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The Role of Horizontal Gene Transfer and Structural Variation in the Adaptation of Goats to Diverse Environments

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Abstract This study analyzed the adaptive traits and genetic basis of goats, focusing on the research progress on HGT and SV in goat environmental adaptation in recent years, analyzing the mechanism of their role in goat adaptation to high-altitude hypoxia, drought, heat and severe cold, as well as the synergistic effect of HGT and SV and their evolutionary significance. The study found that horizontal gene transfer (HGT) and genome structural variation (SV) are two important factors driving the adaptive evolution of goats. New functional genes have been introduced into goats, such as endogenous retrovirus integration to promote placental function, which may improve their ability to adapt to the environment. SV includes large fragment insertion, deletion, duplication, translocation and other variations in the genome, which can significantly change gene dosage and regulatory network, and is a key factor affecting goat phenotypic diversity and environmental adaptability. In addition, this study also looks forward to the use of omics technology and functional experiments to further study HGT and SV, and explores the application prospects of these new knowledge in goat genetic improvement and protection. A deeper understanding of horizontal gene transfer and structural variation will help reveal the genetic mechanisms of goat environmental adaptation, enrich evolutionary biology theory, and provide new ideas for livestock breeding and biodiversity conservation.

Keywords Goat; Horizontal gene transfer; Structural variation; Environmental adaptation; Genome evolution

1 Introduction

Goats are one of the earliest domesticated livestock. They are raised in diverse environments on almost all continents around the world, from alpine tundra to tropical deserts, and show strong environmental adaptability. This wide adaptability makes goats an important model for studying the adaptive evolution of mammals. Under long-term natural selection and artificial breeding, different breeds of goats have formed unique adaptation characteristics to climatic conditions (such as high-altitude hypoxia, drought and heat, severe cold, etc.), and their genomes have left genetic imprints of adaptive evolution (Peng et al., 2024a). Traditionally, genetic studies on the environmental adaptability of goats have focused on single nucleotide polymorphisms (SNPs) and the screening of candidate genes. However, recent advances in genomics have revealed that horizontal gene transfer and structural variation play an important role in the adaptive evolution of species (Dai et al., 2021).

Horizontal gene transfer refers to the "horizontal" transmission process of genetic material from parents to offspring. It has long been believed to occur mainly in the microbial field, but there is increasing evidence that HGT events also occur in eukaryotes (including vertebrates), which have an impact on host evolution (Sun et al., 2015; Huang et al., 2017). On the other hand, structural variation is a large fragment variation of ⩾50 bp in length in the genome, including copy number variation (such as gene duplication or deletion), inversion, translocation and large insertion/deletion, which can cause gene dosage changes or regulatory element rearrangements, thereby having a greater impact on phenotype and adaptability (Bian et al., 2024; Zhang et al., 2024). Because the magnitude of genomic changes caused by structural variation is much greater than that of point mutations, they often play a key role in the evolution of adaptive traits and complex traits (Bian et al., 2024).

With the development of computational biology, more and more dedicated software and pipelines are used to detect HGT events. HGT provides a new perspective for understanding goat genome evolution that is different from the traditional concept, that is, the gene pool is not a closed system, and species can quickly expand their adaptive potential by "borrowing" genes from other species (Ricard et al., 2006; Sun et al., 2015). Structural variation provides rich raw materials for goats to adapt to environmental pressure by causing profound changes in genome structure, and its importance is increasingly valued in the fields of evolutionary biology and population genetics (Bian et al., 2024).

This study will analyze the main phenotypic characteristics and genetic basis of goats' excellent environmental adaptability, summarize the new discoveries of HGT in the field of goat adaptive evolution and the research progress of SV affecting goat adaptability, and further discuss the synergistic effect between HGT and SV and its significance to goat evolution. In addition, the application of HGT and SV research results to goat genetic improvement, protection and future research directions will be prospected, and the core insights and future challenges in this field will be emphasized in the conclusion. This study provides a new perspective for understanding the genetic adaptation mechanism of goats in extreme environments, and also provides a reference for future functional breeding and gene resource development.

2 Characteristics of Environmental Adaptability of Goats And Their Genetic Basis

2.1 Characteristics of environmental adaptability of goats

Goats are known as "poor people's cattle" because of their excellent adaptability. They can survive and reproduce in a variety of extreme environments and have an irreplaceable position in agricultural production. From the hot and arid deserts of Africa (such as Boer goats) and the Middle East, to the cold and oxygen-deficient mountainous areas of the Asian plateau (such as Tibetan goats and Inner Mongolia goats), to the rainy and humid pastures of Europe (such as Angora goats), local goat breeds in various places have formed a wealth of adaptive traits (Figure 1) (Wang et al., 2016). These adaptive traits include: broad-spectrum diet and efficient cellulose digestion in nutrient-poor environments, thirst tolerance and water metabolism efficiency in water-scarce environments, heat stress resistance and efficient heat dissipation mechanism in hot environments, thick and dense fur (such as down) and heat preservation ability in cold environments, and hypoxia tolerance and special physiological regulation ability in high-altitude environments. Genetic studies have shown that these adaptive traits of goats are closely related to multiple genetic variations in their genomes (Peng et al., 2024a).

Figure 1 Different breeds of goats (Adopted from Wang et al., 2016)

By conducting whole-genome selection scans and landscape genomics analysis of goat breeds in different regions around the world, researchers have identified many candidate genes and functional pathways related to local environmental adaptation. For example, a study compared the genomic differences of 51 indigenous goat breeds in different climatic zones and found that about 74 candidate genes were enriched in energy metabolism, endocrine regulation, circadian rhythm and heat stress, reflecting the selective effect of climate factors on the goat genome. These findings show the genetic basis of goats' adaptation to diverse environmental pressures (such as temperature, humidity and nutrition), and are natural "laboratories" (Peng et al., 2024a).

2.2 Adaptation and genetic basis of high-altitude hypoxia environment

In harsh high-altitude environments (such as the Qinghai-Tibet Plateau and the Himalayas), hypoxia (plateau hypoxia) is one of the biggest challenges facing organisms. Goat breeds living on plateaus (such as Tibetan goats) show high tolerance to low oxygen environments and possess a series of physiological adaptations, such as increased erythrocytosis, changes in hemoglobin oxygen affinity, and respiratory metabolic regulation (Zhu et al., 2025). The formation of these adaptations is inseparable from the contribution of genetic factors.

One typical example is the variation of the EPAS1 gene (also known as HIF2A). EPAS1 encodes hypoxia-inducible factor 2α, which is the main regulator of the body's response to hypoxia. Studies on goats at different altitudes in Yunnan, China found that a non-synonymous mutation site (Gln556Leu) in the EPAS1 gene was positively selected in high-altitude goats. The higher the altitude, the higher the frequency of the mutant allele. Goats carrying the mutation showed higher red blood cell counts and hemoglobin concentrations at plateaus above 2,500 meters, which helped improve the blood's oxygen-carrying capacity (Zhu et al., 2025). This finding echoes the adaptive mutation of EPAS1 in humans and other plateau mammals, indicating that different species convergently evolve and utilize the same hypoxia sensing pathway genes (Jin et al., 2020; Tiwari et al., 2024).

In addition to conventional gene mutations, structural variation also contributes to the adaptation of plateau goats. The latest pan-genome study of goats found that a VNTR sequence was inserted near the PAPSS2 gene on chromosome 6 of goats, and the frequency was significantly increased in plateau populations, which is considered to be related to the high-altitude adaptation of goats. PAPSS2 is involved in the sulfate metabolism pathway, and this structural insertion variation may affect the regulation of the gene, thereby affecting plateau hypoxia or other plateau stresses (Bian et al., 2024).

2.3 Adaptation to drought and high temperature environment and genetic basis

The drought and hot environment also poses severe challenges to the survival of goats. In desert and semi-desert areas with scarce water resources, poor vegetation and strong high temperature radiation, local indigenous goat breeds show outstanding characteristics such as heat resistance, drought resistance and roughage tolerance (Silanikove, 2000; Kalıber et al., 2016). For example, goat breeds in the arid zone of sub-Saharan Africa can maintain water balance under long-term water shortage conditions, and dissipate heat and cool down through day and night behavior adjustments and skin physiological regulation; some goat breeds in the Middle East and South Asia can tolerate temperatures as high as 40° C and have evolved the ability to feed on juicy and salty plants.

The genome comparison of the wild relatives living in desert habitats, the Nubian ibex (actually a wild goat subspecies) and domestic goats, provides important clues. A whole-genome analysis of the endangered Nubian antelope identified 22 positively selected genes involved in a variety of biological functions such as immune response, protein ubiquitination, olfactory transduction, and visual development. Among them, three genes (ABCA12, ASCL4, and UVSSA) are closely related to the development and function of the skin barrier (Chebii et al., 2020).

In addition to the skin system, goats' tolerance to high temperatures is also related to metabolic and endocrine regulation. Landscape genomic analysis showed that goat breeds in dry and hot climates showed signs of selection on some genes that control energy metabolism and heat stress response. For example, genes such as PLCβ1, ITPR2, and DENND1A were co-selected in high-temperature environment breeds (Peng et al., 2024a). In addition, heat shock protein (HSP)-related genes play an important role in goat heat tolerance. A study on local Chinese goats reported that several HSP genes were upregulated under high temperature stress conditions, and there were allelic variation differences between breeds.

2.4 Adaptability and genetic basis under severe cold environment and disease pressure

In addition to showing adaptability in tropical deserts and plateau environments, goats also survive well in cold environments such as high latitudes and mountains. For example, some goat breeds from Central Asia and Northern Europe can withstand severe cold of dozens of degrees Celsius below zero. These goats usually have dense fur (including developed undercoat) and thick subcutaneous fat to keep warm, and respond to the cold through behavior (such as curling up, reducing heat loss) and metabolic regulation (such as reducing basal metabolic rate). In goats, FGF5 has been identified as a major gene affecting the length of villi. Some goats in high-altitude cold areas carry FGF5 loss-of-function mutations, which grow longer villi to keep out the cold (Wu et al., 2024). In addition, EDA2R and KRT family genes are also involved in the development of hair and skin, and are selected in the adaptation of goat coat.

In addition to climatic factors, pathogen pressure in the environment is also an important selection pressure driving the evolutionary adaptation of goats. Goats have to deal with a variety of parasites, bacteria and viruses in the wild and on farms, and have evolved strong immune resistance (Luo et al., 2024). For example, during the domestication of goats, a galectin gene cluster (LGALS9 and its analogs) associated with immune response was repeated and expanded, resulting in three additional copies of LGALS9-like genes in domestic goats compared to wild goats (Bian et al., 2024).

Another aspect worth paying attention to is reproductive adaptation. During the domestication and breeding of goats, high fertility is often favored. In sheep, the well-known intron deletion of the BMPR1B gene (FecB mutation) can increase the number of ovulations and the number of lambs. Similarly, a deletion mutation (about ~9 kb in length) of the BMPR1B gene was found in goats to affect reproductive traits (Yang et al., 2024).

3 Research Progress on Horizontal Gene Transfer (HGT) in Goat Adaptation

3.1 Progress in detection and research methods of HGT

In recent years, researchers have developed many bioinformatics tools to assist HGT detection. For example, software such as HGTector, Horizoner, and PHYLOTIC combine abnormal sequence screening and phylogenetic tree construction to perform HGT scanning on massive genomic data (Carpanzano et al., 2022). Some processes adopt the "screening first and then verification" strategy: first screen out suspected exogenous genes based on sequence similarity, and then verify the relationship between genes in different species through phylogenetic tree analysis (Schwarzerova et al., 2024). It should be emphasized that with the increasing size of genome databases, species sampling bias may affect the accuracy of HGT detection (Huang et al., 2017). To this end, new methods have begun to introduce machine learning algorithms to perform pattern recognition on sequence features, which improves the sensitivity to HGT "traces" (Wijaya et al., 2025).

In view of the particularity of vertebrate genomes (isolation of somatic cells and reproductive system, low frequency of HGT), researchers have also adjusted their analysis ideas. Since most HGT events occur between microorganisms or viruses and hosts, viral vectors are often regarded as an important pathway for eukaryotic HGT (Irwin et al., 2022). Therefore, scientists also pay attention to the traces of viral sequences or transposons in the host genome in their research. The appearance of these sequences often means the introduction of horizontal genes in the past (Verneret et al., 2025). In addition, the combination of multi-omics data is also helpful: through transcriptome and proteome, it can be verified whether the suspected HGT gene is expressed and functions in the host, thereby distinguishing true HGT integrated genes from possible experimental/sequencing contamination.

3.2 Examples of HGT in goats and their closely related species

In ruminants, researchers have identified a unique syncytin gene, named Syncytin-Rum1, which is highly conserved in advanced ruminants such as cattle, sheep, and antelopes, and is presumed to have been integrated into the genome of a common ancestor about 30 million years ago (Cornelis et al., 2013). Ruminants such as goats have achieved innovations in placental structure and function by "borrowing" genes from ancient viruses to adapt to their special reproductive needs. , BovB sequences are widely present in unrelated mammals such as ruminants, horses, and kangaroos, but are missing in some more closely related species, which is consistent with the characteristics of cross-kingdom HGT (Huang et al., 2017). For goats, their genomes also carry BovB elements. Since BovB can be inserted at different locations in the genome, its impact on the goat genome structure cannot be ignored.

Goats are typical ruminants, and rumen microorganisms are crucial for their digestion of crude fiber feed. Ricard et al. (2006) sequenced the ESTs of rumen ciliates and found that rumen ciliates acquired many enzyme genes from bacteria and archaea, of which more than 75% were carbohydrate metabolism-related genes. These horizontally acquired bacterial enzymes (such as cellulases, hemicellulases, etc.) greatly enhanced the ability of ciliates to decompose complex plant polysaccharides, allowing them to thrive in the fiber-filled rumen environment. The metabolic functions acquired by ciliates through HGT are further converted into nutritional benefits for the host goats: volatile fatty acids and other nutrients produced by rumen microbial fermentation are absorbed and utilized by goats, enabling goats to digest high-fiber, low-quality plant materials.

3.3 Potential mechanism of HGT in environmental adaptation of goats

HGT gives the host new physiological functions. Through HGT, goats may acquire functional genes that their ancestors never had, expanding their range of adaptation from scratch (Dai et al., 2021). For example, if an ancestor of goats ingested a microorganism containing a gene for antivenom, and the gene was integrated through intestinal HGT, and antivenom was produced in goat serum, then the survival rate of this population in an environment with snakes would be significantly improved. HGT can also accelerate the rate of adaptive evolution. Compared with the traditional mutation-selection process, HGT is equivalent to directly "copying" a ready-made adaptation plan from another species, greatly shortening the generation time to reach an adaptive phenotype (Nakaya and Miyazawa, 2015). When the environment changes suddenly or a new ecosystem expands, the genes provided by HGT may allow goats to quickly break through the limitations.

HGT can provide the raw materials for genetic innovation. Even if an HGT event does not bring significant adaptive advantages at the moment, the new genes introduced may become the starting point of innovation through gene duplication, recombination, etc. in subsequent evolution (Burmeister, 2015; Ravenhall et al., 2015). For example, a silent bacterial gene in the goat genome may confer a new phenotype if structural variation occurs in the offspring to activate its expression. In addition, HGT can also cooperate with structural variation to improve adaptability. Simply put, if a gene acquired through HGT undergoes structural variation such as gene duplication, it can further expand production or multifunctionality and improve environmental adaptability (Dai et al., 2021).

4 The Key Role of Structural Variation (SV) in Goat Adaptation

4.1 Progress in identification technology of structural variation in goat genome

Since 2019, with the rise of third-generation sequencing and graphical pan-genome concepts, scientists have conducted systematic research on goat SV (Bian et al., 2024). After 2020, PacBio high-fidelity long-read sequencing (HiFi) and Oxford Nanopore sequencing were successively applied to goats. In 2024, Bian et al. (2024) constructed the world's first goat graphical pan-genome using de-chimeric diploid assembly of 8 representative goat breeds. Compared with traditional references, the pan-genome adds about 113 Mb of new sequences, including many structural variations that have not been included before. For goat populations with rich genetic diversity, pan-genome + long read length is an effective means to fully capture SV.

In addition to long read length, complementary technologies such as chromosome conformation capture (Hi-C) are also used to assemble and verify large-scale structural variations, and optical mapping technology (Bionano) helps detect ultra-long repeats and translocations. In order to identify the selected functional SVs, researchers usually combine SVs with population genetics statistics. For example, XP-CLR, F_ST, Pi ratio, etc. are used to compare the differences in SV frequency among different ecotypes or breeds. At the same time, functional annotation methods are also being followed up: SVs are located to genes or regulatory regions to evaluate the gene functions that may be affected. In addition, RNA sequencing can be used to detect the effects of SVs on gene expression, thereby inferring their biological significance (Zhang et al., 2024).

4.2 Research findings on the influence of structural variation on goat adaptability

A large amount of evidence supports that structural variation has a profound impact on the adaptive traits of goats, from coat warmth, reproduction patterns to immune resistance, etc., all of which leave traces of SVs. Under multiple selection pressures, the convergent evolution process of sheep and goat animals in morphological traits and adaptability, structural variation (SV) candidate genes played an important role in domestication and improvement (Figure 2) (Yang et al., 2024). These variations shape phenotypes by changing gene dosage (such as gene duplication or deletion changing the number of products) or changing gene regulation (such as

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translocation/inversion changing the upstream and downstream environment of genes, and insertion elements bringing new enhancers, etc.) (Zhang et al., 2024).

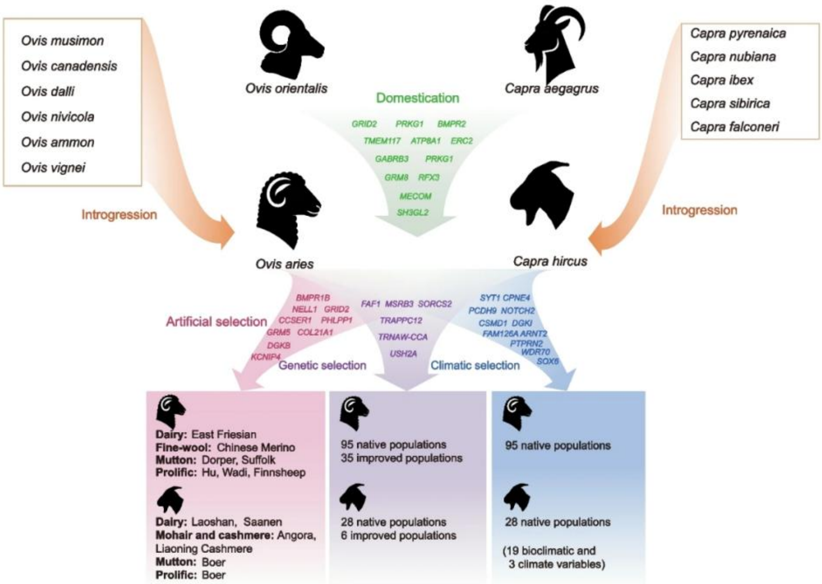

Figure 2 Convergent evolution through molecular parallelism of SV-genes involved in the domestication, genetic selection, climatic selection, and artificial selection of sheep and goats (Adopted from Yang et al., 2024)

Image caption: The genes presented in the modules "Domestication", "Genetic selection", "Climatic selection", and "Artificial selection" are the common candidate genes (i.e., orthologous genes) with important functions identified in the domestication, improvement, environment, and agronomic trait associated analyses of sheep and goats, respectively (Adopted from Yang et al., 2024)

It is worth emphasizing that compared with small variations such as SNPs, SVs can often affect multiple genes or entire pathways at one time, and thus contribute more directly and significantly to complex adaptation (Peng et al., 2024b). For example, a large inversion may simultaneously change the expression coordination of several heat-resistant genes; a large deletion may knock out negative regulatory factors and enhance the activity of disease resistance pathways. These are effects that are difficult to achieve with single point mutations. Therefore, structural variation provides a "macro-genetic lever" for goats to adapt to changing environments. With the in-depth study of the function of goat SV, we can have a more comprehensive understanding of how these "big" variations support the ecological adaptation of goats at the molecular level in the future.

4.3 Discussion on the mechanism of action of structural variation in goat adaptability

Structural variation plays a role in goat environmental adaptation through various mechanisms: changing dosage, changing expression time and space, or directly causing activity changes. These mechanisms of action are often more drastic and complex than single-point mutations, and therefore have a more significant impact on adaptive traits (Di Gerlando et al., 2020). Studies on plants and humans in recent years have also shown that the contribution of SVs to complex trait variation is much higher than the proportion of bases they occupy in the genome (Zhang et al., 2024). For omnivorous species such as goats that are distributed in multiple environments, structural variation undoubtedly provides a strong genetic "ammunition", enabling them to quickly adjust themselves according to different ecological pressures and achieve dynamic matching of genome and phenotype. In the future, by deeply correlating the SVs of goats with trait data, it is expected that a complete "genome structural variation-environmental factors-adaptive phenotype" network map will be drawn, providing a valuable example for adaptive evolution research.

5 The Synergistic Effect of HGT and SV and Their Evolutionary Significance

5.1 The interactive effect of horizontal gene transfer and structural variation

Horizontal gene transfer and structural variation are two completely different genomic variation processes, one involving the acquisition of exogenous genes and the other involving the rearrangement of endogenous genomes.

However, in actual evolution, the two are not isolated from each other, but may interact and cooperate with each other. HGT provides "materials" for SV: When an exogenous DNA segment enters the goat genome through HGT, it becomes part of the host genome and undergoes structural variation processes such as replication, deletion, and recombination like other endogenous sequences (Dai et al., 2021). In addition, SV creates conditions for HGT: Certain structural variations can increase the chance of exogenous DNA integration into the genome. Typical examples include large chromosome translocations or breaks that produce double-stranded DNA break ends, which make it easier for viruses or exogenous DNA to insert and integrate (Huang, 2013).

HGT and SV also participate in functional innovation together: sometimes the new traits exhibited by goats are not caused by a single mechanism, but the result of the combined action of HGT and SV. From a global perspective, HGT increases the compositional diversity of the genome, while SV increases the permutation and combination diversity of the genome. The combination of the two makes the goat genome highly plastic, capable of producing a wide range of variations for selection in response to environmental changes or ecological invasions. HGT tends to cause jump-like changes, while SV can bring about gradual accumulation (a little change in the number of copies). The two complement each other, making goat evolution both leapfrogging and fine-tuning.

5.2 The impact of HGT and SV synergy on adaptation and evolution

The synergy of HGT and SV is not only interesting in terms of specific mechanisms, but also has a profound impact on the adaptive evolutionary pattern and potential of goats at a macro level. Synergy improves the efficiency of goat adaptive evolution. Traditional Darwinian evolution relies on the accumulation of small mutations, while HGT+SV can be regarded as a "warp speed engine": HGT skips the gradual change step and directly provides new features, while SV amplifies the scope of influence of new features in a short period of time. Secondly, synergy enriches the innovation and diversity of evolution. HGT provides genetic elements of different systems, and SV produces new combinations through recombination, which actually gives goats the opportunity to explore phenotypic space that "conventional evolution" cannot reach (Bian et al., 2024).

Synergy is reflected in the evolutionary model as intermittent and continuous coexistence (Nakaya and Miyazawa, 2015). When HGT events occur, they often correspond to rapid differentiation or the generation of new branches on the evolutionary tree; in the HGT gap period, SV leads to slow adjustments, and the population optimizes and adapts based on existing traits. From a broader biological evolution perspective, the synergy of HGT and SV highlights the multidimensionality of evolutionary mechanisms.

5.3 The significance and prospects of co-evolution

From the perspective of evolutionary biology, the synergy of HGT and SV in goats has far-reaching significance, which is the best interpretation of the diversity and flexibility of life evolution. As a mammal, goats use HGT methods similar to those common in microorganisms, and cooperate with large genome variations to open up a wider path for themselves. For conservation biology and livestock genetics, this synergy means that the value of genetic diversity is more multi-level. To maintain the diversity of the goat gene pool, we should not only pay attention to allele frequencies, but also pay attention to the richness of structural variations and the retention of exogenous sequences.

This co-evolutionary model also provides a model for other species. Goats are not the only ones. Many wild or cultivated species also show signs of HGT and SV co-evolution (e.g., the rice genome has HGT from bacteria, accompanied by large fragment duplication; cattle have multiple ERV internalizations and CNVs). The study of HGT and SV co-evolution is still in its infancy, and the future is full of unknowns worth exploring. New sequencing technologies such as metagenomic assembly and long-fragment haplotype typing will help us discover more hidden HGT events and complex SVs.

6 Application Prospects and Future Research Directions

6.1 Application prospects in genetic improvement

The understanding of HGT and SV in goat adaptability is not only of academic significance, but also provides new ideas for practical animal husbandry. In terms of goat breed breeding, traditional breeding mainly focuses on quantitative traits and simple SNP markers. Now SV and potential HGT markers can be included in breeding considerations. For example, through whole genome selection (GWAS), it is found that a certain structural variation is strongly correlated with traits such as disease resistance and heat resistance, which can be used as a target for marker-assisted breeding (Yang et al., 2024). Studies have constructed a pan-genome variation database for goats, which includes unique sequences and SVs of different breeds. Breeding experts can use this to select parent combinations with rich genetic diversity to increase the adaptability potential of offspring (Bian et al., 2024).

In addition, genetic engineering methods have opened the door to directly using HGT to inspire genetic improvement. If a species in nature has the stress resistance gene required by goats, HGT can be simulated and introduced into the goat genome through transgenic or gene editing. In terms of the use of structural variation, genome editing (such as CRISPR/Cas9) can precisely copy or delete certain SVs, thereby verifying their functions and applying them to breeding. In the past decade, CRISPR has been used for goat hornless trait editing, disease resistance gene knock-in, etc. It is natural to expand to environmental adaptability traits in the future.

6.2 Development direction of omics technology and detection methods

Future research on goat HGT and SV will greatly benefit from the promotion of emerging omics technologies. Sequencing technology will continue to develop, providing higher quality genome assembly and more sensitive variation detection. Pan-genome and multi-genome comparison will become routine methods. By constructing a pan-genome of goats containing wild populations and different breeds, we can systematically discover various environmental-related sequence variations. Furthermore, artificial intelligence and big data analysis have broad application prospects in HGT/SV research. Machine learning algorithms can be trained to identify exogenous gene patterns and improve the accuracy of HGT prediction (Wijaya et al., 2025).

In addition, multi-omics fusion will provide new ideas for HGT and SV functional verification. Combining genomic variation data with transcriptome, proteome, and metabolome can map the entire path from variation to phenotype. For example, through the joint analysis of eQTL and GWAS, we can find out which SVs significantly affect gene expression and are associated with adaptive traits (Zhang et al., 2024). New technologies will also help conduct ancient DNA and evolution experiments. Through ancient goat DNA sequencing, we can track the time and frequency changes of HGT fragments or SVs in evolution and verify whether they are selected (Bian et al., 2024).

6.3 Multidisciplinary intersection and functional verification

In terms of multidisciplinary intersection, molecular evolution, biochemistry, structural biology, etc. can all contribute. Through molecular evolution analysis, it can be determined whether HGT genes have undergone positive selection in goats, thereby indirectly confirming their functional importance (Verneret et al., 2025). Biochemistry and structural biology can analyze the functional mechanism of a certain HGT protein, such as determining its three-dimensional structure to see if it has a similar effect to the original species (Sun et al., 2015). This helps to understand whether HGT genes have new functions for goats.

Systems biology is also one of the future directions. Taking the entire physiological system of goats as the research object, simulating the impact of different environmental pressures on multiple organs and multiple levels of goats, embedding relevant HGT genes and SV into the system model, and seeing if they can explain adaptive changes. Comparative genomics is still a powerful tool. Goats can be compared with other species that are resistant to extreme environments to find common HGT or SV patterns. For example, compare plateau goats, yaks, plateau deer, etc. to see if they share certain HGT fragments or have similar gene amplifications. Through multidisciplinary bridging, the genetic variation on paper will be connected with the adaptive behavior of living goats, making the understanding of adaptive evolution more full and three-dimensional.

6.4 Prospects for the study of adaptive evolution of goats

In scientific terms, in-depth analysis of the adaptive evolution of goats will enrich evolutionary theory. In terms of application, research progress will help the sustainable development of animal husbandry. In the context of climate change, how to maintain livestock productivity is a global concern. The reason why goats are popular is largely due to their environmental tolerance (Nair et al., 2021). By exploring the "secret weapons" given to goats by HGT and SV, goats can be better utilized to produce in marginal lands and extreme climates to maintain food security.

In conservation biology, goat research can provide reference for wild relatives and rare species. Many wild goats are facing habitat loss and climate pressure. Understanding how goats adapt to the environment will help formulate conservation strategies. In the academic field, goat HGT and SV research will promote interdisciplinary studies. Genetics, evolutionary biology, ecology, agronomy, computational science, etc. will be integrated here to cultivate comprehensive talents and research teams. This is conducive to promoting innovation in the overall life sciences. Goat research may bring inspiration to human medicine, such as new therapies to combat hypoxia and inflammation (Huang et al., 2017).

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Conflict of Interest Disclosure

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

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