. 比较基因组分析揭示了与山羊品种产奶量和适应性特征相关的候选基因。科学报告, 2023, 13(1): 8722, <https://doi.org/10.1038/s41598-023-35973-0>
- [56] YUAN Y., ZHANG W., LIU C., HE Y., ZHANG H., XU L., YANG B., ZHAO Y., MA Y., ... 和 GUANXIN E. 波尔山羊全基因组选择性分析以研究不同阶段下的动态遗传进化。动物, 2022, 12(11): 1356, <https://doi.org/10.3390/ani12111356>
- [57] SUN Z., LIU Y., HE X., DI R., WANG X., REN C., ZHANG Z., 和 CHU M. 输卵管综合蛋白质组学和转录组学谱揭示山羊 (*Capra hircus*) 发情期多产相关候选生物标志物。国际分子科学杂志, 2022, 23(23): 14888, <https://doi.org/10.3390/ijms232314888>
- [58] LI R., YANG P., DAI X., ASADOLLAHPOUR NANAEI H., FANG W., ... 和 JIANG Y. 山羊遗传和基因组研究的近乎完整的基因组。遗传学、选择、进化, 2021, 53(1): 74, <https://doi.org/10.1186/s12711-021-00668-5>
- [59] LIU Y., QI B., XIE J., WU X., LING Y., CAO X., KONG F., XIN J., JIANG X., WU Q., ... 和 LI W. 通过不同发情期山羊卵巢全基因组分析筛选生殖长链非编码RNA》, BMC 基因组学, 2018, 19(1): 866, <https://doi.org/10.1186/s12864-018-5268-7>
- [60] YAN X., ZHANG T., LIU L., YU Y., YANG G., HAN Y., GONG G., WANG F., ZHANG L., LIU H., LI W., YAN X., ... 和 SU R. 通过模拟研究评估绒山羊和肉山羊重要经济性状基因组选择的准确性。兽医学前沿, 2022, 9: 770539, <https://doi.org/10.3389/fvets.2022.770539>
- [61] GUO J., JIANG R., MAO A., LIU G. E., ZHAN S., LI L., ZHONG T., ... 和 ZHANG H. 全基因组关联研究揭示了 14 个新的 SNP, 并证实了两个与山羊有角/无角表型高度相关的结构变异。BMC 基因组学, 2021, 22(1): 769, <https://doi.org/10.1186/s12864-021-08089-w>
- [62] TOLONE M., SARDINA M. T., SENCZUK G., CHESSARI G., CRISCIONE A., MOSCARELLI A., RIGGIO S., ... 和 MASTRANGELO S. 用于表征当地动物遗传资源的基因组工具: 在马斯卡鲁纳山羊中的应用。动物, 2022, 12(20): 2840, <https://doi.org/10.3390/ani12202840>
- [63] HUSSEN ALI O 和 AL-AZZAWI S. H. 伊拉克当地山羊生长分化因子 9 基因 (GDF9) 外显子 1 的多态性检测及其与产仔数的关联。生物性, 2022, 7(4): 1–5, <https://doi.org/10.21931/RB/2022.07.04.49>
- [64] ZERGANI E., RASHIDI A., ROSTAMZADEH J., RAZMKABIR M. 和 TETENS J. BMP15 基因 c.963A > G 单核苷酸多态性与山羊产仔数关联性的荟萃分析。动物育种档案, 2022, 65(3): 309–318, <https://doi.org/10.5194/aab-65-309-2022>
- [65] FEBRIANA A., SUTOPO S., KURNIANTO E. 和 WIDIYANTO W. KISS1 基因的新型 SNP 与印度尼西亚山羊品种的产仔数密切相关。热带动物科学杂志, 2022, 45 (3): 255–269, <https://doi.org/10.5398/tasj.2022.45.3.255>
- [66] ZHANG S., GAO X., JIANG Y., SHEN Y., XIE H., PAN P., HUANG Y., WEI Y., 和 JIANG Q. 努比亚山羊生殖基因突变位点的群体验证及其与产仔数的关联。动物育种档案, 2021, 64(2): 375–386, <https://doi.org/10.5194/aab-64-375-2021>
- [67] ERNIE MUNEERAH M. A., MD TAMRIN N. A., SALISI M. S., ZULKIFLY S., GHAZALI S. S. M. 和 MAMAT-HAMIDI K. 基于微卫星的马来西亚半岛本土卡姜山羊遗传特征分析。动物, 2021, 11(5): 1328, <https://doi.org/10.3390/ani11051328>
- [68] NORHAZIRAH A. H., NULIT R., SHOHAIMI S. 和 SHIKH MAIDIN M. 评估农场系统和饲养方式对波尔山羊生殖性能和流产发生率的影响。马来西亚动物科学杂志, 2016, 19(2): 107–115. [https://mjas.my/mjas-v2/rf/pages/journal/v19i2-11-Nurhazirah%20Mashitah\(Assessment\)_r4.pdf](https://mjas.my/mjas-v2/rf/pages/journal/v19i2-11-Nurhazirah%20Mashitah(Assessment)_r4.pdf)
- [69] BAKAR A. 和 MARINI A. 使用微卫星评估马来西亚四种山羊品种的遗传特征。马来西亚博特拉大学硕士论文, 马来西亚, 2014. <http://psasir.upm.edu.my/id/eprint/52528>
- [70] AMIE MARINI A. B., MOHD HIFZAN R., JOHARI J. A., TAN S. G. 和 PANANDAM J. M. 利用微卫星多态性标记对马来西亚四种山羊品种进行遗传变异分析。马

- 来西亚动物科学杂志, 2013, 16(2): 1–8.
[https://msap.my/mjas16-2/1\(GENETIC-Amieza_1-8\)rev3.pdf](https://msap.my/mjas16-2/1(GENETIC-Amieza_1-8)rev3.pdf)
- [71] AMIE MARINI A.B., MOHD HIFZAN R., JOHARI J. A., TAN S. G. 和 PANANDAM J. M. 使用微卫星标记评估马来西亚山羊品种的遗传多样性。马来人。动物科学杂志, 2014, 17(1): 19–26.
https://www.msap.my/pdf/2-Assesment-Amie_rev6.pdf
- [72] CORTE PAUSE F., CROCIATI M., URLI S., MONACI M., DEGANO L. 和 STRADAIOLI G. 影响意大利西门塔尔公牛繁殖效率的环境因素。《动物》, 2022, 12(18): 2476, <https://doi.org/10.3390/ani12182476>
- [73] CREAM A. J. 和 IMMLER S. 环境影响对配子表现的进化后果。《哲学学报》。英国皇家学会 B: 生物科学, 2021, 376(1826): 20200122, <https://doi.org/10.1098/rstb.2020.0122>
- [74] FURSTOSS V., DAVID I., FATET A., BOISSARD K., CLÉMENT V. 和 BODIN L. 与奶山羊人工授精成功相关的遗传和非遗传因素。动物, 2015, 9(12): 1935–1942, <https://doi.org/10.1017/S1751731115001500>
- [75] MUCHA S., TORTEREAU F., DOESCHL-WILSON A., RUPP R. 和 CONINGTON J. 动物委员会邀请评审: 山羊和绵羊恢复力和效率特征遗传参数的荟萃分析。动物, 2022, 16(3): 100456, <https://doi.org/10.1016/j.animal.2022.100456>
- [76] EVANS T. J. 饲料和谷物中的生殖性能下降和选择性毒物。北美兽医诊所: 食用动物实践, 2011, 27(2): 345–371, <https://doi.org/10.1016/j.cvfa.2011.03.001>
- [77] RHIND S., RAE M. 和 BROOKS A. 营养和环境因素对生殖轴胎儿编程的影响。生殖, 2001, 122(2): 205–214, <https://doi.org/10.1530/rep.0.1220205>
- [78] LOZANO-JARAMILLO M., KOMEN H., WIENTJES Y. C. J., MULDER H. A. 和 BASTIAANSEN J. W. M. 优化设计以估计具有常见环境影响的环境之间的遗传相关性。动物科学杂志, 2020, 98(2): skaa034, <https://doi.org/10.1093/jas/skaa034>
- [79] HAMEL S., CÔTÉ S. D. 和 FESTA-BIANCHET M. 母性特征和环境影响雌性山羊的繁殖成本。生态学, 2010, 91(7): 2034–2043, <https://doi.org/10.1890/09-1311.1>
- [80] CUMMINGS A. M. 和 KAVLOCK R. J. 基因-环境相互作用: 对生殖和发育影响的综述。毒理学评论, 2004, 34(6): 461–485, <https://doi.org/10.1080/10408440490519786>
- [81] PARK T. S. 基因编辑技术及其在畜牧业及其他领域的应用。动物生物科学, 2023, 36(2): 333–338, <https://doi.org/10.5713/ab.22.0383>
- [82] GARCIA A. 50 基因编辑在畜牧业生产中的应用。动物科学杂志, 2023, 101(Supplement_1): 43–44, <https://doi.org/10.1093/jas/skad068.050>
- [83] POLEJAEVA I. 利用体细胞核移植产生转基因牲畜。繁殖, 2021, 162(1): F11–F22, <https://doi.org/10.1530/REP-21-0072>
- [84] YÁÑEZ J. M., XUP, CARVALHEIRO R. 和 HAYES B. 基因组学应用于畜牧业和水产养殖。进化应用, 2022, 15(4): 517–522, <https://doi.org/10.1111/eva.13378>
- [85] BAES C. F., ROCHUS C. M., HOULAHAN K., OLIVEIRA JR G. A., VAN STAVEREN N. 和 MIGLIOR F. 22 可持续畜牧业育种: 挑战与机遇。动物科学杂志, 2022, 100 (补充3): 13–13, <https://doi.org/10.1093/jas/skac247.023>
- [86] BISHOP T. F. 和 VAN EENENNAAM A. L. 基因组编辑方法增强牲畜育种计划。实验生物学杂志, 2020, 223 (补充1): jeb207159, <https://doi.org/10.1242/jeb.207159>
- [87] TU C.-F., CHUANG C. 和 YANG T.-S. 基于基因编辑的新型育种技术在养猪业中的应用——综述。动物生物科学, 2022, 35(6): 791–803, <https://doi.org/10.5713/ab.21.0390>
- [88] ISLAM R., LIU X., GEBRESELASSIE G., ABIED A., MA Q. 和 MA Y. 全基因组关联分析揭示了中国阿尔巴斯绒山羊高繁殖性状的基因位点。基因组学, 2020, 42(8): 893–899, <https://doi.org/10.1007/s13258-020-00937-5>
- [89] PROUDFOOT C., MCFARLANE G., WHITELAW B. 和 LILLICO S. 21 世纪的畜牧育种: 编辑革命的希望。农业科学与工程前沿, 2020, 7 (2): 129, <https://doi.org/10.15302/J-FASE-2019304>
- [90] YUAN M., GAO Y., HAN J., WU T., ZHANG J., WEI Y., 和 ZHANG Y. 基因组编辑技术在反刍动物中的发展与应用: 综述。农业科学与工程前沿, 2020, 7 (2): 171, <https://doi.org/10.15302/J-FASE-2019302>
- [91] ALMEIDA M. 和 RANISCH R. 超越安全: 绘制可遗传基因组编辑干预的伦理辩论图。人文与社会科学通讯, 2022, 9(1): 139, <https://doi.org/10.1057/s41599-022-01147-y>
- [92] MATTAR C. N. Z., LABUDE M. K., LEE T. N. 和 LAI P. S. 胚胎和胎儿受孕前和产前基因改造的伦理考虑。人类生殖, 2021, 36(12): 3018–3027, <https://doi.org/10.1093/humrep/deab222>
- [93] BRANDT R. 道德基因。生物伦理学, 2022, 36(4): 403–410, <https://doi.org/10.1111/bioe.13006>
- [94] XAFIS V., SCHAEFER G. O., LABUDE M. K., ZHU Y., ... 和 CHADWICK R. 通过新颖的政治、伦理和社会视角进行种系基因组改造。PLOS 遗传学, 2021, 17(9): e1009741, <https://doi.org/10.1371/journal.pgen.1009741>
- [95] KRISHAN K., KANCHAN T. 和 SINGH B. 人类基因组编辑和伦理考虑。科学与工程伦理, 2016, 22(2): 597–599, <https://doi.org/10.1007/s11948-015-9675-8>
- [96] YEAGER A. 种系基因改造临床试验中代际监测引发的伦理问题。医学伦理杂志, 2021, 47(4): 267–270, <https://doi.org/10.1136/medethics-2020-106095>
- [97] KORMOS A., LANZARO G. C., BIER E., SANTOS V., NAZARÉ L., PINTO J., AGUIAR DOS SANTOS A. 和 JAMES A. A. 基因驱动的伦理考虑: 平衡包容性、权力和观点的挑战。生物工程与生物技术前沿, 2022, 10: 826727, <https://doi.org/10.3389/fbioe.2022.826727>
- [98] SUGARMAN J. 伦理与种系基因编辑。EMBO 报告, 2015, 16(8): 879–880, <https://doi.org/10.15252/embr.201540879>

- [99] QIU R. 讨论基因组编辑技术的伦理问题。亚洲生物伦理评论, 2016, 8(4): 307–326, <https://doi.org/10.1353/asb.2016.0026>
- [100] KAUMBATA W., NAKIMBUGWE H., NANDOLO W., BANDA L. J., MÉSZÁROS G., GONDWE T., ... 和 WURZINGER, M. 马拉维和乌干达实施社区山羊育种计划的经验: 一种保护和改良小农农场本土小反刍动物的潜在方法。可持续性, 2021, 13(3): 1494, <https://doi.org/10.3390/su13031494>
- [101] HAILE A., GIZAW S., GETACHEW T., MUELLER J. P., AMER P., REKIK M., RISCHKOWSKY B. ... 和 WURZINGER M. 以社区为基础的育种计划是埃塞俄比亚小反刍动物基因改良的可行解决方案, 但需要公共和私人投资。动物育种与遗传学杂志, 2019, 136(5): 319–328, <https://doi.org/10.1111/jbg.12401>
- [102] SOW F., CAMARA Y., TRAORE E., CABARAUX J.-F., MISSOHO A., ANTOINE-MOUSSIAUX N., HORNICK J.-L. 和 MOULA N. 塞内加尔法蒂克地区小农户山羊生产系统的特征。畜牧业, 2021, 11(1): 12, <https://doi.org/10.1186/s13570-021-00195-4>
- [103] MONAU P., RAPHAKA K., ZVINOROVA-CHIMBOZA P. 和 GONDWE T. 可持续利用南部非洲的本土山羊。多样性, 2020, 12(1): 20, <https://doi.org/10.3390/d12010020>
- [104] BRAGA LOBO R. N. 巴西小型反刍动物育种计划的投资机会。动物育种与遗传学杂志, 2019, 136(5): 313–318, <https://doi.org/10.1111/jbg.12396>
- [105] SILVA S. R., SACARRÓ-BIRRENTA L., ALMEIDA M., RIBEIRO DM., GUEDES C., GONZÁLEZ MONTAÑA J. R., ... 和 DE ALMEIDA, A. M. 绵羊和山羊的广泛生产: 新技术对可持续发展和动物福利的作用。动物, 2022, 12(7): 885, <https://doi.org/10.3390/ani12070885>
- [106] THOMPSON W. M. 和 MAGNAN N. 预测生产性资产转移计划的成功: 海地的山羊计划。应用经济观点与

政策, 2017, 39(2): 363–385, <https://doi.org/10.1093/aep/px021>

- [107] WANG L., NGULUMA A., LEITE-BROWNING M. L. 和 BROWNING R. 美国东南部四种肉用山羊品种在母鹿健康指标性状方面的差异。动物科学杂志, 2017, 95 (4): 1481–1488, <https://doi.org/10.2527/jas.2016.1283>

Word count: 5,955 words, excluding references.

Peer review information:

Whether the manuscript was fast tracked? - No

Number of reviewer report submitted in first round: 3 reports

Number of revision rounds: 2 rounds

Final revised version submitted: March 8, 2025

Disclaimer/Publisher's Note:

The views and conclusions expressed in this review are those of the author(s) and do not necessarily reflect the official policy or position of the Journal of Hunan University (Natural Sciences). The information provided is for educational and informational purposes only, intended to contribute to academic discussions and to guide further research in the field. The authors have made every effort to ensure the accuracy of the data and insights presented, but readers are encouraged to consult additional sources and verify the information before applying it to any practical, breeding, or policy-related decisions. Neither the authors nor the publisher accepts liability for any errors, omissions, or outcomes associated with the use of this information.