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检索报告

根据委托人王靖轩委托, 通过网络检索, 王靖轩发表的 1 篇论文被《科学引文索引》扩展版 (SCI-Expanded) 数据库收录。数据库具体检索结果如下:

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根据委托人王靖轩委托,通过网络检索,王靖轩发表的1篇论文于2025年2月5日网络在线发表。数据库具体检索结果如下:

标题: A functional SNP of the core promoter region within goat C DC25A gene affects litter size

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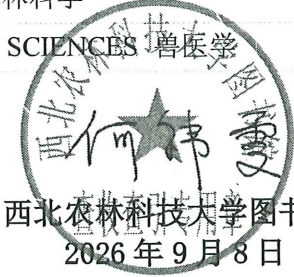
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A functional SNP of the core promoter region within goat *CDC25A* gene affects litter size

Taiyuan Zhang^{1†}, Jingxuan Wang^{1†}, Yangyang Bai¹, Qian Wang¹, Ke Wang¹, Haijing Zhu², Lei Qu², Zhengang Guo³, Chuanying Pan^{1*} and Xianyong Lan^{1*}

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The *Cell division cycle 25A* (*CDC25A*) gene has been considered as a candidate gene associated with reproductive traits for goat breeding. In this study, five truncated fragments divided at position -2285 nt to +198 nt were amplified and cloned into the luciferase reporter vectors to identify the core promoter. The luciferase reporter assay showed that the core promoter of *CDC25A* was located at position -663 nt to -237 nt. Afterwards, a single nucleotide polymorphism (NC_030829.1:g.51731829A > C) at the core promoter was detected using sequencing and KASP in a population of 1,016 goats and luciferase reporter vectors carrying the A allele or C allele were transfected into cells, respectively. The results displayed that the higher relative luciferase activity was observed in plasmids carrying the A allele rather than the C allele. The litter size of individuals with the AA genotype was significantly better than those with other genotypes, which corresponded to increased transcriptional activity in plasmids carrying the A allele. In short, our study provides a potential molecular genetic marker for improving reproductive efficiency in goat breeding.

KEYWORDS

goat, litter size, *CDC25A* gene, promoter activity, SNP, KASP

1 Introduction

For thousands of years, goats (*Capra hircus*) have provided humans with meat, milk, and fiber products. In today's goat industry, improving economic returns through breeding programs remains a key focus. Reproductive traits, as critical phenotypic characteristics, have a significant impact on the economic viability of goat production. However, reproductive traits are quantitative traits with low heritability, and traditional breeding programs have difficulty to improve these traits in a short time. Marker-assisted selection (MAS) is a method based on morphological, biochemical or DNA/RNA makers to select individuals with better phenotypic traits, which is quicker and more effective than traditional breeding programs (1, 2). Using MAS to identify and choose genotypes that enhance fertility can significantly boost reproductive efficiency in goats over a short period.

The *CDC25A* is a dual-specificity phosphatase of the *CDC25* family, which plays a crucial role in the regulation of the eukaryotic cell cycle (3, 4). In reproduction, *CDC25A* plays a crucial role in spermatogenesis, where its decreased expression is linked to infertility and failed sperm retrieval (5). Additionally, overexpression of miR-15b, which targets the 3'-UTR of *CDC25A*, negatively impacts *CDC25A* activity and is vital for proper spermatogenesis (6). In mouse oocytes, downregulation of *CDC25A* leads to the release from metaphase II arrest, demonstrating its importance in maintaining the cell cycle during meiosis (7). Among livestock, the goat *CDC25A* gene shares a closer evolutionary relationship with other species

within the *Bovidae* family (Supplementary Figure S1). Dong et al. (8) found that *CDC25A* showed lower expression levels in cattle-yak (*Bos taurus* × *Bos grunniens*) testis than those in cattle (*Bos taurus*) and yak (*Bos grunniens*), which was considered to correlate the infertility in cattle-yak. The gene expression heat map referring to the Ruminant Genome Database¹ (9) displayed that *CDC25A* showed relatively high expression levels in testis and ovary of goats, which may imply its potential function in reproduction (Supplementary Figure S3). For goat breeding, nucleotide polymorphisms of goat *CDC25A* were considered as potential molecular markers. For instance, an insertion/deletion mutation located in the intron of *CDC25A* has been found to be correlated with goat litter size (10) as well as growth traits (11). In a study by Wang et al. (12), *CDC25A* was identified as a candidate gene underlying strong selection signature with goat body size. Genes in the same family generally have similar structure and functions (13). Wang et al. (2) used whole genome sequencing (WGS) to identify a variant in *CDC25C*, another member of the *CDC25* family, was significantly related to goat litter size. These findings stimulated our interest in exploring the relationship between *CDC25A* and goat reproductive traits.

Most studies in the *CDC25A* gene have been limited to coding region and intron variants that may affect protein function and mRNA splicing, yet polymorphisms within the promoter have been ignored. A promoter is a DNA sequence, which is needed to turn a gene on or off (14). Generally, the promoter region ranges from 2,000 bp upstream to 500 bp downstream of the transcription start site (TSS) in animals (15). The core promoter, including the RNA polymerase binding site and cis-acting elements, etc., plays a crucial role in regulating transcription of the gene (16). Mutations in the core promoter probably alter transcriptional activity and thus affect phenotypic traits. Hence, identifying the core promoter in goat *CDC25A*, scanning the mutation within it, and assessing the correlation of the mutation and reproductive traits are of great significance.

Herein, we identified promoter activity in different truncated fragments of the goat *CDC25A* gene, discovered a novel SNP in the core promoter that affected the transcriptional activity, and analyzed the correlation between the novel SNP and litter size in goat. These findings would provide a potential molecular genetic marker to improve reproductive efficiency in goat breeding.

1 <http://animal.nwsuaf.edu.cn/code/index.php/RGD>

Abbreviations: AOD, Animal Omics Database; CDC25A, Cell division cycle 25A; CDS, coding sequence; CHO-K1 cell, Chinese hamster ovary K1 cell; He, heterozygosity; HEK293T cell, human embryonic kidney 293T cell; Ho, homozygosity; HOXA5, Homeobox A5; MAS, marker-assisted selection; NF-Y, Nuclear Transcription Factor Y; PCR, polymerase chain reaction; PIC, polymorphism information content; POU1F1/POU1F1a, POU Class 1 Homeobox 1/POU Class 1 Homeobox 1a; SBWC goat, Shaanbei white cashmere goat; SNP, single nucleotide polymorphism; TSS, transcription start site; UTR, untranslated region; WGS, whole genome sequencing; KASP, kompetitive allele-specific PCR.

2 Materials and methods

All animal experiments were approved by the Animal Care and Use Committee of Northwest A&F University (protocol No.314020038) and conformed to the animal welfare laws and guidelines in this study.

2.1 Samples and data

A total of 1,016 ear samples of adult female Shaanbei White Cashmere (SBWC) were randomly collected in Yulin city, Shaanxi Province, China (17). All individuals were healthy, mated naturally and kept under the same nutritional and living conditions. In addition, the litter size data for all goats were recorded by the stockmen.

The goat genomic DNA was extracted from tissue samples using a high-salt extraction protocol and then diluted to 10 ng/ μ L-concentration solution, keeping at -40°C (18, 19). The purity and quality of nucleic acid were detected using NanoDrop 1,000 instrument (Thermo Fisher Scientific Inc., America).

2.2 Plasmid construction

Five truncated fragments with different length divided in the -2285 nt ~ +198 nt region (F1: position -2285 nt to +198 nt; F2: position -1176 nt to +198 nt; F3: position -663 nt to +198 nt; F4: position -237 nt to +198 nt; F5: position -115 nt to +198 nt) were amplified and cloned into the pGL3-Basic luciferase reporter vectors using seamless cloning technology, respectively (Takara Bio, Kyoto, Japan) (Figure 1A, Information of primers was shown in Table 1). According to the target transferred fragments, plasmids were named as pGL3-F1, pGL3-F2, pGL3-F3, pGL3-F4 and pGL3-F5. Besides, the luciferase reporter vectors carrying various alleles were constructed according to the protocol described above after scanning the core promoter sequences. Recombinant vectors were used for transient transfection after identification. The pRL-TK vectors were used to normalize the luciferase signal, as the internal reference.

2.3 Cell culture

Chinese hamster ovary K1 (CHO-K1) cells and Human embryonic kidney 293 T (HEK293T) cells were cultured in complete medium consisting of Ham's F 12 nutrient medium (Sangon Biotech, Xi'an, China), 10% fetal bovine serum (Zeta life, America) and 1% penicillin-streptomycin (Gibco, America) at 37°C in a humidified 5% CO_2 atmosphere (20–22).

2.4 Transient transfection and dual-luciferase reporter assay

Before transfection, the cells were seeded into 96-well plates at a density of 5×10^4 cells per well. 100 μ L of complete medium was added to each well and transient transfection was conducted after 12 h. 100 ng of reporter plasmids and 4 ng of transfection

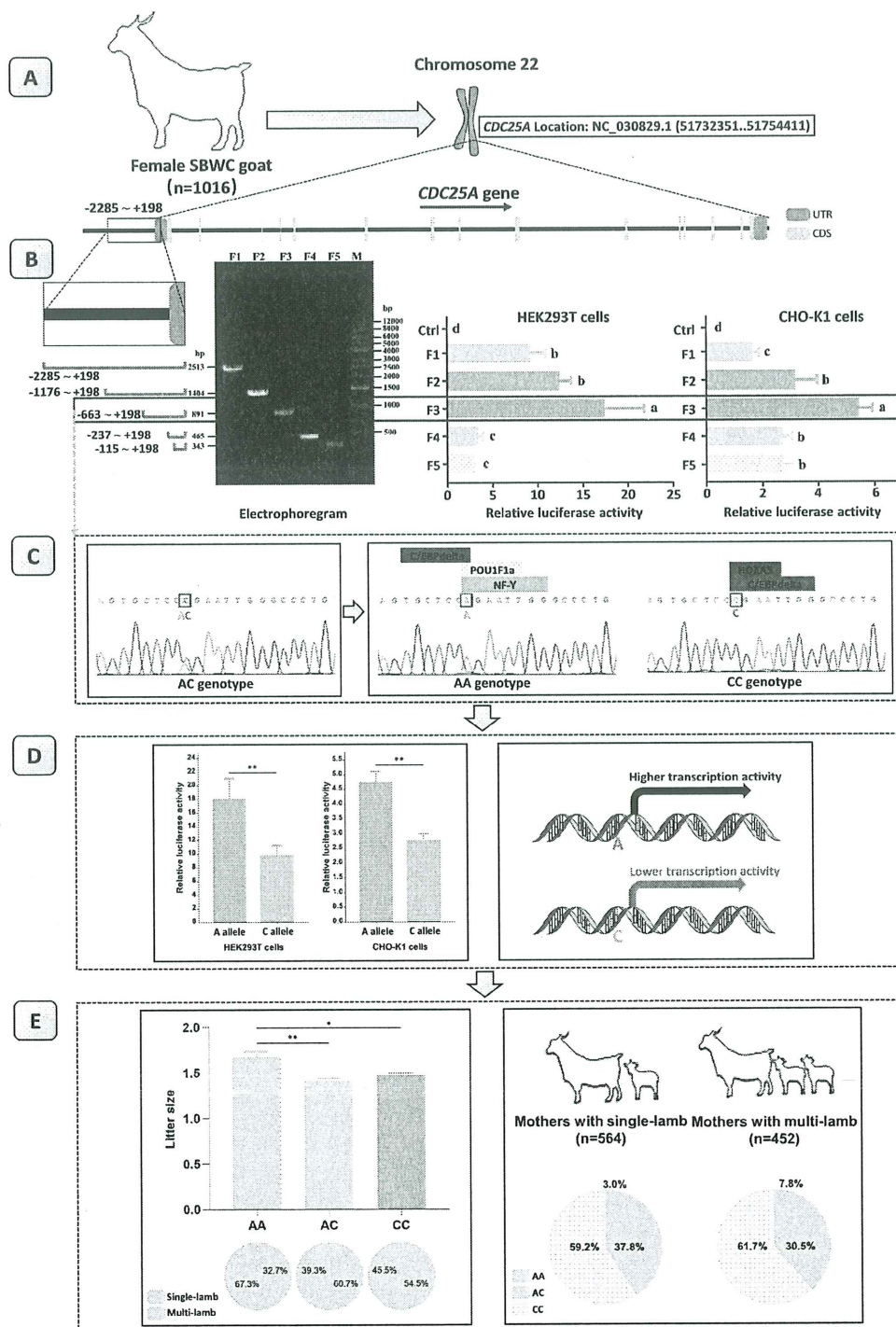


FIGURE 1

Mechanism diagram. (A) The structure patterns of goat *CDC25A* gene. (B) The core promoter of goat *CDC25A* gene was located at position -663 to -237. The electrophoregram on the left displayed that the five fragments were amplified successfully. The bar plots in the middle and on the right displayed the relative luciferase activity of different fragments within *CDC25A* gene promoter detected in HEK293T and CHO-K1 cells, respectively. (C) One novel SNP (NC_030829.1:g.51731829A > C) within the core promoter of goat *CDC25A* gene was found, which might change the binding of transcription factors. (D) The novel SNP significantly affected the transcriptional activity of *CDC25A* gene. (E) Left: associations between the novel SNP and litter size in goat *CDC25A* gene and the proportion of different types of litter size in individuals with AA, AC and CC genotypes. Right: the proportion of AA, AC and CC genotypes in single-lamb and multi-lamb groups. SBWC goat, Shaanbei white cashmere goat; UTR, untranslated region; CDS, coding sequence; ** $p < 0.01$. Bars with different letters (a, b, c, d) means $p < 0.05$.

TABLE 1 Information of primers for goat *CDC25A* gene.

Primer name	Primer sequences (5' → 3')	Product length/bp	Utility
P1	F: <u>ATCTGCGATCTAAGTGGCGAAAAACAGAGGTAGTGGT</u>	2,513	F1 amplification and promoter activity detection
	R: <u>GTAAGAGCTCGGTACCGGCAACCTTAAGATTAAATCCAAACA</u>		
P2	F: <u>TTTCTCTATCGATAGGACAAGTAATTTTCAGGACTGACAGCTG</u>	1,404	F2 amplification and promoter activity detection
	R: <u>GTAAGAGCTCGGTACCGGCAACCTTAAGATTAAATCCAAACA</u>		
P3	F: <u>TTTCTCTATCGATAGCGAGAGAAGGAAATGGTTCTGAG</u>	891	F3 amplification and promoter activity detection
	R: <u>GTAAGAGCTCGGTACCGGCAACCTTAAGATTAAATCCAAACA</u>		
P4	F: <u>TTTCTCTATCGATAGCAGCTGGGAGTTTTCATTGACC</u>	465	F4 amplification and promoter activity detection
	R: <u>GTAAGAGCTCGGTACCGGCAACCTTAAGATTAAATCCAAACA</u>		
P5	F: <u>CCGAGCTCTTACGCGATTGGTTCAGCCTAGCTGCC</u>	343	F5 amplification and promoter activity detection
	R: <u>GTAAGAGCTCGGTACCGGCAACCTTAAGATTAAATCCAAACA</u>		
P6	F: AACGCAGGCCATAGGTTAAG	710	Mutation detection
	R: CAGGGGTCACACTCTCTTC		
	FAM:GAAGGTGACCAAGTTCATGCTACAGGAGCCTCAGTGCTCCA	68	KASP detection
P7	VIC: GAAGGTCGGAGTCAACGGATTACAGGAGCCTCAGTGCTCCC		
	R:TTGCCTCACAACACAGGGC		

f, forward primer; r, reverse primer. The underline indicates the homology arms for seamless cloning. F1, fragment 1 (location-2285 ~ +198); F2, fragment 2 (location-1176 ~ +198); F3, fragment 3 (location-663 ~ +198); F4, fragment 4 (location-237 ~ +198); F5, fragment 5 (location-115 ~ +198).

control plasmids (pRL-TK) to normalize the luciferase signal were co-transfected into CHO-K1 and HEK293T cells with Lipofectamine 2000 (Invitrogen, America). Then cells were cultured for 24 h and a Dual-Luciferase-Assay-System (Promega, Heidelberg, Germany) was employed to monitor luciferase activity (20–22).

2.5 Mutation detection and genotyping

A 25 µL polymerase chain reaction (PCR) system and the Kang's program (21) were used to amplify the target fragments and products were validated by electrophoresis using 1.5% agarose gels stained with GoldView (Zhonghuihecai Biotech, Xi'an, China) (Information of primers was shown in Table 1 and the primer P6 was used to detect the novel mutation). Qualified PCR products were sent to sequencing to detect mutation located in the goat *CDC25A* core promoter (Sangon Biotech, Xi'an, China), which were then compared with variant tables of Ensembl Database² and Animal Omics Database (AOD)³ to search novel nucleotide polymorphisms.

Besides, genotyping was performed with the KASPTM genotyping technology (Kompetitive Allele-Specific PCR assay, FLU-ARMS, Videgene, China), and results were visualized with fluorescence ration PCR instrument (Quant Studio 5, Thermo Fisher Scientific, US). Genotype data for each animal were exported for the statistical analysis.

2.6 Statistical analyses

The frequencies of genotypes and alleles, heterozygosity (He), homozygosity (Ho), and polymorphism information content (PIC) of the mutation were calculated adopting Nei's methods (23). Welch's ANOVA, *Post Hoc* Multiple Comparisons (Tamhane's T2 test) and χ^2 test were used to analyze the correlation between the mutation and litter size. Hardy-Weinberg equilibrium was tested in SHEsis software⁴ (24). The following general linear model of ANOVA was used: $Y_{ijk} = \mu + A_i + G_j + \varepsilon_{ijk}$, where Y_{ijk} is the phenotypic data of litter size of each animal, μ is the mean of population, A_i is the fixed effect of age, G_j is the fixed effect of genotype, and ε_{ijk} is the random error (25).

2.7 Prediction of CpG island and transcription factors

Promoter regions often contains CpG islands (26), which have been linked to promoter activity (27). DNA methylation at CpG islands is crucial for gene transcription and tissue-specific processes (28). Thus, we predicted the CpG islands in the *CDC25A* promoter using the EMBOSS CpGplot software.⁵ Besides, a mutation in the core promoter may affect transcriptional activity by changing transcription factors bound with core promoters (29), and thus potential transcription factors were predicted via the PROMO software⁶ (factors predicted within a dissimilarity margin less or equal than 5%).

2 <http://asia.ensembl.org/index.html>
3 <http://animal.nwsuaf.edu.cn/>

4 <http://analysis.bio-x.cn>
5 https://www.ebi.ac.uk/Tools/seqstats/emboss_cpgplot/
6 http://algggen.lsi.upc.es/cgi-bin/promo_v3/promo/promoinit.cgi?dirDB=TF_8.3

3 Results

3.1 Identification of the goat *CDC25A* gene core promoter

Five truncated *CDC25A* promoter fragments were successfully amplified (Figure 1B) and cloned into luciferase reporter vectors, which were co-transfected with pRL-TK into CHO-K1 and HEK293T cells, respectively. The dual-luciferase reporter assay displayed that the pGL3-F3 vector had significantly stronger luminescence activity than the others in both cell lines ($p < 0.05$) (Figure 1B), suggesting that the core promoter was located at position -663 nt to -237 nt of *CDC25A* gene.

3.2 Detection and genetic parameter analysis of a novel SNP within the goat *CDC25A* core promoter

The core promoter sequences were amplified and sent to sequencing in order to scan the nucleotide polymorphisms among a population of 413 goats. One SNP (NC_030829.1:g.51731829A > C) within the core promoter was identified and three genotypes, AA, AC and CC, were detected, which had never been recorded in the Ensembl Database and AOD (Figure 1C). Then, the nucleotide diversity of the remaining 603 individuals was detected by KASP technique (Supplementary Figure S2). The frequencies of AA, AC and CC were 0.051, 0.346 and 0.603, and the A and C allele frequencies were 0.224 and 0.776, respectively. The genetic parameters were calculated as follows: $H_o = 0.652$, $H_e = 0.348$, $N_e = 1.533$, and $PIC = 0.287$ (Table 2). These observations indicated that the frequency of the novel SNP was high, and it had a moderate level of genetic diversity ($0.25 < PIC < 0.5$). Besides, the mutation is at the Hardy-Weinberg equilibrium in this population ($p = 0.5318$) (Table 2).

3.3 The novel SNP might change the binding of transcription factors

In this study, the CpG islands in promoter and transcription factors bound with the promoter have been predicted. A same CpG island, located at position +96 to +445, and 350 bp in length, was predicted in both alleles and 43% length of the CpG island region was

coincident with the core promoter using the online software EMBOS Cpgplot (Supplementary Figure S4). However, the transcription factors binding at the SNP locus varied between different alleles. Homeobox A5 (HOXA5) was observed to bind to the C allele, and POU Class 1 Homeobox 1 (POU1F1/POU1F1a) and Nuclear Transcription Factor Y (NF-Y) were observed to bind to the A allele.

3.4 The novel SNP significantly affected the transcriptional activity of *CDC25A*

The core promoter can regulate gene expression activity via binding transcription factors. Consequently, a mutation in the core promoter can alter transcriptional activity and then affect phenotypic traits in animals. In order to confirm whether the SNP would affect the transcriptional activity of the *CDC25A* gene, luciferase reporter vectors were constructed. The results demonstrated that the luminescence activity of vectors carrying the A allele was significantly higher than vectors carrying the C allele in both CHO-K1 and HEK293T cells (Figure 1D).

3.5 Correlation between the novel SNP and goat litter size

We examined the relationship between the novel SNP and litter size using Welch's ANOVA, followed by Tamhane's T2 *post hoc* test for multiple comparisons to assess the significance of litter size differences across genotypes. Additionally, the χ^2 test was applied to evaluate differences in genotype distribution among goats with varying litter sizes in the population. The association analysis revealed a significant correlation between the novel SNP and litter size in goats. Individuals with the AA genotype had a higher litter size compared to those with the CC and AC genotypes ($p < 0.05$). Moreover, goats with the AA genotype were more prevalent among mothers with multiple lambs than among those with single lambs ($p < 0.05$) (Table 3, Figure 1E).

4 Discussion

MAS, a modern approach within the field of molecular breeding (30), offers the advantages of high efficiency and precision. It has been

TABLE 2 Genetic parameters of the SNP (NC_030829.1:g.51731829A > C) within *CDC25A* in SBWC goats ($n = 1,016$).

Genotypic frequencies			Allelic frequencies		Population parameters				H
AA	AC	CC	A	C	H_o	H_e	N_e	PIC	
0.051 ($n = 52$)	0.346 ($n = 351$)	0.603 ($n = 613$)	0.224	0.776	0.652	0.348	1.533	0.287	0.5318

H_o , homozygosity; H_e , heterozygosity; N_e , Number of effective alleles; PIC , polymorphism information content.

TABLE 3 Genotype distribution between mothers with single and multi-lamb in SBWC goats.

Types	Sample sizes	Genotypes			Independent χ^2 , (p value)
		AA	AC	CC	
Mothers with single-lamb	564	17	213	334	$\chi^2 = 15.027$, ($p = 0.001$)
Mothers with multi-lamb	452	35	138	279	

applied to enhance reproductive traits and overall productivity in goats (17). The *CDC25A* gene has been demonstrated to be essential for spermatogenesis and oocyte development (5–7, 31) and selected as a candidate gene for goat breeding (2, 10–12, 32). Previous research has demonstrated that mutations in the coding regions and introns of the *CDC25A* gene influence litter size in goats. However, there have been limited studies examining the relationship between promoter polymorphisms and reproductive traits in goats.

We first investigated the regional coverage of the *CDC25A* core promoter. Five truncated fragments with different length located from position –2285 to +198 were amplified and linked to pGL3-Basic plasmids. A dual-luciferase reporter assay was used to detect luminescence activity and the CHO-K1 and HEK293T cell lines were implied for transfection. The results displayed that maximum luminescence activity was observed at the PGL3-F3 vector in both cell lines, suggesting the core promoter of *CDC25A* was located at position –663 to –237 (Figure 1B).

Mutations in gene promoters were demonstrated to alter animal phenotypic traits, including litter size, milk traits, and body measurement traits, etc. (21, 33, 34). In our study, one novel SNP (NC_030829.1:g.51731829A > C) located in the *CDC25A* core promoter was successfully detected among 1,016 goats (Figure 1B). Genetic parameter analysis demonstrated that the frequency of the C allele was higher than the A allele in SBWC breed. Besides, the SNP had a moderate level of genetic diversity and at the Hardy–Weinberg equilibrium ($p = 0.5318$) in this population (Table 2) (17).

A mutation within the core promoter can impact epigenetic processes and alter transcription factor binding. Thus, CpG islands in the promoter and transcription factors bound to the SNP locus were predicted. We found that the mutation did not affect the existence of CpG island but changed the binding of the transcription factors (Supplementary Figure S4). Notably, POU1F1a, a key transcription factor that influences development and growth through direct regulation of pituitary hormone secretion (35), could combine with the A allele rather than the C allele (Figure 1C). The missense mutation within *POU1F1a* has been reported to be strongly related to litter size in goat (25), suggesting that the novel SNP might cause binding changes of important transcription factors and affect growth or reproduction phenotypes in goat.

The changes in transcription factor binding can alter the transcriptional activity of genes (36). Therefore, to investigate whether the SNP influences gene transcriptional activity, vectors containing the A allele and C allele were constructed. The results revealed that the vector with the A allele exhibited significantly higher luminescence activity, confirming that the SNP in the *CDC25A* core promoter affects the gene's transcriptional activity (Figure 1D). Notably, the up or down-regulation of the transcriptional activity of genes could alter phenotypic traits of animals. We found that the litter size of goats with the AA genotype was significantly better than those with the AC or CC genotype, which corresponded to increased transcriptional activity in plasmids carrying the A allele, and amounts of mothers with single/multi-lamb were significantly correlated with genotype frequencies. Goats with the AA genotype accounted for a higher proportion in the multi-lamb population compared with the single-lamb population. It has been indicated that *CDC25A* activity is crucial for both spermatogenesis (5, 6, 31) and oocyte development, particularly during the metaphase II arrest in oocytes (7). Therefore, the SNP may affect the expression of the *CDC25A* gene,

thereby influencing downstream physiological processes, particularly reproductive performance. In summary, the novel SNP within the core promoter of the *CDC25A* gene changed promoter activity and was remarkably associated with litter size in goat.

Our findings would provide a potential molecular genetic marker for improving goat reproductive efficiency. However, more evidences are required to determine whether the correlation between the novel SNP and litter size is direct or indirect.

5 Conclusion

In the present study, the core promoter of the goat *CDC25A* gene was identified and a novel SNP in the core promoter was associated with the litter size presumably by affecting transcriptional activity. The novel SNP locus could be a potential molecular genetic marker to improve goat reproductive efficiency.

Data availability statement

The variant data for this study have been deposited in the European Variation Archive (EVA) at EMBL-EBI under accession number PRJEB84361, <https://www.ebi.ac.uk/eva/?eva-study=PRJEB84361>.

Ethics statement

The animal study was approved by Animal Care and Use Committee of Northwest A&F University. The study was conducted in accordance with the local legislation and institutional requirements.

Author contributions

TZ: Formal analysis, Investigation, Software, Writing – original draft, Writing – review & editing. JW: Formal analysis, Investigation, Software, Writing – original draft, Writing – review & editing. YB: Investigation, Software, Writing – review & editing. QW: Investigation, Software, Writing – review & editing. KW: Software, Writing – review & editing. HZ: Resources, Software, Writing – review & editing. LQ: Funding acquisition, Supervision, Writing – review & editing. ZG: Resources, Software, Writing – review & editing. CP: Conceptualization, Funding acquisition, Project administration, Supervision, Validation, Writing – review & editing. XL: Conceptualization, Data curation, Project administration, Resources, Writing – review & editing.

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Conflict of interest

The authors declare that the research was conducted in the absence of any commercial or financial relationships that could be construed as a potential conflict of interest.

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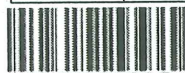
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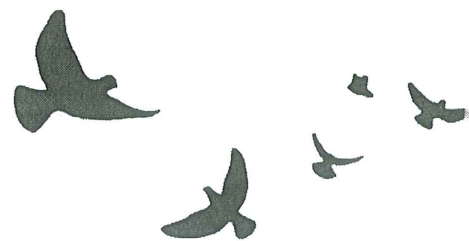


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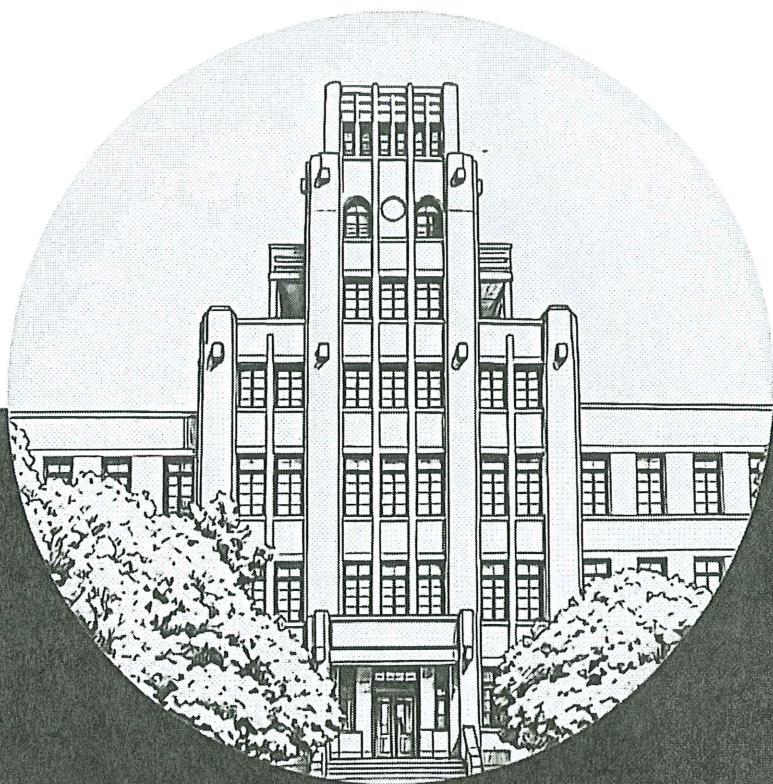
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60 名本科生的保研、考研之路

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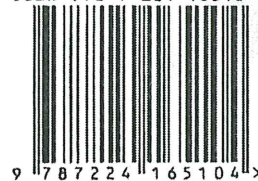
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Article

Investigation of a Rare *CSN1S1*⁰¹ Allele in Goats Using Allele-Specific PCR and Mathematical Expectation Analysis

Jingxuan Wang ^{1,†}, Yuta Yang ^{1,†}, Yuhuan Gao ¹, Ebadu Areb ¹ , Xianyong Lan ¹, Haijing Zhu ² and Chuanying Pan ^{1,*}

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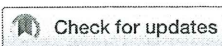
Simple Summary

The *casein alpha s1* (*CSN1S1*) gene is a critical milk protein locus in goats, characterized by extensive genetic polymorphism. The *CSN1S1*⁰¹ allele is a key ‘null’ variant. However, its distribution across diverse breeds and large populations remains unclear. Furthermore, its associations with economic traits have not been fully elucidated. In this study, a cost-effective genotyping approach was employed to screen 2319 goats from 11 Chinese breeds for the *CSN1S1*⁰¹ allele. Our results show that the “1” allele predominates across all populations, whereas the “0” allele occurs at a low frequency, indicating limited genetic diversity at this locus. Association analysis revealed that *CSN1S1*⁰¹ genotypes are significantly correlated with body length, third-parity litter size, and average litter size, specifically in Laoshan dairy goats. This study provides important evidence for the association of *CSN1S1*⁰¹ genetic variation within goat populations.

Abstract

The *casein alpha s1* (*CSN1S1*) gene plays an important role in milk protein synthesis and has been associated with milk quality and calcium-related physiological processes in mammals. To date, 19 *CSN1S1* variants have been reported. Among them, the *CSN1S1*⁰¹ allele has been described as a key “null” variant that may influence goat milk production traits through its effect on *CSN1S1* gene expression. However, the association between this allele and economically important traits in goats remains poorly understood. Therefore, the present study aimed to investigate the *CSN1S1*⁰¹ allele in goats using economical and rapid approaches, including mathematical expectation (ME) analysis and allele-specific PCR (AS-PCR), and to evaluate its association with economic traits in Chinese goat breeds. A total of 2319 goats from 11 breeds were analyzed. Compared with the “0” allele, the “1” allele showed a higher frequency across all populations and exhibited low genetic diversity. Significant associations were detected between *CSN1S1*⁰¹ genotypes and body length, third parity, and average kidding number in Laoshan dairy goats ($p < 0.05$). In addition, the low-frequency distribution of the *CSN1S1* “0” allele was further confirmed. Overall, this study provides population-based association evidence supporting the consideration of *CSN1S1*⁰¹ genetic variation in goat breeding programs.

Keywords: goat *CSN1S1*; AS-PCR; genotyping; mathematical expectation method



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1. Introduction

Casein is a unique phosphoprotein in milk that contains high levels of calcium and phosphorus. In goats (*Capra hircus*), caseins consist of four polypeptide chains: α_{s1} , α_{s2} , β , and κ caseins [1]. The *CSN* genes encoding casein are linked as *CSN1S1-CSN1S2-CSN2-CSN3*, and the gene cluster spans about a 250 kb region on goat chromosome 6 [2,3]. Polymorphisms in these four genes are associated with milk yield and quality traits (fat, protein, and total solids), regulation of milk enzyme activity and edible suitability, body measurement traits, and reproductive traits [4–6].

As we know, the α_{s1} -casein (*CSN1S1*) is one of four caseins synthesized by the lactating mammary gland. The goat *CSN1S1* gene is generally polymorphic; at least 19 *CSN1S1* protein variants have been identified in goats and used for breed characterization, biodiversity, and phylogenetic research. Detailed information on the identified alleles is summarized in Table 1. Most of the mutations contributing to *CSN1S1* allele differentiation have been characterized. The B1 allele is considered the ancestral form and has given rise to two major lineages: type A (A, A2, A3, O1, O2, I, G, and H) and type B (B2, B3, B4, C, E, F, and L) [7]. Previous studies have suggested that interallelic recombination events between type-A and type-B alleles may have contributed to the formation of the *CSN1S1* N and M alleles [8]. Certain alleles, such as the F allele, are distinguished by specific intronic insertions or deletions [9,10]. Molecular approaches including PCR-SSCP have been widely used to identify alleles such as N and F, and previous studies reported associations with milk yield and composition in Chinese dairy goats [11]. The O2 allele has been described as a null allele containing a large insertion that has not yet been fully characterized. In addition, alleles O1 and O2 are called ‘null’ alleles and cause the deficiency of α_{s1} -casein [12]. An 11 bp indel of this gene was associated with litter size and body measurement traits in goats, suggesting a potential link between *CSN1S1* polymorphisms and multiple traits [6,13]. However, the association between different *CSN1S1* alleles and body measurements and reproductive traits of goats has not been reported. The low-frequency *CSN1S1*^{O1} allele of the goat *CSN1S1* gene was mentioned in previous studies, and the mutational origin of this allele is the large deletion of a DNA segment of approximately 8.5 kb, starting from the 181st nucleotide of intron 12 [14]. Although the *CSN1S1*^{O1} allele is considered a null allele and has multiple functions such as goat milk allergenicity [15]. Milk obtained from goats carrying the “null” allele may be more suitable for specific nutritional or dietary purposes, specific transformation technology processes, or for “humanized” milk production [16]. Given the diversity of *CSN1S1* gene functions, its influence on growth and reproductive traits requires further exploration. Previous studies have shown that the polymorphism of the *CSN1S1*^{O1} allele in goat breeds [17]. Thus, we detected this rare mutation in 11 goat breeds by combining the allele-specific polymerase chain reaction method (AS-PCR) and the mathematical expectation (ME) method [18] and explored the relationship between mutation and its association with growth and reproductive traits.

Table 1. Details on the goat *CSN1S1* alleles.

Alleles	Variations	References
A	Glu (77) → Gln	[19]
A2	uncharacterized	NA
A3	uncharacterized	NA
B1	Reference 199 residues	[20]
B2	Leu (16) → pro	[21]
B3	Leu (16) → pro, Arg (100) → Lys	[21]

Table 1. Cont.

Alleles	Variations	References
B4	Leu (16) → pro, Arg (100) → Lys, Thr (195) → Ala	[21]
C	Leu (16) → Pro; Arg (100) → Lys; Thr (195) → Ala; His (8) → Ile	[19]
D	Leu (16) → Pro, deletion 59 to 69	[19]
E	a 457 bp insertion within exon 19 (last untranslated exon)	[22]
F	presence of short insertions of 11 bp (CGTAATGTTTC) (nucleotides 9972–9982) and 3 bp (AAT) (nucleotides 10,639–1042) inside the 9th intron, and by the deletion of 7 bp (TTATCTA) at the 14th intron between the 14,647 and 14,648 nucleotides	[9]
G	Glu (77) → Gln, deletion 14 to 26	[21]
H	Glu (77) → Gln; Arg (1) → Lys	[9]
I	unknown	[23]
L	Leu (16) → Pro; Arg (90) → His	[23]
M	Ser (66) → Leu a single nucleotide transition C → T (nucleotide 23/exon 9)	[23]
N	the deletion of cytosine at the 23rd nucleotide of the 9th exon, without the insertion of 11 and 3 bp in the subsequent intron	[8]
01	the deletion of a DNA segment of about 8.5kb starting from the 181st nucleotide of the intron 12, and including the last 7 exons of the gene	[9]
02	A large insertion, so far uncharacterized	NA

“NA” indicates: Not Available.

In this study, we described an economical and rapid method for analyzing the goat *CSN1S1*⁰¹ allele and found a significant association between different genotypes of the *CSN1S1*⁰¹ allele and goat growth and reproductive traits. Therefore, this study provides population-based association evidence that may inform future investigations into the role of *CSN1S1*⁰¹ genetic variation in goat breeding programs.

2. Materials and Methods

2.1. Samples and Data Collection

In this study, 2319 goats representing 11 breeds were used. Samples of Shaanbei white cashmere goats (SBWC) were collected from Yulin, Shaanxi Province. Guizhou Heima goat (GZHM) and Nubia goat (NG) samples were collected from Guizhou province. Guanzhong (GZ) and Xinong Saanen (SA) dairy goats were collected from Qianyang County in Shaanxi Province. Inner Mongolia white cashmere goats (IMWC) were collected from Ordos City in the Inner Mongolia Autonomous Region. Goats of the same breed were raised and managed under identical conditions, and individuals included in this study were randomly selected. Body measurement traits were recorded following the protocol described by Zhang et al. [24]. Sample collection and storage procedures were performed according to the previously reported method [6].

2.2. DNA Isolation and Primer Design

Genomic DNA was extracted from the collected ear tissue samples using the high-salt extraction method [25]. A Nanodrop 2000 spectrometer (Thermo Fisher Scientific, Waltham, MA, USA) was used to determine the DNA purity and quality. Subsequently double-distilled water was added to dilute the extracted DNA to 20 ng/μL and stored at −20 °C. A set of allele-specific primers was designed based on previously published methods to amplify a region spanning part of exon 12 and the adjacent intron 12 of the goat *CSN1S1* gene, which contains the deletion characteristic of the *CSN1S1*⁰¹ null

allele [17]. The primers used were: goat-*CSN1S1*-AS-a (5'-CCCCAGCTGGTAATGTTTAA-3'), goat-*CSN1S1*-AS-b (5'-GGTCCATCAATTCCCTGTGT-3'), and goat-*CSN1S1*-AS-c (5'-TGTATGGATCCCTGATTCCTTC-3'). The amplified fragment is approximately 249 bp for the *CSN1S1*⁰¹ allele and 281 bp for the reference allele, allowing clear discrimination of homozygous, heterozygous, and reference genotypes. Primer positions relative to the gene structure are illustrated in a schematic diagram. The PCR was performed in a 20 µL reaction mixture containing 2 µL of DNA solution (20 ng) goat genomic DNA (constructed from four different individuals), 10 µL of 2× *Eco Taq* PCR Super mix (Vazyme Biotech Co., Ltd., Nanjing, China; Cat# No. P222-01), 0.6 µL of forward primer, 0.4 µL of reverse primer, and 6.6 µL of double distilled. The protocols for the PCR reaction mixture and amplification conditions used in the present study were based on Yang et al. [26]. A 3.5% agarose gel was used for electrophoresis of the PCR products to identify the indel locus [27].

2.3. Statistical Analysis

Previously reported methods were used to examine the Hardy–Weinberg equilibrium (HWE) and population-genetic parameters, such as homozygosity (*H_o*), effective allele numbers (*N_e*), and polymorphism information content (PIC) [28]. The association between the goat *CSN1S1*⁰¹ allele and economic traits was analyzed using *t*-test on SPSS software (version 24.0). A linear model of the relationship between goat genotypes and each growth trait was constructed using Hui's method [29].

3. Results

3.1. Identification of Indel Variations and Genotyping

The AS-PCR amplification results showed that there were two genotypes in the goat population: the A¹A¹ genotype showed one band (281 bp), and the A¹A⁰ genotypes showed two bands (281 and 249 bp) (Figure 1). However, only the A¹A¹ genotype was detected in IMWC, GB, BJ, MT, GW, SBWC, and NG goats (Table 2).

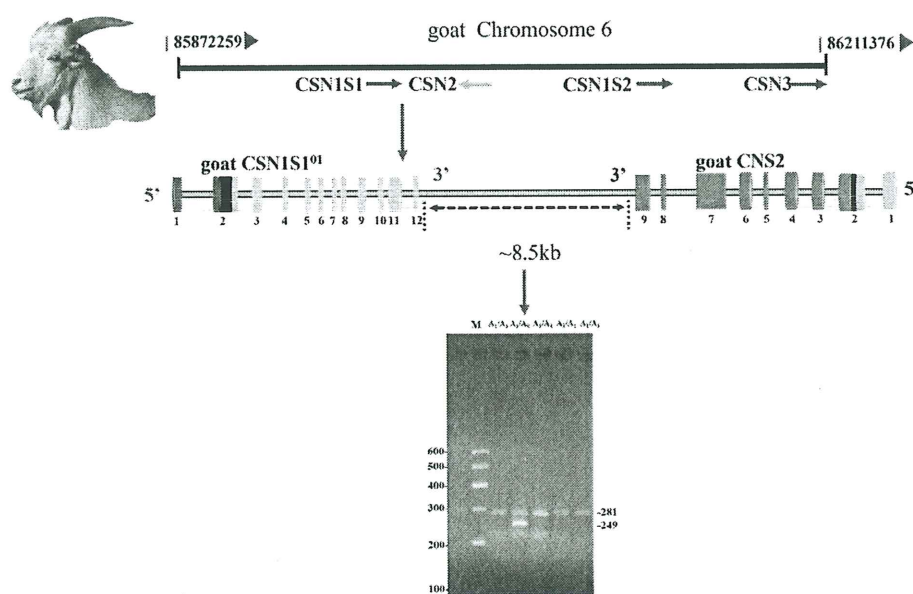


Figure 1. Electrophoresis of AS-PCR products of goat *CSN1S1* gene. Note: Red arrows indicate the transcription orientation of genes, colored boxes represent exonic regions, the blue arrow denotes the deletion locus analyzed in this study, and the dashed line indicates the genomic distance between *CSN1S1* and *CSN2* (~8.5 kb).

Table 2. The population genetic metrics of the *CSN1S1* locus for different populations.

Types	Breeds	A ¹ A ¹ Genotype	A ¹ A ⁰ Genotype	Total	A ¹ A ⁰ Alleles	Ho	He	Ne	PIC	χ ² Value
Cashmere type	IMWC	689	14	703	0.985/0.015	0.969	0.031	1.032	0.03	0.11
	SBWC	1031	0	1031	1.000/0	1	0	1	0	0
Meat type	GZHM	200	1	201	0.995/0.005	0.995	0.005	1.005	0.005	0.001
	NG	69	0	69	1.000/0	1	0	1	0	0
	GZBG	21	0	21	1.000/0	1	0	1	0	0
	BJ	25	0	25	1.000/0	1	0	1	0	0
	MT	22	0	22	1.000/0	1	0	1	0	0
	GW	31	0	31	1.000/0	1	0	1	0	0
Dairy type	Sa	66	8	74	0.946/0.054	0.898	0.102	1.114	0.097	0.24
	LS	76	4	80	0.975/0.025	0.951	0.049	1.051	0.048	0.05
	GZ	60	2	62	0.984/0.016	0.968	0.032	1.033	0.031	0.02

Note: Sa = Saanen dairy goat, LS = Laoshan dairy goat, GZ = Guanzhong dairy goat, IMWC = Inner Mongolia white cashmere goat, GZBG = Guanzhong black goat, BJ = Banjiao goat, MT = matou goat; GW = Guizhou white goat; SBWC = Shaanbei White Cashmere Goat; GZHM = Guizhou heima goat; NG = Nubia goat.

3.2. Genetic Parameter Analysis

The frequency of the A¹ allele ranged between 0.946 and 1.000, and this locus was in Hardy–Weinberg equilibrium in all populations ($p > 0.05$). The genotypic distribution among the 11 goat breeds was determined by calculating the genetic parameters associated with the *CSN1S1*⁰¹ allele, such as genotype and allele frequencies (Table 2). Compared with the “0” allele, the “1” allele had a higher frequency in the 11 goat breeds. Based on the PIC values, this allele showed low genetic diversity in all breeds.

3.3. Association Analysis of Genotypes and Body Measurement Traits

The association between the *CSN1S1*⁰¹ allele and economic traits in Laoshan dairy goats is shown in Tables 3 and 4. The *CSN1S1*⁰¹ allele was highly associated with third parity and average kidding number ($p < 0.05$, Table 3). A doe with A¹A⁰ genotype produces approximately 0.6 more kids per parity (2.25 vs. 1.61) represent a major economic benefit through more replacement stock. Similarly, the *CSN1S1*⁰¹ allele was also associated with body length ($p < 0.05$, Table 4). For all other traits (weight, height, chest, cannon), the A¹A⁰ genotype had numerically higher averages than A¹A¹ but statistically non-significant.

Table 3. Association between different genotypes of the *CSN1S1* gene with litter size (means ± SE) in Laoshan dairy goats.

Fixed Effects	A ¹ A ¹ Genotype (n = 76)	A ¹ A ⁰ Genotype (n = 4)	p-Value
The third parity	1.67 ± 0.10 ^a	2.50 ± 0.29 ^b	0.02
Average	1.61 ± 0.08 ^a	2.25 ± 0.43 ^b	0.05

Note: Different lowercase letters (a, b) indicate significant differences at $p < 0.05$. “The third parity” refers to the number of kids born at the third kidding. “Average” refers to the mean number of kids per kidding.

Table 4. Association between different genotypes of *CSN1S1* gene and goat economic traits (Mean ± SE) in Laoshan dairy goat.

Traits	A ¹ A ¹ Genotype (n = 76)	A ¹ A ⁰ Genotype (n = 4)	p-Values
body weight (kg)	47.30 ± 1.09	51.00 ± 5.00	0.490
body height (cm)	76.05 ± 0.52	80.50 ± 0.50	0.119
body length (cm)	78.29 ± 0.52 ^a	85.50 ± 1.50 ^b	0.014
chest circumference(cm)	79.34 ± 0.52	83.00 ± 0.53	0.215
cannon circumference (cm)	9.63 ± 0.13	10.00 ± 0.12	0.601

Note: Different lowercase letters (a, b) indicate significant differences at $p < 0.05$.

4. Discussion

In this study, the *CSN1S1*⁰¹ polymorphism was systematically characterized across multiple goat populations using AS-PCR and ME methods. Only two genotypes (*A*¹*A*¹ and *A*¹*A*⁰) were detected, and the *A*⁰ allele was observed at a very low frequency and only in a limited number of breeds. This distribution pattern indicates that *CSN1S1*⁰¹ is a low-polymorphism locus in goats, which is consistent with previous reports describing the rarity of the *A*⁰ allele in different geographic and production populations [13,17,30,31].

The investigation of genetic variation in the *CSN1S1* gene and its association with production traits is of considerable interest. Previous studies have demonstrated that polymorphisms in *CSN1S1* are associated with variation in milk casein content as well as milk structure and nutritional properties. To date, ruminants—including cattle, sheep, and goats—remain the primary source of milk for human consumption worldwide, and most studies on *CSN1S1* have therefore focused on these species. In cattle, ten *CSN1S1* protein variants (A, B, C, D, E, F, G, H, I, and J) have been reported, and several alleles have been associated with differences in milk composition traits, such as milk fat percentage and *CSN1S1* content [32,33]. In sheep, seven *CSN1S1* phenotypes (A, B, C, D, E, F, and X) have been identified [34]. Beyond milk composition, *CSN1S1* polymorphisms have also been examined in association studies involving other economically relevant traits in livestock. For instance, *CSN1S1* polymorphisms have been associated with lower yearling weights in cattle [35]. In goats, *CSN1S1* polymorphisms have also been linked to reproductive and growth traits [14,24]. However, the biological basis of these associations remains unclear. Overall, existing evidence indicates that genetic variation at the *CSN1S1* locus is primarily relevant to milk-related traits, while reported associations with non-milk traits should be considered descriptive and population-specific rather than indicative of direct functional effects.

In the present study, we focused specifically on the *CSN1S1*⁰¹ allele across different goat populations. Methods including ME and AS-PCR were established for reliable identification of the 01 allele, and the reported mutation frequency of this allele in other goat populations is summarized in Table 5. Notably, while the frequency of the *CSN1S1*⁰¹ allele varies across breeds, it reaches an exceptionally high level (approximately 70–73%) in Norwegian Dairy goats, significantly impacting milk composition and technological properties [36,37]. Genetic parameter analysis revealed that the *CSN1S1* locus adheres to the Hardy–Weinberg equilibrium (HWE) across all studied populations, with PIC values indicating a low genetic diversity. These results suggest a relatively stable allelic distribution and imply that strong directional selection is unlikely to be acting on this locus. However, the limited polymorphism observed necessitates caution when interpreting downstream association analyses, particularly concerning rare genotypes. Association analysis demonstrated that the *CSN1S1*⁰¹ allele is significantly correlated with the third-parity litter size and body length in Laoshan dairy goats, whereas no significant associations were detected for other morphological traits. Notably, these associations were inconsistent across breeds and traits, highlighting a clear population- and trait-specific pattern. The absence of significant effects on most growth-related parameters suggests that *CSN1S1* polymorphisms do not exert a broad influence on overall body conformation. Reproductive performance and body measurements are complex quantitative traits governed by polygenic inheritance and environmental-management interactions. The parity-specific associations observed here further reflect the complexity of reproductive traits, potentially influenced by sample structure, breeding history, or management practices. Consequently, the identified associations should be interpreted as localized statistical correlations rather than evidence of a universal or direct genetic effect.

Table 5. The allele frequency of the *CSN1S1* locus for the reported populations.

Breeds	Total	A ¹ /A ⁰ Alleles	References
GSB (White shorthaired)	123	0.976/0.024	[12]
	333	0.981/0.019	[12]
BSH (Brown shorthaired)	45	0.989/0.011	[12]
	165	0.985/0.015	[12]
Sarda goats	935	0.999/0.001	[31]
Frisa	70	0.893/0.107	[30]
Orobica	66	0.977/0.023	[30]
Verzasca	67	0.993/0.007	[30]
Camosciata	88	0.9890/0.011	[30]
Neapolitan goats	285	1.000/0	[7]
Alpine breeds	83	0.990/0.010	[38]
Kilis	60	1.000/0	[39]
Sanliurfa	66	1.000/0	[39]
Siirt	55	1.000/0	[39]
Norwegian dairy goat	575	0.263/0.737	[36,37]

From a methodological perspective, this study establishes a practical framework for the detection and population-level screening of the *CSN1S1* allele in goats. The integrated application of AS-PCR and ME methods ensures reliable genotype differentiation across diverse breeds, facilitating future investigations into *CSN1S1* polymorphisms within various genetic backgrounds. However, several limitations must be acknowledged. First, the low frequency of the A⁰ allele constrained the statistical power of our association analyses, particularly in breeds where only the A¹A¹ genotype was present. Second, this study focused on a single locus without integrating functional or expression data. Finally, environmental and management factors, which can influence reproductive performance and growth traits [40], should be considered in future investigations as their potential effects were not explicitly modeled here. These constraints underscore the necessity for further validation in independent cohorts and integrated omics research to fully elucidate the biological significance of *CSN1S1* variations.

In summary, this study systematically characterized the genetic variations in *CSN1S1* across Chinese goat populations and elucidated population-specific associations with key growth and reproductive traits. While these findings are preliminary and descriptive in nature, they expand the current understanding of *CSN1S1* polymorphisms and provide a valuable foundation for subsequent functional validation.

5. Conclusions

AS-PCR and mathematical expectation (ME) methods can be used to rapidly and efficiently detect goat *CSN1S1*⁰¹ allelic mutations. The low-frequency characteristics of the *CSN1S1*⁰¹ allele are universal in the goat breeds. The *CSN1S1*⁰¹ allele shows population- and breed-specific associations with selected growth and reproductive traits in Laoshan dairy goats.

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Institutional Review Board Statement: All animal procedures were conducted in accordance with the national guidelines for the care and use of laboratory animals and were approved by the Institutional Animal Care and Use Committee of Northwest A&F University (IACUC-NWAFU).

Informed Consent Statement: Written informed consent was obtained from the owner of the animals involved in this study.

Data Availability Statement: All data analyzed during this study are available from the corresponding author upon reasonable request.

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Abbreviations

Sa: Saanen dairy goat; LS: Laoshan dairy goat; GZ: Guanzhong dairy goat; IMWC: Inner Mongolia white cashmere goat; GZBG: Guanzhong black goat; BJ: Banjiao goat; MT: matou goat; GW: Guizhou white goat; SBWC: Shaanbei White Cashmere Goat; GZHM: Guizhou Heima goat; AS-PCR: allele-specific polymerase chain reaction; ME: mathematical expectation.

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基于专利计量的山羊产业技术发展态势与创新路径研究

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[摘 要] 研究旨在探讨中国山羊产业专利技术的发展格局、技术优势及创新驱动因素, 以评估其农业科技创新能力与竞争力。通过对全球山羊领域专利进行可视化分析, 系统研究山羊产业的专利布局策略、技术领域及产学研协同机制。研究表明: 中国在山羊相关专利数量上具有显著优势, 技术创新活跃, 尤其在基因育种、智能养殖和分子检测等关键领域持续突破, 其中, 西北农林科技大学发挥了重要的引领和枢纽作用。然而, 国内专利质量与转化率仍待提升, 核心技术与高价值专利存在短板。当前, 中国山羊产业面临技术代际更替与专利竞争挑战, 亟需通过政策引导、科研协同与企业转化加强战略布局和技术路线引导, 推动产业向数字化、精准化和低碳化高质量发展。

[关键词] 山羊产业; 专利创新; 可视化分析; 创新驱动

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专利作为科技创新成果的重要载体, 其蕴含的技术信息与创新线索已成为衡量国家、科研机构以及学科创新能力的关键指标^[1-3]。专利兼具新颖性、创新性和实用性, 是衔接技术研发、学术研究和产业应用的桥梁, 因此, 高质量专利既体现创新价值与转化潜力, 又对国家知识产权战略实施具有重要的实践意义^[4]。研究表明: 跨学科专利的引用强度显著高于单一领域专利^[5], 特别在农业生物领域, 专利布局直观反映产业的技术发展方向和创新活跃度。

专利制度是知识产权体系的核心支柱^[6], 在推动政产学研协同创新中具有枢纽作用。专利分析不仅能追溯技术发展轨迹, 更能前瞻性地识别研究热点、技术迭代趋势和潜在突破点^[7], 对优化创新资源配置具有重要指导意义。高校作为国家创新体系的重要主体之一^[8], 其专利布局直接影响创新效能^[9], 国内外普遍将专利作为衡量学术影响力与技术转化水平的关键指标^[10]。专利布局的质量和密度直接关系到国际话语权, 为此, 《国家知识产权战略纲要》将知识产权人才队伍建设列为重点任务^[11-12], 以满足日益增长的专利运营和保护需求。

中国山羊产业具有显著的规模优势和区域特

色, 存栏量和羊肉产量全球领先, 随着消费升级呈现出科技创新驱动、产业链延伸、绿色可持续发展等新特征。然而, 该领域专利研究仍属空白, 难以系统把握技术发展态势。因此, 本研究通过构建专利分析框架, 系统挖掘全球山羊技术专利数据, 旨在揭示技术演进路径、识别创新热点, 为技术创新、成果转化和科研布局提供数据支撑和决策参考。

1 材料与方法

1.1 数据来源

本研究所分析山羊专利数据来源于 PatYee 壹专利-专利检索分析系统 (<https://www.patyee.com/>), 专利检索式为: TI=(山羊) OR TI_T=(山羊) NOT SS=(山羊草), 专利检索时间为 1949 年 1 月 1 日至 2025 年 3 月 31 日。初始检索获得 5891 条专利数据, 经申请号合并去重后得到 4857 个专利族, 筛选去除不相关专利, 最终获得有效专利 4495 条数据集包含专利号、公开时间、标题、类型、申请人、发明人、专利状态、专利价值度等信息。

1.2 研究方法

根据以下研究技术路线(图 1), 借助 Python、

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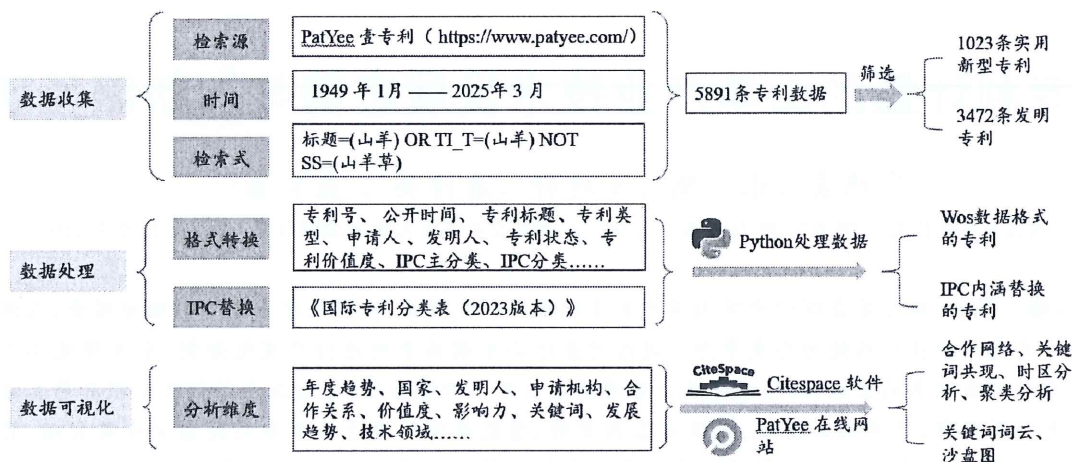


图 1 研究技术路线图

Fig.1 Research technology roadmap

文本聚类软件、Excel 等工具对全球与中国山羊领域专利的发表情况进行可视化分析。

2 结果与分析

2.1 山羊专利总体发展趋势

基于全球专利数据分析发现:1949 年 1 月 1 日至 2025 年 3 月 31 日期间山羊领域公开专利 4495 件,其中发明专利申请 2 365 件,占比 52%,为山羊技术领域的主导类型;发明授权专利 1 107 件,占比

25%;实用新型专利 1023 件,占比 23%。

从专利年度公开数量变化趋势来看(图 2):我国山羊专利整体公开数量呈现稳步增长态势,呈现三个阶段特征:萌芽期(1975—1993):首件专利聚焦乳房炎防治,此后发表较为零星;稳定增长期(1994—2016):2012 年公开量首次突破 100 件,技术积累逐步加深;快速发展期(2017—至今):2017 年出现申请高峰,达 445 件,其中 87%为发明专利,显示该阶段的创新活动主要集中在核心技术突破和知识产权保护的强化。

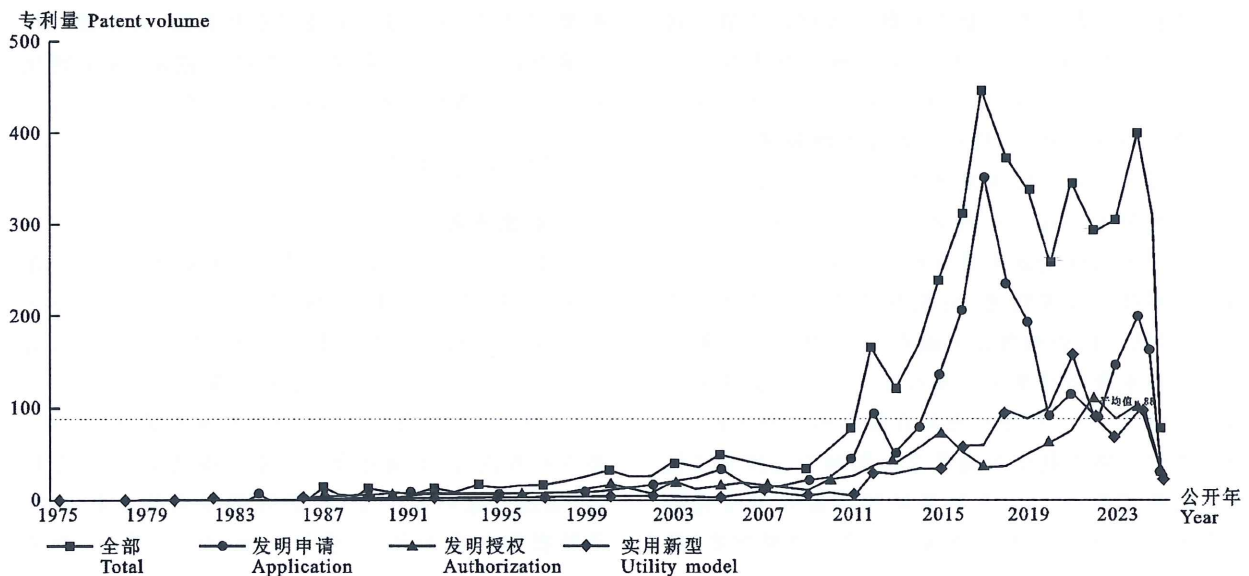


图 2 山羊专利发表量年度趋势

Fig.2 Annual trend of goat patent publications

这一增长趋势主要源于三方面因素的驱动:技术创新与市场需求拉动,科研能力提升,知识产权保护力度持续加强。而 2020 年数据回落可能由于疫情导致科研活动、企业研发和专利申请节奏放缓,同

时专利审查周期(约 18 个月)和数据收录滞后性也是重要影响因素。

2.2 山羊专利申请国家、地区分析

专利的申请地区是指专利权人申请专利保护的

31.78%)位居榜首,其次是福建省农业科学院畜牧兽医研究所、内蒙古农业大学等科研机构,以及合肥合丰牧业等企业,共同构建了“高校引领-院所支撑-企业参与”的创新梯队。这些机构展现了山羊领域的技术创新活跃度、技术集中度及潜在的市场垄断格局。

从技术布局来看,不同机构呈现出多元发展态势(图 6)。西北农林科技大学在专利申请和授权数量上均保持领先,展现出深厚的科研底蕴与学科优势;福建省农业科学院更注重应用导向型技术创新,

实用新型专利占比达 37%,技术集中于养殖设备、饲料配方等实践环节;企业主体如合肥合丰牧业主要聚焦产品加工和疫病防控等产业化应用方向,展现出强烈的市场导向。这种差异化布局形成了从基础研究到产业转化的完整创新链条:高校主导前沿技术突破,科研院所推动技术落地应用,企业实现市场价值转化。这些机构的不同专利策略共同推动着我国山羊产业的技术进步和转型升级,为全球山羊产业的发展提供了中国方案。

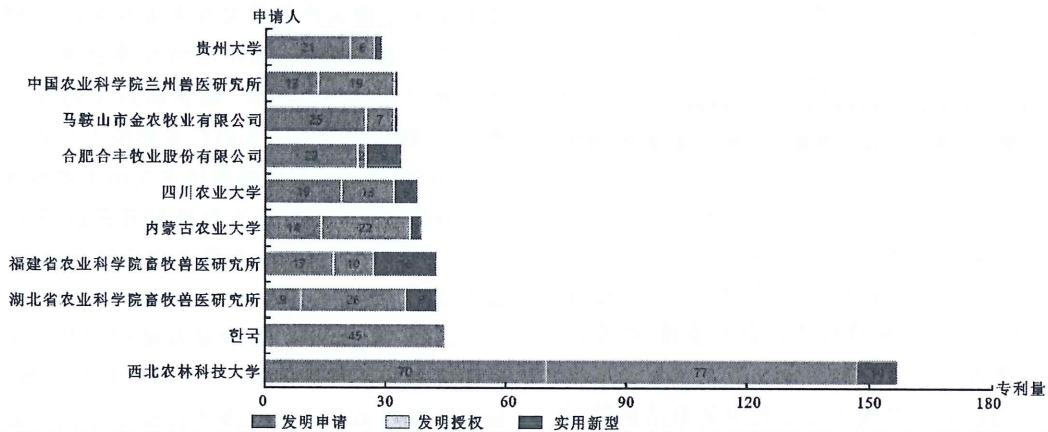


图 6 山羊专利申请量前 10 机构的专利类型

Fig.6 Patent types of the top 10 goat patent applications by organizations

2.4.2 山羊专利申请机构类型与合作关系 山羊专利申请机构类型涵盖高校、企业、科研院所、事业单位及机关团体等多种形式,高校与企业合计超过 60%的专利申请量呈现“双轮驱动”格局(图 7)。我国山羊技术创新具有“产学研”协同发展的区域集群特征,形成陕西(以西北农林科技大学为核心)、内蒙

高质量的技术成果,还通过与企业协同合作,促进科研成果的转化与落地;企业则更关注技术转化、市场导向及产业实施,在技术供给与市场需求之间发挥桥梁作用,使遗传改良等关键技术有效实现市场对接,加速其产品化进程,更快速、高效地服务于生产实践。

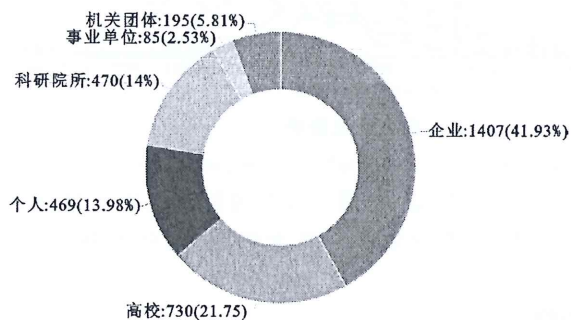


图 7 山羊专利申请人所属机构合作分析

Fig.7 Analysis of the cooperation among institutions of the goat patent applicants

古(内蒙古农业大学牵头)、福建(省农科院主导)三大创新集群。在知识经济时代,以专利为代表的知识产权蕴含巨大经济价值。高校和科研机构作为知识创新的重要主体^[13],凭借其雄厚的科研积累与理论基础,在基础研究和关键技术攻关方面持续输出

这一合作机制不仅为企业带来市场价值,也为高校提供了实践平台与资金支持,推动科研成果的落地与迭代优化。例如,内蒙古农业大学与蒙羊牧业联合持有的绒山羊育种专利实现了高达 280%的转化收益率,成为产学研深度融合的典型实例。

此外,地方特色种质资源(如关中奶山羊、戴云山羊、宜昌山羊等)的丰富性与多样性提高了持续创新的沃土,借助现代生物技术不断提升种质资源的生产性能,增强了山羊研究的深度与广度,形成了从基础研究到产业落地的完整创新链条。随着生物技术与信息技术的深度融合,未来山羊专利技术将朝着智能化、精准化的方向发展,为产业高质量发展提供持续动能。这种创新生态既体现了知识经济的特征,也彰显了我国在山羊育种领域的特色优势。

2.4.3 山羊专利申请机构影响力分析 本研究从引用数量、被引用数量、发明人数量、涉及行业数及

专利有效期五个维度,综合评估了山羊专利发表量前 10 位机构的技术影响力(表 1)。中国农业科学院兰州兽医研究所等单位的引用数量领先,体现突出的技术实用性;福建省农科院等科研机构则凭借高被引专利展现学术引领作用。这种“企业推动产业化-科研机构注入科技活力”的协同格局,体现出我国山羊产业技术创新的产研融合特征。

此外,领先机构普遍具备三大特征:规模化、协同力强的研发团队、跨行业技术渗透以及长效专利

布局(平均有效期 6.99 年)。有效期较长的专利往往具备更高的技术壁垒和持久的市场价值,为企业和科研机构提供了持续的技术支持和竞争优势。这种格局下,企业加速技术产业化应用,科研院所专注前沿突破,形成良性互动。生物育种是国家重大发展战略,我国“十四五”规划和 2035 年远景目标纲要中,明确提出有序推进生物育种产业化应用。随着生物育种产业化进程加速,这种创新模式将持续提升我国山羊种业的国际竞争力。

表 1 山羊前 10 机构影响力分析
Table 1 Impact analysis of the top 10 goat institutions

维度名称 Dimension	西北农林科技大学 Northwest A&F University	福建省农业科学院畜牧兽医研究所 Institute of Animal Husbandry and Veterinary Medicine, Fujian Academy of Agricultural Sciences	湖北省农业科学院畜牧兽医研究所 Institute of Animal Husbandry and Veterinary Medicine, Hubei Academy of Agricultural Sciences	内蒙古农业大学 Inner Mongolia Agricultural University	合肥合丰牧业股份有限公司 Hefei Hefeng Animal Husbandry Co., Ltd.	马鞍山市金农牧业有限公司 Mianshan Jinrong Animal Husbandry Co., Ltd.	中国农业科学院兰州兽医研究所 Lanzhou Veterinary Research Institute, Chinese Academy of Agricultural Sciences	四川农业大学 Sichuan Agricultural University	贵州大学 Guizhou University	内蒙古盛健农牧业工程技术研究有限公司 Inner Mongolia Shengjian Animal Husbandry Engineering Technology Research Co., Ltd.
引用数量 Number of citations	243226	146512	337209	257885	102941	308091	340625	206667	286207	288889
被引用数量 Times cited	0.89032	2.25581	0.23256	0.81579	0.35294	0.75758	1.3125	1.66667	1.41379	0.44444
发明人数量 Number of inventors	667742	562791	108372	726316	197059	145455	76875	533333	641379	57037
涉及行业数 Number of industries involved	202381	2	206977	218421	338235	318182	2375	136667	172014	296236
专利有效期 Patent validity period	6.87178	3.84409	9.42568	14.2782	2.61015	2.73159	9.79426	2.50721	4.6581	13.19

2.5 专利价值度分析

Innography 提出的专利强度(Patent Strength)用于识别核心技术专利并追踪技术发展的前沿动态^[14],得分越高,代表该专利在创新性、市场价值和法律保护等维度上的综合优势越强。对山羊领域专利价值度评估发现(图 8),61.5%的专利价值度集中在 21~40 区间,呈现以 30 为中轴的正态分布趋势,表明行业整体具备一定的技术创新性和初步的市场

应用潜力,处于技术转化初期。少数高价值专利如“山羊支原体肺炎二联灭活疫苗”、“山羊绒制品加工方法”等主要集中在具有关键技术突破和实际应用成效的领域。即当前专利布局呈现“金字塔”结构:底层以实用型技术为主,顶层则聚焦核心领域。这种价值分布格局既反映了现有技术成熟度,也预示着未来随着市场需求升级和技术迭代加速,创新重点将向高壁垒、高附加值领域集中。

2.6 专利技术领域分析

2.6.1 研究领域分析 专利技术主题演化分析的代表性方法包括专利分类法、引文分析法以及文本挖掘法等^[15]。其中,专利分类法通过统计专利分类号(IPC)随时间的变化趋势,识别技术发展的演化路径^[16]。基于 IPC 分类的山羊专利技术主题分析显示,当前研发主要集中于 A 部(2 603 件)和 C 部(1 036 件):畜牧管理(A01K 类)与饲料生产(A23K 类)等基础环节,表明当前山羊技术研发重点集中于畜禽养殖管理优化、新品种培育及饲料加工技术等,对于提升山羊生产效率、动物健康和饲养成本控制

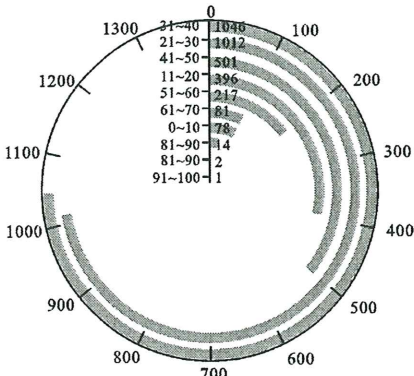


图 8 山羊专利价值度分析
Fig.8 Analysis of goat patent value

利集群优势。

在市场端,消费升级,例如人均羊肉消费量由2010年的3.2 kg提升至2022年的4.8 kg,加速技术创新迭代,如智能饲喂设备专利3年内完成产业化,显著缩短研发周期;抗病育种专利使羔羊成活率从82%提高至94%,大幅提升养殖效益与产业稳定性。并且,中国专利优势与全球最大的山羊养殖规模和消费市场形成正向循环。未来,中国有望进一步强化在全球山羊产业的技术主导权,为全球畜牧业可持续发展提供了重要技术支撑和创新范式。

3.3 技术代际更替下的风险预警

中国山羊领域专利发展面临双重挑战:技术代际更替风险与关键领域短板并存。一是传统技术专利影响力持续下滑,例如表型选择育种专利被引频次年均下降,反映出中国部分传统专利技术在持续创新与市场适配能力上的瓶颈。同时,随着环保政策趋严,粗放饲料类专利申请数量明显减少,体现出政策环境对低效技术的倒逼淘汰作用。二是中国在关键新兴技术领域仍存在短板:CRISPR-Cas9等核心工具类专利主要被美国Broad研究所垄断,养殖机器人、智能感知与算法控制类核心专利中约70%归属德国(Lely公司)和日本(Kubota)企业,凸显出技术壁垒问题。这种结构性风险可能制约产业数字化转型,在技术更替周期不断缩短的大背景下,中国一方面应强化对颠覆性技术(如合成生物学、细胞培养肉等)的全球专利动态监测,防范外部替代技术对传统产业模式的冲击;另一方面应聚焦关键工具技术,推动本土核心技术平台的开发应用,提升在国际科技博弈中的话语权与主动权。

3.4 对策

3.4.1 政府层面:构建制度性保障体系 政府作为科技创新体系中的宏观引导者和制度供给者应重点构建三大机制推动山羊产业专利高质量发展:一是建立国家级山羊技术专利池,借鉴水稻产业联盟的成功经验,通过星级评价体系甄选高价值专利,推动专利高效流转和技术快速落地。二是优化审查流程,在前沿领域设立专利绿色通道,例如山东知识产权保护中心试点将授权周期从22个月压缩至12个月。三是建设全国专利数据库与专利导航系统,设立专项知识产权维权体系,比如2023年某绒山羊核心基因专利侵权案件成功获赔287万元,彰显出法律保护的震慑效力和制度化维权的必要性。未来,通过政府对山羊产业核心专利的引导性扶持,将构建稳定、高效、协同的山羊知识产权体系,为我国山

羊科技产业的高质量发展提供坚实支撑。

3.4.2 科研机构:深化产学研协同创新 科研机构作为农业科技创新的重要源头,应着力推动创新链与产业链深度融合,构建协同高效的产学研一体化创新体系。一是建立联合研发机制,促进科研成果快速转化,例如:四川农业大学动物营养研究所与铁骑力士集团联合将“山羊用复合益生菌制剂”的研发周期从54个月压缩至32个月。二是打破单一专利孤岛化问题,围绕育种-养殖-加工等关键环节,构建系统化、协同化的专利组合布局。例如,西北农林科技大学在选育新品种时同步部署多维度知识产权保护策略,涵盖基因标记、养殖技术以及肉质检测方法专利,实现从品种创新到养殖管理再到产品品质控制的全链条技术覆盖,不仅有效提升了知识产权的系统防护能力,也增强了科技成果的市场竞争力。未来,科研机构应推动跨学科交叉融合,加强与龙头企业的深度战略合作,推动关键核心技术专利的高质量输出与高效转化。

3.4.3 企业层面:专利组合战略实施 企业作为科技成果落地转化和产业化应用的主体,其专利布局不仅直接关系到产品市场竞争力,也决定了其在产业链中的话语权和技術壁垒构建能力。当前,领先企业正积极构建专利组合战略,通过横向与纵向协同布局,形成技术闭环与产业链控制双重优势。例如蒙牛集团的“奶山羊全链条专利链”组合专利布局不仅提升了企业对产业链关键环节的技术控制力,也增强了其在高端市场中的品牌议价能力和国际竞争力。此外,温氏集团的“饲料+设备+数据”三位一体战略协同构建了完整的技术闭环,使企业在山羊智能养殖领域形成强有力的技术壁垒和商业模式护城河,竞争对手难以绕开其核心技术体系,将创新成果沉淀为战略性资产。

4 结 论

本研究基于专利计量系统分析了全球山羊技术专利发展态势,发现当前呈现三大特征:全球山羊专利申请以发明专利为主,中国专利量占比全球领先,产学研协同效应显著。尽管中国在山羊领域技术创新活跃,但技术代际更替背景下仍存在风险隐患,面临国外技术垄断与自主能力不足的问题。未来应进一步强化创新驱动战略,充分发挥政策引导,优化产学研协同机制,短期突破“卡脖子”技术,中期构建全球专利监测系统,长期打造国家级创新平台,形成具有中国特色的“学科-专利-产业”融合创新高地,推

动高价值专利产业化,迈向科技强农的更高阶段。

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Research on the Development Trend and Innovation Path of Goat Industry Based on Patent Metrology

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Abstract: This study aimed to explore the development landscape, technological advantages, and innovation-driving factors of China's goat industry patents, evaluating its agricultural innovation capacity and competitiveness. Through a visual analysis of global patents in the goat sector, this research systematically investigated patent layout strategies, key technological domains, and industry-academia-research collaboration mechanisms. The results revealed that China holds a significant advantage in the quantity of goat-related patents, demonstrating strong innovation activity, particularly in key areas such as genetic breeding, intelligent farming, and molecular diagnostics. Northwest A&F University has played a pivotal leading and bridging role in this field. However, challenges remain in patent quality and commercialization rates, with gaps in core technologies and high-value patents. Currently, China's goat industry faces challenges related to technological generational shifts and patent competition, necessitating strategic policy guidance, enhanced research collaboration, and enterprise-driven technology transfer to strengthen industrial layout and guide technological roadmaps. This will drive the industry toward digital, precision-based, and low-carbon high-quality development.

Keywords: goat industry; patent innovation; visual analytics; innovation-driven



畜牧科学研究

全球 1992 ~ 2024 年山羊研究发展态势解析

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摘 要:为全面了解国内外山羊研究领域的现状及最新发展趋势,本研究采用文献计量学方法,对 1992~2024 年在 Web of Science 数据库收录的全球山羊研究论文及中国知网(CNKI)数据库中的中文相关论文进行了精准检索与分析。本研究全面解析了国内外山羊研究论文的分布特点,并利用 Excel 2019、GraphPad Prism v5.01 和 VOSviewer 等软件,对 1992~2024 年的文献发表情况进行了可视化分析,重点关注 2017~2019 年(新冠疫情前)、2020~2022 年(新冠疫情期间)、2023~2024 年(疫情后)三个时间阶段的动态变化,分析内容涵盖年度发表文献数量、各国发文情况、研究机构、作者分布、期刊、关键词共现以及研究方向演变等多个维度,并对不同阶段的数据进行了横向与纵向的对比研究。研究结果表明,1992~2024 年中国山羊研究整体处于全球领先地位,总发文量位列全球第一,展现出巨大的发展潜力。全球山羊研究领域 TOP10 学者主要来自中国和美国,其中尤以中国西北农林科技大学和美国兰斯顿大学为代表。全球山羊领域的研究深度与广度显著拓展,国际间的合作交流日益加强。国内山羊研究的学科布局与国际趋势基本保持一致,并逐步形成跨学科、跨领域、多学科交叉融合的发展态势。然而,在新兴学科方向上,中国仍需加大关注与投入,增强研究的创新性与实践应用,进一步提升学术质量,以扩大中国在国际山羊研究领域的影响力。本研究的成果将为提高山羊育种效率、促进农业生产发展及优化产业布局提供理论支持和决策依据。

关键词: 山羊; Web of Science; 中国知网; 文献; 可视化; 引文分析; 文献计量学

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Analysis of the Global Goat Research and Development Trend from 1992 to 2024

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Abstract: In order to comprehensively understand the current status and latest development trends of goat research both domestically and internationally, this study employed bibliometric methods to systematically search and analyze global goat research papers from

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the Web of Science database and Chinese-related papers from the CNKI database spanning the period from 1992 to 2024. The distribution characteristics of these publications were analyzed across multiple dimensions, including the number of annual publications, country-wise publication distribution, research institutions, authors, journals, keyword co-occurrence, and the evolution of research directions. Visual analysis was conducted using Excel 2019, GraphPad Prism v5.01, and VOSviewer, with a focus on dynamic changes across three key time periods: 2017–2019 (pre-COVID-19 pandemic), 2020–2022 (during the pandemic), and 2023–2024 (post-pandemic). The results show that China has maintained a leading position in global goat research, ranking first in total number of publications and demonstrating significant development potential. The top 10 scholars in this field are mainly from China and the United States, notably represented by Northwest A&F University (China) and Langston University (USA). The depth and breadth of goat research have expanded considerably, accompanied by growing international cooperation and academic exchange. The disciplinary structure of goat research in China has become increasingly aligned with global trends and is evolving toward interdisciplinary and multidisciplinary integration. However, in emerging research areas, China still needs to increase investment and focus, enhance innovation and practical application, and further improve academic quality to strengthen its influence in international goat research. The findings of this study provide theoretical support and a decision-making basis for improving goat breeding efficiency, promoting agricultural development, and optimizing industrial layout.

Key words: goat; Web of Science; CNKI; literature analysis; visualization; citation analysis; bibliometrics

畜禽种业是畜牧业发展的根基,是畜牧业核心竞争力的重要体现^[1]。作为现代畜牧业中至关重要的一环,山羊产业在推动畜牧业高质量发展方面发挥着关键作用^[2]。加快山羊育种进程、促进养羊业发展,不仅对畜牧业升级具有深远意义,也对农业农村经济的可持续发展至关重要。山羊起源于多个独立的野生山羊种群,其中野生山羊(*Capra aegagrus*)是其主要祖先。这些山羊在早期农业社会被逐步驯化,并成为最早的家畜之一。山羊因其适应性强、饲养成本低、繁殖能力快、管理要求低、养殖方式灵活,以及产品多样化的特点,广泛分布于全球,形成了丰富的品种资源,并适应了多种生态环境^[3]。

在中国,山羊是畜牧业的重要养殖品种,在衣食住行、医疗保障及国民经济等方面发挥着不可替代

的作用。山羊产业不仅有助于乡村振兴、提高农民收入、优化优质畜产品供给^[4],还为提升人类生活质量提供了有力的物质保障^[5]。此外,山羊凭借其独特的食性和消化特性,在维持草原生态平衡、降低野火风险等生态保护方面也具有重要价值^[6]。当前,中国山羊产业正处于关键的转型升级期,呈现出规模化、集约化、标准化和现代化的发展趋势。新设备、新技术和新理念的不断引入,推动了产业的持续健康发展^[7],并促进了全产业链的不断延伸。然而,随着国民消费水平的提高,山羊相关畜产品的市场需求持续增长,而现有供给仍显不足。因此,深入开展山羊研究,优化优良种质资源,提升高品质山羊肉、奶、绒等产品的供给能力,已成为当前亟待解决的重要任务。

文献计量分析(bibliometric analysis)是一种融合统计学、信息学及数学建模的方法,通过对文献数据的定量统计和特征分析,揭示特定研究领域的发展趋势、研究热点、学术影响力及合作网络,从而为科学研究提供客观、量化的数据支持。其核心分析维度包括文献引用情况、出版趋势、合作网络、关键词共现及主题演化,能够有效追踪学科发展脉络,为科研管理和学术评价提供科学依据^[8]。它不仅帮助学者和科研机构更系统地梳理某一领域的研究进展、技术演变和科研合作模式,从而优化研究布局和资源配置,还在科研管理、政策制定及产业发展等方面发挥着重要作用。此外,文献计量分析能够从海量文献的发展脉络中,敏锐捕捉新兴理论的发展轨迹,为前沿研究提供早期预警,并推动交叉学科的深度融合。目前,该方法已广泛应用于多个学科领域,如生态环境、气候变化、土壤污染分析^[9-11],以及医药卫生^[12-15]、人类生理疾病等生命科学领域。此外,在畜牧业研究中,文献计量分析已被用于奶牛、牦牛、奶绵羊等反刍动物的研究^[16-17],为动物遗传育种、疾病防控及产业优化提供数据支撑。

本文基于 Web of Science 核心合集数据库和中国 CNKI 数据库,运用可视化技术对 1992~2024 年的山羊研究文献进行系统分析,重点关注 2017~2019 年(新冠疫情前)、2020~2022 年(新冠疫情期间)和 2023~2024 年(疫情后)三个阶段的动态变化。分析内容涵盖年度发表文献数量、研究国家(地区)、研究机构、作者、期刊、被引频次、研究方向及关键词等多个维度,以客观揭示研究发展态势、梳理学科演化脉络,并探讨前沿研究热点,以期为中国山羊科学研究提供数据支持和新的研究思路。

1 数据来源与统计方法

1.1 国际研究相关数据

本文所分析的数据来源于 Web of Science 核心合集,该数据库具备数据全面、检索灵活等优势,能够确保检索结果的权威性和覆盖广度。本研究检索式为 $TI=[\text{goat NOT}(\text{"goat grass"} \text{ OR } \text{"Aegilops"})]$ 和 $TI=[\text{goat NOT}(\text{"goat grass"} \text{ OR } \text{"Aegilops"})]\text{ AND CU=China}$,检索时间范围设定为 1992~2024 年,数据来源于 SCI-Expanded 索引。检索结果显示,在全球范围内,共收录 27 888 篇与山羊相关的 SCI 论文,其中中国贡献 3 958 篇。本研究数据检索日期为 2025 年 1 月 12 日。对 1992~2024 年山羊研究的发展趋势系统分析,并将检索结果划分为 3 个关键阶段:2017~2019 年(新冠疫情前)、2020~2022 年(新冠疫情期间)、2023~2024 年(新冠疫情后),本研究通过动态分析各阶段的研究趋势、热点演化及影响因素,并运用 Excel 2019、GraphPad Prism v7.00 和 VOSviewer 等软件对数据进行可视化处理,以直观展现不同时间段的研究变化特征和发展趋势。

1.2 中文研究相关数据

本文对 CNKI 中国期刊全文数据库进行了精准检索,关键词设定为“山羊”且排除“山羊草”,检索时间范围为 1992~2024 年。初步检索共获得 27 056 条学术期刊文献记录。为确保数据的准确性和可信度,剔除了文学、戏剧等非相关领域的文献,最终筛选出 25 874 篇有效文献。同时,为进一步提高研究数据的学术质量,本文将数据筛选范围限定为 EI 来源期刊、CSSCI 来源期刊、CSCD 来源期刊及核心期刊,进行主题词检索,最终筛选得到 6 922 篇文献。在此基础上,本研究对 1992~2024 年的筛选结果按照不同时间阶段进行对比分析,并运用可视化软件

进行数据展示,以直观呈现研究趋势及发展态势。

2 山羊研究领域论文可视化分析

2.1 全球山羊论文数量年度变化趋势

在 Web of Science 平台的 SCIE 数据库中检索到 1992~2024 年,全球共发表山羊相关文献 27 888 篇,其中中国文献 3 958 篇。从全球年度发文总量来看,2007 年和 2018 年的年增长量最高,分别为 59.54% 和 30.65%(图 1)。自 2017 年起,山羊相关论文的产出呈阶梯式上升,并于 2022 年达到了峰值(1 831 篇),此后增长有所放缓。国内发展趋势紧跟国际,特别是 2007 年,国内的年增长率高达 187%,随后出现较大幅度的波动增长趋势,并在 2022 年同样达到峰值(433 篇),这表明山羊产业作为中国养殖业的重点扶持产业,具备可持续的研究价值,并且与国际发展趋势同步。这一变化可能与 2022 年作为实施“十四五”规划的承上启下之年,也与乡村振兴全面展开的关键年份密切相关。政府在促进乡村振兴、加强食品安全、提高农业生产效率等方面提供了更多支持,从而推动了相关研究的增长。同时,随着新冠肺炎疫情防控措施的优化和调整,科研活动逐渐恢复,尤其是在动物健康、疫病防控等领域研究得到了更多关注和资金投入。

2.2 全球山羊研究的 TOP10 国家/地区论文影响力分析

引文分析(citation analysis)作为文献计量学中的一项重要方法,通过对学术文献的引用情况进行分析,评估文献、期刊、作者、机构以及学科领域的学术影响力。本文通过对 1992~2024 年不同国家/地区山羊相关文献发表情况的统计,筛选出了论文发表数量排名前十的国家/地区,并将 1992~2024 年的检索结果进行系统性分析,划分为以下 3 个阶段:2017~2019 年(新冠疫情前)、2020~2022 年(新冠

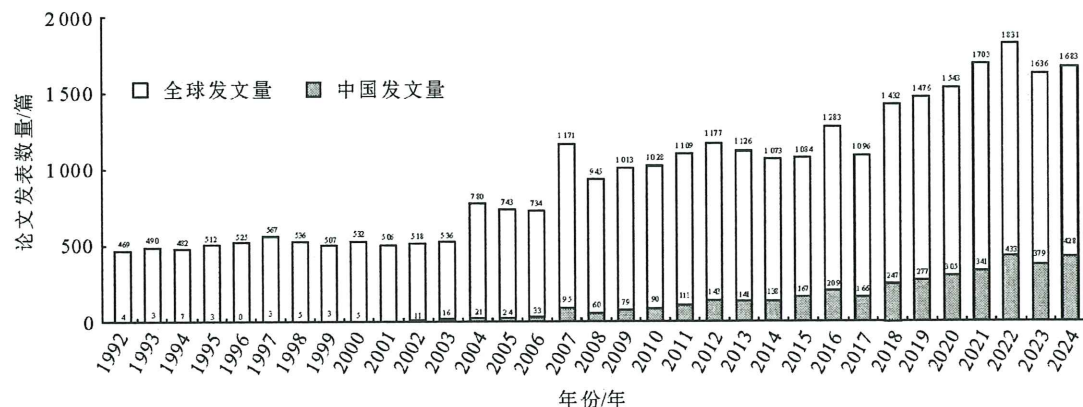


图 1 1992~2024 年国内外山羊研究论文数量的年度变化趋势

Fig.1 Annual trend of the number of goat research papers at home and abroad from 1992 to 2024

疫情期间)、2023~2024 年(疫情后)。同时,选取篇均被引频次作为分析指标,对各国研究的影响力进行综合评价。分析结果表明(表 1):从总发文量来看,1992~2024 年中国的发文量居全球首位,美国位列第二,印度排名第三。巴西和西班牙的论文数量变化相对平稳,处于第二梯队。值得注意的是,大多数国家在 2020 年后维持了较高的发文数量,但中国在 2020~2024 年的发文量已经增至其他国家的三倍左右,显示出中国在山羊研究领域的关注度显著提升,研究进展加速。印度的发文量较之前有所下降,但仍排名第三,其文章的参考价值与质量仍然有待商榷^[18]。尽管法国的发文量排名全球第六,但其篇均被引频次却位居全球第一,达到了 27.95,较 2022 年增长了 0.3。紧随其后的是意大利和西班牙。目前,中国虽然在发文数量上发展迅速,但在篇均被引频次上仅位列第六。由此可见,尽管中国山

羊研究在数量上取得了显著进展,但与全球领跑国家在学术影响力和文章质量上的差距仍需正视。只有在提升研究质量的同时,才能在国际山羊研究领域占据更为重要的话语权。

2.3 山羊研究的 TOP10 机构影响力分析

2.3.1 全球前 10 的研究机构变化趋势 采用相同的统计方法,本文对 1992~2024 年全球发文量排名前十的机构在三个时间阶段的动态变化进行了深入分析,并以总被引频次作为指标进行统计(表 2)。从发文量的角度来看,中国的研究机构在 2020~2024 年迅猛发展,呈现出指数式增长趋势。在总被引频次方面,中国西北农林科技大学(Northwest A&F University)凭借多年的研究积累,以 10 657 次的总被引频次领先其他机构,已成为山羊研究领域的核心力量。自该校畜牧学学科于 2022 年入选“双一流”建设名单以来,学校持续加大对学科建设

表 1 1992 ~ 2024 年山羊研究发文量前 10 的国家/地区发文变化趋势

Table 1 Trends in the top 10 countries/regions in terms of goat research publications from 1992 to 2024

发文量 排名	国家	发文量				篇均被 引频次	篇均被 引排名
		2017~2019	2020~2022	2023~2024	1992~2024		
1	中国	690	1 105	871	3 958	12.74	6
2	美国	447	450	277	3 871	16.52	4
3	印度	288	352	210	3 301	6.41	10
4	巴西	349	399	156	2 172	11.09	7
5	西班牙	233	236	137	2 116	18.78	3
6	法国	115	104	70	1 390	27.95	1
7	意大利	192	200	124	1 376	19.03	2
8	德国	105	126	64	901	15.82	5
9	土耳其	144	177	5	872	10.17	9
10	墨西哥	121	127	74	861	10.79	8

表 2 1992 ~ 2024 年山羊研究发文量前 10 的机构发文变化趋势

Table 2 The trend of the top 10 institutions in goat research from 1992 to 2024

排名	机构	国家	发文量				篇均被 引频次	篇均被引 频次排名
			2017~2019	2020~2022	2023~2024	1992~2024		
1	西北农林科技大学 Northwest A&F University	中国	134	175	120	616	17.30	8
2	Autonomous University of Barcelona	西班牙	21	16	8	130	23.88	1
3	西南大学 Southwest University	中国	17	43	36	126	5.60	10
4	University of California Davis School	美国	9	16	13	124	17.59	6
5	Utrecht University	荷兰	17	13	4	122	22.52	2
6	Vetsuisse Faculty Bern and Zurich	瑞士	17	17	9	120	17.31	7
7	University Putra Malaysia	马来西亚	28	23	7	116	13.64	9
8	Aristotle University of Thessaloniki	希腊	19	17	8	106	19.58	4
9	University of Pretoria	南非	12	12	8	106	20.56	3
10	Norwegian School of Veterinary Science	挪威	5	6	5	105	19.36	5

的投入,强化科研成果的转化与应用,充分发挥畜牧学科优势,进一步提升其在全球山羊研究领域的学术地位。这一系列举措不仅巩固了该校在国内的领先地位,也为中国山羊产业的高质量发展奠定了坚实基础。值得一提的是,中国西南大学(Southwest University)作为近年来的后起之秀,其发文量跻身TOP3,排名第三,显示出中国研究机构逐步领先的趋势,尽管国际上其他国家在山羊研究领域起步较早。此外,西班牙的巴塞罗那自治大学(UAB)发文量位居全球第二,但呈现逐年下降的趋势。法国国家农业研究院(INRA)已退出前十,这一变化与前期的研究结论一致^[18]。此外,前十名机构中有半数机构的山羊领域论文数量有所下降,可能与国家政策的变化及研究投入的优先级调整密切相关。从篇均被引频次来看,西班牙的研究机构在山羊领域的论文被引用频次最高,其次是荷兰,而南非的相关机构排名第三。机构的总被引频次不仅反映了其在山羊研究领域的学术影响力,也标志着其在学术研究方向上的领导地位,引领着山羊研究的发展方向,为全球山羊产业的市场分析及政策制定提供了重要的学术支持和实践参考。这提示各个机构,在增加山羊相关论文数量的同时,也应注重提升论文质量。

2.3.2 国内英文文献发表的研究机构分析 基于1992~2024年国内山羊研究论文发表的机构数据,本文选取了2023年发文量排名前十的机构,并以篇均被引频次作为分析指标。在发文量方面,论文数

量最多的机构分别为西北农林科技大学、中国农业科学院、南京农业大学和中国科学院,其总论文数量依次为932篇、351篇、284篇和237篇。此外,西北农林科技大学在1992~2024年的论文数量超过900篇,是国内发表论文数量最多的机构,并在全球范围内排名第一。在篇均被引频次方面,位居前十的机构中有九所来自农业高校或研究院,这表明在国内山羊研究领域,涉农机构更具学术话语权,且农业科研领域的重点机构对山羊研究起到了重要推动作用。根据篇均被引频次排名,南京农业大学、中国农业科学院和西北农林科技大学分列前三。

2.3.3 国内中文文献发表的研究机构分析 对1992~2024年发表于山羊领域的中文文献进行的研究机构发文量统计分析,结合是否发表于核心期刊的因素,筛选出了以西北农林科技大学为首的十大研究机构,并对其发文情况进行了可视化呈现(表3)。分析结果表明,是否限定为核心期刊发文量基本一致(表4)。其中,西北农林科技大学的发文量最为突出,达到1885篇,是排名第二机构发文量的两倍多,远超其他机构,充分体现了西北农林科技大学在国内山羊研究领域的重要地位与话语权,为中国在全球山羊研究领域的声誉提升做出了显著贡献。与2019年之前相比,西南民族大学在近5年发文量显著提升。此外,通过对发文量排名前五的机构所属地区的观察分析,可以发现,这些地区均有地方特色山羊品种。例如,陕西拥有陕北白绒山羊、关

表 3 1992 ~ 2024 年山羊研究中文发文量排名前 10 的机构

Table 3 The top 10 institutions in terms of the number of Chinese papers published in goat research from 1992 to 2024					
排名	发文量	机构	排名	发文量	机构
1	1 885	西北农林科技大学	6	277	贵州大学
2	786	内蒙古农业大学	7	256	西南民族大学
3	592	南京农业大学	8	245	山东农业大学
4	476	扬州大学	9	232	中国农业大学
5	273	四川农业大学	10	214	河北农业大学

表 4 1992 ~ 2024 年山羊研究中文发文量排名前 10 的机构(核心期刊)

Table 4 Top 10 institutions(core journals) in terms of the number of Chinese published articles in goat research from 1992 to 2024					
排名	发文量	机构	排名	发文量	机构
1	891	西北农林科技大学	6	172	贵州大学
2	355	内蒙古农业大学	7	156	中国农业大学
3	255	南京农业大学	8	122	中国农业科学院北京畜牧兽医研究所
4	222	扬州大学	9	116	四川农业大学
5	179	西南民族大学	10	114	甘肃农业大学

中奶山羊和萨能奶山羊;内蒙古则有内蒙古白绒山羊;江苏拥有南通白山羊和苏北山羊;四川则有川滇山羊、藏山羊和川白山羊等。由此可见,西北农林科技大学在国内山羊研究领域具有较高的话语权,且当地山羊品种的研发和推广,有助于推动相关科研成果的产出。

2.4 山羊研究的 TOP10 作者分析

2.4.1 山羊领域全球英文文献发表的作者分析

以 1992~2024 年山羊研究领域的论文作者为统计数据来源,本研究共统计了 61 294 位国内外相关领域的研究作者,并根据发文量进行排序。在此基础上,优先筛选出发文量前 20 名的作者,并针对作者姓名缩写可能存在重复的情况进行了逐一核对,最终确定发文量排名前十(TOP10)的作者(表 5)。

从作者所属国家来看,发文量排名前十的作者中,7 位来自中国,3 位来自美国。其中,美国的 3 位作者均来自兰斯顿大学(Langston University),而中国的 3 位作者则来自西北农林科技大学(Northwest A&F University)。这一结果表明,西北农林科技大学与兰斯顿大学在山羊研究领域具有较高的学术影响力和研究活跃度。在发文量方面,兰斯顿大学的 GOETSCH AL 和 SAHLU T 位居榜首;紧随其后的是甘肃农业大学的张勇教授在山羊生产性能的遗传改良方面取得了重要进展,特别是在山羊性状遗传与繁殖机制研究方面具有深远影响。此外,西北农林科技大学的罗军教授长期致力于奶山羊研究;陈宏教授在山羊的重要经济性状相关功能基因研究方面取得了进展;蓝贤勇教授专注于反刍

动物(羊等)遗传育种,围绕优异性状形成机理、基因挖掘与开发利用展开深入研究并获得了科学成果,持续助推学科发展。

相比 2020 年之前,中国学者在全球山羊研究中的影响力日益提升。尽管部分知名教授陆续退休,但新生代科研力量源源不断,研究团队规模持续扩展,推动中国在该领域的学术地位稳步提升。此外,从发文量排名来看,美国学者占据前四名,表明美国在山羊研究领域仍处于全球领先地位。这一数据提示中国应进一步集中科研资源,提升高质量文献的产出,加强国际学术合作,以进一步增强中国在全球山羊研究领域的话语权和学术影响力。

2.4.2 全球文献发表的作者共现 本研究绘制了 2017~2024 年山羊研究领域英文论文的作者合作网络图谱(图 2),以分析主要作者及其合作关系。网络分析结果显示,该合作网络由 411 个节点(N=411)、1 090 条连线(E=1 090)构成,整体网络密度

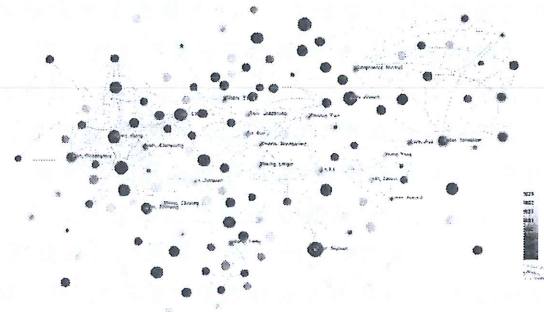


图 2 2017 ~ 2024 年国际山羊研究文献发表作者共现
Fig.2 Authors of international goat research publications from 2017 to 2024

表 5 1992 ~ 2024 年全球山羊研究发文量排名前 10 作者

Table 5 The top 10 authors in the number of global goat research papers from 1992 to 2024

排名	作者	发文量	机构	国家
1	GOETSCH AL	188	Langston University	美国
2	SAHLU T	188	Langston University	美国
3	张勇 ZHANG Y	171	甘肃农业大学 Gansu Agricultural University	中国
4	PUCHALA R	165	Langston University	美国
5	罗军 LUO J	156	西北农林科技大学 Northwest A&F University	中国
6	WANG Y	155	中国科学院-昆明研究所 Chinese Academy of Sciences-Kunming Inst Zool	中国
7	蓝贤勇 LAN XY	143	西北农林科技大学 Northwest A&F University	中国
8	陈宏 CHEN H	139	西北农林科技大学 Northwest A&F University	中国
9	谭支良 TAN ZL	137	Chinese Academy of Sciences	中国
10	WANG ZY	129	首都医科大学-宣武医院 Capital Medical University- Xuanwu Hospital Capital Medical University	中国

(density)为 0.011 2,由多个紧密的合作关系群体组成,并以核心作者为中心形成合作集群。其中,Li Li、Guo Jiazhong、Zhang Hongping、Wang Linjie、Luo Jun、Lan Xianrong、Kaba Jaroslaw、Cao Jiaxue、Zhan Siyuan、Qu Lei、Chen Hong等学者处于网络的核心位置,体现出较强的学术影响力和合作关系。整体来看,多数学者的合作主要集中在团队内部,但近年来跨团队合作的趋势日益增强,呈现出分散性与聚集性并存的特点。核心作者之间整体联系较强,合作关系较为密切,而部分学者的合作相对稀疏,使得整体网络呈现出“大分散、多聚集”的特征。

在合作网络中,Li Li 是关键节点之一,在 2017 年发表论文 70 篇,位居首位,并且多数研究涉及跨团队合作。究其原因,中国学者在山羊研究领域的显著合作表现,主要受以下因素的推动:首先,山羊研究涉及多个学科领域,亟需跨学科合作以应对复杂的研究问题;其次,科研资金与资源的共享促进了跨机构合作,从而提升了研究效率;再者,山羊产业的快速发展对技术创新与应用提出了迫切需求;此外,政府政策鼓励科研团队间的联合攻关,推动了技术成果的转化;最后,现代信息技术的迅猛发展促进了学术交流与合作。

综上所述,近年来中国山羊研究领域的作者间合作日趋紧密,不仅提高了研究效率,也推动了重大科研问题的联合攻关,为学术研究的持续发展奠定了基础。未来,随着跨学科合作与国际合作的深化,中国山羊研究领域有望进一步提升学术影响力,推动行业发展。

2.5 全球山羊领域出版期刊的变化趋势

基于 Web of Science 核心合集数据库对 1992~2024 年山羊研究论文的期刊发表情况进行的统计分析显示,在刊载山羊研究论文的 2 136 种国际期刊中,载文量排名前 10 的期刊累计载文达 7 604

篇,占总文献量的 27.27%(图 3)。其中,排名前三的期刊为《Animals》(瑞士,MDPI)、《Small Ruminant Research》(荷兰,Elsevier)、《Journal of Dairy Science》(美国,Elsevier)。《Animals》尽管创刊较晚,但迅速成为动物学领域的重要开放获取(Open Access,OA)期刊之一,在全球山羊研究领域的载文量排名跃升至第一,可能由于在新冠疫情时期疫情期间提供快速审稿机制,吸引了大量相关研究;开放获取、提升了论文可见度;并且该期刊涵盖多个动物科学领域,尤其聚焦于动物福利、行为学和疾病预防,契合当前研究热点。《Small Ruminant Research》和《Tropical Animal Health and Production》主要关注小型反刍动物(如山羊、绵羊)的生产管理、育种和健康与生产,影响因子均在 2.0 左右,自 2000 年后逐步成为小型反刍动物研究的核心期刊之一。《Journal of Dairy Science》作为历史悠久的高影响因子期刊,在乳业研究的持续发展推动下,逐步增加了对山羊乳及其产品的关注,特别是在动物健康、乳品质、营养价值及技术应用方面具有重要影响,其载文量位列全球山羊研究期刊第三位。而印度出版的期刊的载文量呈下降趋势,其影响因子相对较低,期刊质量亟需提升。综上现象反映了全球范围内不同出版机构在山羊研究领域的影响力差异,同时展现了高质量期刊的竞争格局和研究热点的转移。

综上所述,全球山羊研究领域的核心期刊格局正发生动态变化,开放获取(OA)期刊的影响力持续上升,特别是《Animals》已成为该领域的重要学术传播平台。此外,荷兰和美国的专业期刊仍然保持较强竞争力,而部分国家的传统期刊影响力有所下降。这一趋势表明,未来高影响因子期刊将更加关注山羊研究的前沿方向,如基因育种、精准营养、健康管理和可持续生产,为全球山羊产业的发展提供重要的学术支撑。

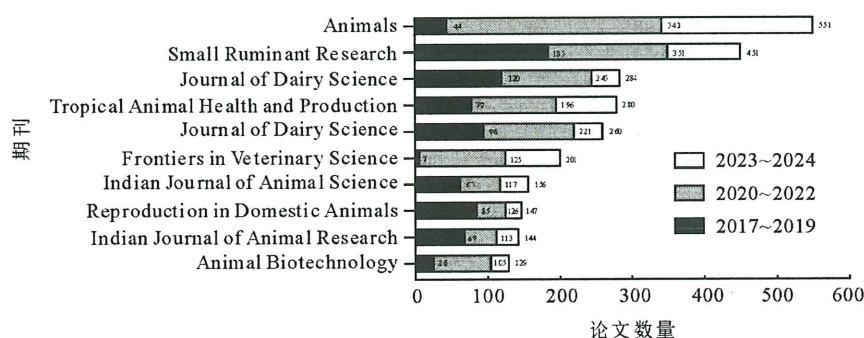


图 3 国际发文量前 10 的期刊各阶段论文数量变化

Fig.3 Changes in the number of papers in the top 10 journals with the largest number of papers published in each stage

2.6 全球山羊前 10 的研究方向的变化趋势

基于 Web of Science 数据库,对 2017~2024 年全球山羊研究领域发文量排名前十的研究方向进行了系统分析,并进一步按时间段划分为 2017~2019 年(新冠疫情前)、2020~2022 年(疫情期)、2023~2024 年(疫情后)三个时间段,动态追踪国内外研究趋势的变化。由于大多数论文具有多学科属性,为确保各阶段数据的可比性,本研究将每个时间段内各领域的学科分类占比标准化为 100%,以便进行后续可视化分析。

从雷达图(图 4)可见,农业相关研究(黄色)在全球及中国均处于核心地位,并随时间推移呈持续增长趋势。至 2023~2024 年,全球农业类研究占比已接近 45%,中国亦保持较高水平。这表明山羊研究仍主要围绕养殖管理、品种改良和生产性能优化等核心农业主题展开,全球对可持续农业的关注度不断提升,呈现出稳步上升的趋势。2020~2024 年间,兽医学研究显著增长,尤其在中国,这一趋势可能源于:国家对动物健康、疫病防控及抗生素替代策略的重视不断提高;饲料添加剂、生物安全及疫苗研发等方面的深入推进;食品科学与相关技术研究亦呈上升趋势,反映出市场对山羊奶、山羊肉及其加工产品的需求增长,促使食品加工、质量控制及安全评估等研究方向持续扩展。尽管全球在遗传学、生物化学及分子生物学等基础学科的研究占比较为稳定,但中国在这些领域的研究占比仍相对较低。近年来,山羊遗传改良、基因组学及分子育种方向已取得一定进展,然而,与全球领先水平相比,仍存在较大差距。未来需要进一步加强精准育种与分子标记

辅助选择(MAS)技术的应用,优化山羊繁殖性能;推进基因组学研究,深化对山羊性状遗传机制的解析,提升中国在该领域的国际竞争力。

此外,雷达图显示,中国在化学、生殖生物学及应用微生物学领域的研究占比仍较低,而全球在这些方向上的发展趋势较为明显,表明这些领域在山羊研究中的重要性日益突出,反映了山羊研究正向多学科交叉融合的趋势发展。其中生殖生物学在提高繁殖效率及解析生殖调控机制方面至关重要,未来可结合分子生物学和基因组学,推动山羊繁殖性能优化。应用微生物学在动物肠道健康、饲料发酵、益生菌研究等方向具有广阔应用前景,而中国在该领域的研究尚未充分展开,仍需加强投入与关注。

整体来看,国内山羊研究在学科布局上逐步紧跟国际趋势,并不断拓展研究方向。全球范围内,山羊研究正朝着多学科交叉融合的方向发展,推动该领域迈向更加精细化、高技术化的阶段。特别是在基因组学、分子生物学和食品科学的驱动下,山羊研究的深度与广度均得到显著扩展,形成了一个跨学科、跨领域的研究网络。未来,随着精准育种、营养调控、生殖调控和食品加工技术的不断优化,中国在全球山羊研究中的影响力有望进一步提升。

2.7 全球山羊领域高频关键词共现

高频关键词指的是在文献中频繁出现的词汇,能够有效反映文章的研究方向和核心内容,精准提炼主题信息并传达研究主旨^[19]。为了深入探索全球山羊研究的热点与发展趋势,本研究利用 VOS-viewer 可视化软件,对 1992~2024 年山羊研究领域的 27 888 篇文献进行关键词共现分析,设定引用频

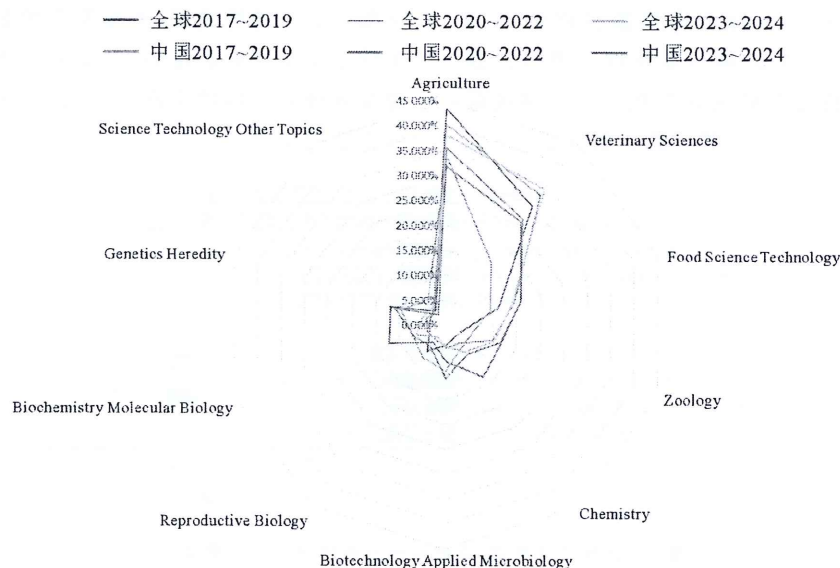
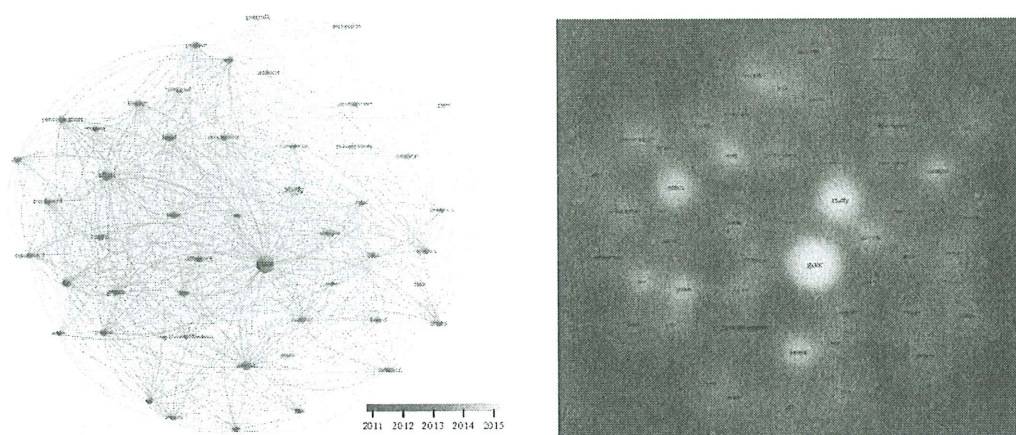


图 4 2017~2024 年国内与国际山羊研究领域热门学科分布

Fig.4 Distribution of popular disciplines in the field of goat research at home and abroad from 2017 to 2024



气泡越大表示被引频次越多;色卡越偏右表示研究更为新颖

图 5 1992 ~ 2024 年全球山羊领域研究关键词分析图共现分析

Fig.5 Co-occurrence analysis of key words in global goat research from 1992 to 2024

次>118 次作为筛选条件,生成关键词共现标签视图(图 5)。

共现分析结果可见,“milk”这一关键词的节点最大,表明山羊产品的功能性与营养价值已成为该领域研究的核心重点。随着消费者对健康与营养的关注不断提升,山羊乳制品的品质、营养成分及健康益处吸引了越来越多的学术关注,进一步推动了技术创新与应用研究的快速发展。除此之外,“treatment”、“gene”、“concentration”、“diet”和“protein”等主题也构成了山羊研究的重要基础,涵盖了营养学、遗传学、繁殖学、疫病防控及动物健康等关键领域。“gene”、“supplementation”、“goat milk”、“PCR”和“isolate”等关键词的高频共现,显示出近年来新兴的研究热点,这一趋势与当前营养科学、遗传育种、分子生物学及生物技术等领域的快速发展高度契合。

通过进一步分析高频关键词所涉及的学科方向,可以验证前述热门学科分析结果的可靠性与全面性。国内外学者的研究方向高度一致,特别是在遗传学、分子生物学和生物技术方面取得了突破性进展。随着基因组学和分子技术的迅猛发展,山羊研究逐渐向遗传改良、疾病防控及功能性食品等领域拓展,逐渐成为新的研究热点。

关键词共现分析不仅揭示了山羊研究的热点主题,还反映出该领域未来的发展趋势。在遗传育种、营养优化、动物健康与食品科学等方向,全球研究格局正不断调整,中国在基因组学应用、精准营养及功能性食品开发等方面的研究仍需进一步强化。未来,交叉学科融合将成为推动山羊研究深化的重要动力,为提升该领域的科技创新与产业化应用提供更多机遇。

3 讨论

文献计量学分析是一种高效的研究方法,广泛应用于揭示特定领域的最新科研动态、研究热点及未来发展方向^[20]。通过分析科学文献的数量与质量,文献计量学能够有效评估该领域的科学技术水平及发展态势。本研究基于 Web of Science 核心合集数据库和 CNKI 数据库,检索 1992~2024 年间的山羊科学研究相关文献,并按照时间节点划分为 2017~2019 年(新冠疫情前)、2020~2022 年(新冠疫情中)、2023~2024 年(新冠疫情后)三个阶段。采用文献计量学和统计学方法,以年发文量、国家、研究机构、作者、研究方向、关键词及被引频次等指标进行动态可视化分析,系统总结研究成果,以揭示 1992~2024 年山羊研究领域的演变趋势及热点方向。

3.1 发文量时序演变特征

全球山羊研究整体呈现出积极发展的态势,自 1990 年代初以来,年度发文量显著增长,逐步迈入上升轨道。特别是中国、美国和印度等国家,在山羊科学研究中始终占据领先地位。本研究发现山羊研究发展过程中的三个关键增长节点:2007 年是基础研究取得突破的重要年份,国际上首个山羊基因组草图的构建为分子育种和功能基因研究奠定了基础,极大地推动了后续遗传改良相关研究的开展;其次,2017 年是山羊遗传改良和疾病抗性研究加速发展的时期,分子生物学与基因组学技术的创新推动了研究热潮;最后,2022 年疫情后科研活动的恢复带来发文量激增。疫情导致发文量的短期抑制,全球科研活动因疫情封锁一度受限,但 2022 年发文量呈现“V 型”反弹,反映出山羊研究具有较强韧性。

2022 年山羊养殖业在全球范围内的市场需求和技术创新达到新高,可能源于三方面因素:一是疫情后科研活动补偿性恢复,随着新冠疫情防控措施的优化,动物健康和疫病防控等方面的研究得到了更多关注与资金支持;二是山羊奶制品因其营养价值和健康功能获得市场关注,激发了以乳品品质、功能性成分和消费者需求为导向的新一轮研究热潮;三是各国对畜牧业稳产保供的政策支持,反映出国家对农业科研的持续投入,尤其是山羊产业作为稳产保供的重要环节,未因疫情中断研究进程。

综上所述,山羊研究的发展历程不仅受到科技进步的推动,也与全球农业政策导向、公共卫生事件及市场需求密切相关。其稳定增长与快速反弹的态势,充分体现了该领域较强的科研韧性和现实需求牵引力。

3.2 国家/地区科研格局分析

从整体趋势来看,2020 年后各国加大了对山羊研究的科研投入,发文量普遍增加。中国以 3958 篇总发文量居全球首位,展现出显著的数量优势,这得益于政策支持如“十四五”规划等对畜牧业的重点部署,为山羊研究提供了坚实保障。美国则在研究质量和影响力方面保持领先,其优势源于完善的科研生态体系。印度等发展中国家发文量增长迅速,显示出较强的发展潜力,但整体研究质量有待提升。疫情后,各国普遍加大科研投入,但呈现出不同的发展模式:中国通过政策驱动实现跨越式增长,美国依托科研体系的韧性维持稳定产出,欧盟国家则更关注动物福利和可持续发展等议题,反映出各国在科研导向和战略重点上的差异。

具体而言,国家政策的出台和国际大事件的发生是驱动山羊研究发展的关键因素。近年来,中国陆续出台了多项支持山羊养殖业升级的政策《畜牧业发展规划(2016—2025 年)》明确提出要推动山羊等小型反刍动物的品种改良和技术提升,倡导科技创新和绿色养殖,推动山羊产业的可持续发展;《农业农村部关于推进畜牧业高质量发展的意见》(2019 年)强调加强基因改良和生态养殖模式的建设,推动山羊养殖品质提升;2021 年发布的《“十四五”畜牧业发展规划》聚焦技术创新和绿色转型,推动山羊产业向现代化、生态化方向发展。这些政策的持续落地,为科研工作提供了明确方向和资金支持,尤其在肉用山羊品种改良与产业转型方面起到显著推动作用。

尽管中国在山羊研究中已取得数量上的领先,但在研究质量和国际学术影响力方面仍存在差距。

与之相比,美国在各阶段均保持高水平产出,研究更具原创性和实践价值。这一优势源于其先进的科研平台、稳定的资金投入、跨学科合作机制以及完善的人才培养体系。为实现从“数量优势”向“质量优势”的转变,中国需进一步优化科研资源配置,提升研究的创新性与国际影响力。一方面,应鼓励开展高水平原创性研究,注重基础理论与应用实践的結合;另一方面,应加强国际合作与跨学科融合,推动科研成果向产业应用转化。唯有如此,中国方能在全球山羊研究领域占据更具影响力的学术地位,为畜牧业的高质量与可持续发展提供坚实支撑。

3.3 机构竞争力评估

在研究机构层面,全球山羊科研呈现出“国内一超多强、国际多极分布”的格局。:西北农林科技大学凭借长期积累和政策支持成为领军机构,农业农村部及中国农业科学院构成第二梯队。西北农林科技大学的成绩既得益于其在畜牧科学方面的长期积淀,也离不开国家与地方在农业科技创新上的持续政策倾斜,尤其在品种选育、种质保护和智能养殖等方面持续发力。在国际范围内,美国加州大学戴维斯分校(UC Davis)、法国国家农业研究院(INRA)等机构在跨学科研究方面表现突出,尤其在基因组学、营养代谢与动物健康交叉领域成果显著。相比之下,中国研究机构虽在承担国家科研项目(如重点研发计划、国家自然科学基金等)方面具有优势,但在国际合作网络构建和高影响力成果产出方面仍存在差距。

近年来,随着国家对山羊产业战略定位的不断提升,国内研究机构获得了大量科研资金支持。“十三五”科技支撑计划、“十四五”畜牧业发展规划等一系列政策的实施,为山羊遗传资源保护、优良品种选育及产业现代化发展提供了强大支撑,进一步推动了山羊产业的现代化和绿色可持续发展。特别是在疫情期间,国家出台的畜牧业稳产保供政策进一步强化了山羊科研投入,尤其在种质资源保护、智慧养殖技术等领域。此外,疫情推动了数字化协作模式的普及,促进了数字技术与智能养殖的深度融合,为国内外研究机构之间的远程合作创造了新机遇。

中国积极推动国际科研合作,与澳大利亚、美国、法国等国家展开深度合作,围绕山羊养殖技术、基因组学研究及疫病防控等关键领域开展联合攻关,有效提升了整体科研水平和国际竞争力。然而,与全球顶尖研究机构相比,中国在科研成果的原创性、论文的国际影响力以及跨国合作的深度与广度方面仍有提升空间。未来,应进一步聚焦高水平原

创性研究,推动重大科研成果的国际发表,加强与全球领先机构的合作交流,从而增强中国在全球山羊研究领域的学术影响力与话语权,助力畜牧业高质量、可持续发展。

3.4 学术共同体特征

聚焦于全球视野,国际学术界在山羊研究领域呈现“西方引领—东方追赶”的态势。美国凭借高水平科研人才的持续涌现及其紧密、高效的科研合作网络,持续产出具有原创性和引领性的研究成果,在山羊基因组学、营养调控、疫病防控等多个关键领域保持全球领先地位,有力推动了全球山羊产业的科技进步。在国内,张勇、罗军、蓝贤勇、陈宏、王永、张涌、朱江江、张燕军、潘传英、林亚秋及屈雷等知名学者在山羊科研领域持续深耕,取得了诸多突破性进展。通过长期系统深入研究,这些学者逐步构建起覆盖遗传育种、营养调控、疫病防治等方向的高效协同网络,推动了中国山羊研究体系的构建与优化,并不断拓展理论深度,为产业发展提供了坚实的科学基础。

尽管如此,中国在跨机构、跨学科、跨国界的科研协作深度尚不足,高水平成果的国际影响力仍待加强。未来需更加注重优质科研资源的统筹配置,加快高水平科研团队的建设与人才培养,推动原创性成果的持续产出,提升科研成果的应用转化效率。同时,应加强与国际顶尖机构和研究团队的深度合作,聚焦山羊遗传改良、疫病防控及生态养殖等关键方向,在解决全球性农业问题中发挥更大作用,提升中国在国际畜牧科研舞台上的影响力。值得注意的是,值得关注的是,疫情期间虚拟学术社区的兴起推动了线上科研合作的普及,合著论文数量显著增长。这一新型科研合作模式正在逐步改变传统协作结构,有望在未来科研实践中发挥更为重要的作用,进一步促进全球科研资源的高效流动与协同创新。

3.5 国际热门期刊发表特征

近年来,新兴期刊的崛起与发展显著加快了科研成果的发表进程,也有效提升了学术论文的可发表性与可见度,成为推动全球山羊研究发文量增长的重要驱动因素。OA 期刊凭借其开放共享特性,加快了科研成果在国际学术界的传播效率,显著增强了论文的学术影响力和引用率^[21]。此外,国际重大事件如新冠肺炎(COVID-19)大流行,不仅影响了全球科研方向,也重塑了山羊研究的期刊分布格局。研究显示,近年来期刊呈现出三大显著趋势:第一,疫情相关研究在 2020~2022 年频繁占据期刊特殊版面,突显动物健康与公共卫生交叉议题的研究

热度;第二,传统研究主题如遗传育种与繁殖技术依然保持稳定的发表节奏,说明该领域的基础研究持续稳健发展;第三,面向新兴交叉学科的研究成果更倾向于发表在综合性或主题拓展性更强的期刊上,反映出研究内容边界的不断拓展。

诸如《Animals》、《Small Ruminant Research》、《Journal of Dairy Science》等期刊在 2000 年后迎来快速发展,其学科定位与山羊研究的增长趋势高度契合,成为该领域成果传播的核心载体。这一现象表明,随着生物技术、动物福利、疫病防控和营养调控等研究方向的深化,科研社区对高质量、国际化学术平台的需求愈加迫切。与此同时,印度出版的期刊在整体学术质量方面仍存在较大提升空间。当前,这些期刊面临质量提升与国际化双重挑战,亟需提升学术标准、拓展研究边界,主动对接全球研究热点,如公共健康、生物安全、环境友好型养殖等交叉领域,以避免边缘化风险。通过强化国际合作、推动高水平同行评审制度以及聚焦可持续发展议题,印度相关期刊有望提升其全球学术竞争力,更有效地参与全球畜牧研究的发展进程。

3.6 学科演进动态

近年来,全球山羊研究正朝着精准化、健康化与可持续化方向发展,呈现出学科交叉融合与研究持续深化的总体趋势。本研究分析识别出当前山羊研究发展的三大转型特征:(1)研究范式由单一农业向“农—医—工”跨学科融合转变:农业科学研究仍占据主导地位,并持续呈现稳步增长态势;兽医学、食品科学技术等学科的参与程度不断提升,尤其是在动物疫病防控和食品安全领域贡献显著。相较之下,遗传学与生物技术尚有进一步发展的空间,而真正实现跨学科深度融合,仍需加强政策引导与科研机制创新。(2)研究方法从经验主导向精准化升级:科研热点正向精准育种、健康养殖及环境可持续性方向拓展。例如精准育种与基因编辑,随着基因组学与生物技术的突破,利用基因编辑(如 CRISPR-Cas9)优化山羊品种,改善生长性能、抗病能力及繁殖效率已成为研究前沿,推动种质改良从传统经验育种向分子层面精准调控转变,显著提升山羊的生产性能、抗病能力与繁殖效率,成为种业创新的核心驱动力。(3)可持续发展理念深度融入研究体系:研究焦点正逐步转向绿色养殖与动物健康管理,例如抗生素替代,全球山羊研究正逐步向减少抗生素使用、疫苗研发、益生菌制剂及植物提取物等方向拓展,体现出动物福利与生态环境双重驱动下的健康养殖新模式。同时,低碳排放与环境友好型

养殖成为全球关注重点,智能化养殖技术、环境调控系统以及减少氨气和温室气体排放的研究不断增加,旨在降低畜牧业对生态系统的负面影响,助力构建可持续发展的绿色畜牧体系。

总体而言,中国在保持农业和兽医学研究优势的同时,应进一步加强前沿科技引领、推动学科交叉协同创新,积极布局基因组育种、智能养殖与绿色养殖等新兴领域,持续提升中国在全球山羊研究体系中的学术话语权与竞争力。

3.7 研究热点变迁

尽管全球各国在山羊研究的论文数量与质量方面存在一定差异,但整体发展态势呈现出一致性,体现为多学科交叉融合、聚焦核心技术与实际应用的趋势。通过关键词演化分析,山羊研究的热点变迁主要呈现以下四大特征:(1)传统核心持续强化:围绕羊奶的研究始终处于该领域的核心地位,形成了涵盖“成分—功能—加工”完整链条的知识体系。同时,“treatment”、“gene”、“concentration”等关键词频繁出现,构建了山羊研究的基础框架,涉及山羊产品的营养成分、功能特性及其对动物健康的影响,反映了学界长期以来对生产性能提升与产品质量优化的持续关注。(2)新兴热点引领跨学科融合:近年来,“gene”、“supplementation”等关键词的显现,标志着研究重心正由传统生产技术向分子精准育种与营养优化转移。这些新兴热点反映出山羊领域正积极引入遗传学、生物技术和现代分子检测方法,以实现更精准的品种改良和健康管理,基因组研究从初期的测序工作逐步深入至功能注释、调控机制和性状关联等层面^[22]。此外,后疫情时期“抗生素替代”、“精准营养”等议题快速升温,突显山羊研究正朝着综合营养学、疫病防控、动物健康与生产等多个学科领域扩展,形成了更为广泛和深入的跨学科融合趋势。(3)向精准与健康导向转型:全球山羊研究正由传统的生产性能提升,转向精准育种、健康管理及分子生物技术的广泛应用。这一变化不仅体现在传统研究热点的延续与深化上,也体现为新兴研究领域的不断拓展,展现出技术驱动与问题导向并重的研究模式。(4)疫病防控优先级显著提升:新冠疫情期间(2020~2022年),与动物健康管理如“vaccine”、“immunity”等频繁出现,人畜共患病防控与生物安全研究引发广泛关注,与全球对公共卫生风险的关注同步。进入后疫情阶段(2023~2024年),研究焦点进一步向“抗生素替代”、“益生菌”等绿色防控技术延申,体现出全球畜牧业对可持续养殖模式的重视。同时,遗传育种(如“gene editing”)与营

养学(如“supplementation”)等传统研究方向保持稳定,未受明显冲击,并更趋于与健康性状(如抗病基因筛选)相结合,呈现出更加紧密的学科融合趋势。

综上所述,山羊研究正在经历由传统向现代、由单一向多元、由粗放向精准的深度转型。未来,随着学科融合程度的不断提高与技术手段的持续创新,山羊研究有望在产品质量提升、动物健康保障与绿色高效生产等方面实现更大突破,从而推动整个领域向更加高质量和可持续的发展方向迈进。

3.8 新冠疫情对山羊科学研究的影响分析

新冠疫情对全球科研格局产生了深远影响,山羊研究领域也经历了从短期冲击到长期转型的过程,主要体现为以下五个方面:(1)科研节奏阶段性调整与恢复性增长。疫情初期,全球科研活动普遍受到限制,实验室关闭、田间试验中断、国际合作推迟,导致部分山羊研究项目进度放缓。然而,随着各国防控政策的优化与远程协作机制的逐步完善,科研活动逐步恢复,并在2022年实现强劲反弹,展现出山羊科研体系良好的韧性与恢复能力。(2)研究主题向动物健康与疫病防控倾斜。疫情突显了动物健康与公共卫生之间的密切关联,激发了对动物疫病防控、生物安全管理及跨种传播机制的广泛关注。在山羊研究中,疫苗研发、抗病品种培育、病原体快速检测等方向快速升温,相关研究成果显著增长,体现出科研热点向“健康优先”导向的明显转移。(3)科研投入与政策支持持续加码。为应对公共卫生挑战,中国等国家加大了农业与畜牧科研的政策扶持与资金投入,重点推动山羊健康养殖、生态养殖等绿色发展方向的技术创新。(4)国际合作形式多样化与开放获取趋势强化。疫情限制了传统线下学术交流,但也加速了线上会议与远程协作机制的发展,降低了跨国合作的门槛,增强了学术交流的灵活性与包容性。同时,开放获取(OA)期刊快速发展,如《Animals》等期刊显著提升了稿件处理效率与研究成果传播速度,有力推动了山羊科研的国际可见度与影响力。(5)研究热点加速转向“精准”与“绿色”。疫情促使全球科研进一步聚焦精准农业与生态农业。在山羊研究中,基因编辑、精准营养、抗应激管理、微生物生态调控等新兴方向快速发展,标志着山羊养殖从传统经验模式加速迈向精准化、智能化与绿色可持续发展路径。

总体来看,尽管新冠疫情在短期内对山羊科研活动造成一定冲击,但其长期效应却加速了研究范式的革新,推动了研究内容、协作机制与成果传播方

式的深度变革。未来,中国应继续发挥政策支持、技术积累与学术资源的综合优势,积极应对全球科研新格局,提升山羊科研质量与国际影响力,为全球畜牧业的绿色可持续发展贡献更多中国智慧。

3.9 未来的发展建议

为了进一步提升中国山羊研究的整体质量与层次,并推动全球山羊研究向更深层次发展,亟需从以下几个方面加大工作力度:(1)强化科研基础与应用技术:需要进一步加强科研基础和应用技术研究,完善论文评价体系,提升期刊质量及对国内学术期刊的扶持力度,从而稳步提高山羊研究的整体水平。中国需从“高产”转向“高质量”,尤其在原创性技术(如 CRISPR 育种)和跨学科融合(如“One Health”框架下的疫病研究)方面对标美国等领先国家。(2)优化产业结构与解决现存瓶颈:当前国内山羊养殖面临地域资源分配不均、畜群结构不合理、优良品种比例偏低、性别比例失衡,这些因素严重制约了行业的可持续发展^[23-24]。同时,基础研究与应用开发投入比例失衡,也限制了包括基因编辑在内的新技术的高效利用,进而影响了产业向高端化与精细化发展的进程。此外疫情期间暴露的产业链断裂风险(如饲料供应中断)提示需加强“研产结合”,例如通过数字化技术(物联网监测)提升养殖韧性。(3)加大资金投入与技术转化:国家应增加对山羊产业的资金支持,特别是在品种改良和饲养管理现代化方面,加快品种改良步伐,提升整体竞争力。科研投入也应进一步加强,推动新技术的推广应用,通过科技创新提高生产力和产业效益。科研人员需与产业界紧密对接,注重技术研发的实践性和可操作性,实现前沿科研成果向实际生产力的高效转化。(4)推动跨学科合作与国际交流:国家应加强政策支持,促进各级科研机构间的合作与资源共享,推动跨学科、跨领域的协同创新,为山羊产业提供坚实的技术保障与发展动力。加强遗传育种与生物技术研究,提升在基因组学、分子标记辅助选择等领域的竞争力;拓展与微生物学、化学、生殖生物学等学科的交叉合作,推动精准养殖与疾病防控技术创新;鼓励国内研究者在《Small Ruminant Research》、《Journal of Dairy Science》等高影响力期刊上发表论文,提升科研成果的国际影响力;并借鉴美、欧、澳等国家在疫病防控、营养调控及基因育种等领域的先进经验,以不断增强中国山羊产业的全球竞争力。后疫情时代需重建国际信任,优先在公共健康关联领域(如人畜共患病预警系统)开展合作,同时提升本土期刊学术标准。(5)市场需求变化的驱动:疫情期间山羊奶

制品因营养健康属性受到关注,推动相关研究(如乳成分优化、功能性产品开发)增长。疫情后,消费者对食品安全的更高要求促使研究向“全产业链追溯”、“低碳养殖”等方向拓展。未来通过科技、政策和产业的多维度协同,中国将逐步破解山羊养殖面临的瓶颈问题,实现产业升级转型,迈向更高质量、更可持续的发展道路。

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