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Book of Abstracts

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Contents

PART 1: Anatomy, Physiology, Welfare	1
1 Feeding and high ambient temperature effects on carbon dioxide and methane emissions in crossbred dairy goats under tropical conditions.....	2
2 Impact of Human Presence on the Cardiac Autonomic Profile of Periparturient Goats: A Biologging Approach.....	3
3 Significant Shifts in Autonomic Nervous System Activity During Parturition in Dairy Goats	4
4 Evaluation of Cardiac Autonomic Response and Welfare in Dairy Goats During Milking via Subcutaneous Biologgers	5
5 Effects of different housing conditions on behaviour and stress in Shiba goats	6
6 Metabolic and productive responses to heat stress in heat-sensitive and heat-tolerant Murciano-Granadina dairy goats	7
7 Effects of microplastics of varying particle sizes on testicular injury in goats (<i>Capra hircus</i>)	8
8 Rumen Microbiome Responses to Heat Stress and their Association with Thermotolerance in Indigenous Goats	9
9 Effect of intramammary infections and dry-off treatment on whole blood haematological profile and leukocytes differential of Alpine dairy goats.....	10
10 Assessing the role of horns in the short-term thermoregulation of lactating dairy goats submitted to heat stress	11
11 Boosting PRRSV-Specific Cellular Immunity Development of an Fc-fused Multi-CTL Epitope Vaccine	12
12 Metabolic and sensor-based stress assessment of milk-fed goat kids transported by road at short-distances and two different densities	13
13 Tolerance and Adaptive Responses of Goats to Saline Drinking Water: Evidence from a Systematic Review.....	14
PART 2: Diseases	15
14 Nationwide investigation of respiratory problems in goat kids in Greece.....	16
15 Lameness in adult goats in Greece: prevalence, predictors, treatment, importance for farmers	17
16 Healthcare Management Practices Adopted by goat Farmers in the Rif region of Northern Morocco	18
17 Inter-scorer reliability of animal-based welfare indicators in subtropical goats	19
18 Development of Nanopore sequencing Nematobiome and mixed amplicon metabarcoding for anthelmintic resistance detection and gastrointestinal nematode species identification in	

European goat herds.....	20
19 Prevalence of helminth infections in the goat population in Poland.....	21
20 Application of nanopore sequencing mixed amplicon metabarcoding for surveillance of benzimidazole resistance in Polish goat herds	23
21 Protective Effects of Lactobacillus Reuteri Isolated from Goats in a Murine Model of Salmonella Infection	25
22 Heat stress induces apoptosis and ferroptosis in goat (<i>Capra hircus</i>) skeletal muscle satellite cells via oxidative stress and disruption of iron homeostasis	26
23 Gastrointestinal strongyles epidemiology in goats in Japan	27
24 Predicting somatic cell count in goat milk using explainable Machine Learning and Deep Learning approaches	28
25 First detection and pathogenicity of caprine kobuvirus and caprine bocaparvovirus in diarrheic goats in Southwest China.....	29
26 Research on portable detection of subclinical mastitis in dairy goats based on Vis-NIR absorption spectroscopy.....	30
27 A type 2 immune circuit and arachidonic acid metabolism role in anti-nematode infection: evidence from transcriptome and targeted metabolome data in goat.....	31
28 Diagnostic performance of a rapid on-farm test for detecting CNS subclinical mastitis in dairy goats	32
29 Epidemiological Surveillance and Clinical Management of High rated infection in Goats under intensive Environment: A Longitudinal Analysis.....	33
30 The Healthier Goats Project: Lessons learned after eliminating CAE, CLA and Paratuberculosis from the Norwegian dairy goat population.....	34
31 An Intelligent Interpretation Method for Brucellosis Rose Bengal Plate Test Based on YOLOv8-CNN Machine Vision Machine Vision.....	35
32 Reflecting on the Journey Towards Peste des Petits Ruminants (PPR) Eradication.....	36
33 Research on Gene-Edited Goats Resistant to Prions.....	37
34 Lactobacillus pentosus W17 alleviates intestinal inflammation and oxidative stress by regulating AEA and the intestinal microbiota.....	38
PART3: Economy, Sociology, Production systems, Housing	39
35 Goat farming: a viable livelihood avenue in semi-arid communal rangelands in KwaZulu-Natal, South Africa	40
36 Dynamics and Management of Extended Lactations in French Dairy Goat Herds: From Reproductive Adjustment to Strategic Choice.....	41
37 Life on the Edge of Changthang: An Overview of Threatened Nomadic Culture of Ladakh	43
38 Effects of grazing and adding supplementary feeding on goats (<i>Capra hircus</i>) and forage	

biomass	44
39 Development of digital tools to support decision-making processes in the dairy goat sector using collaborative methodologies.....	45
40 Integrating the concept of resilience into a decision support tool for dairy goat farming: a methodological proposal	46
41 The China’ s goat milk way: Opportunities and limitations in a growing market	47
42 Effects of Compound Microbial Inoculants on Bacterial Community Succession and Functional Association During Goat Manure Aerobic Composting.....	48
43 The Role of Climate-Induced Hazards in Farmers’ Knowledge and Adoption of Risk-Mitigating Technologies_ Evidence from Low- and High-Risk Goat Farming Areas in India	49
44 Effects of compound lactobacillus plantarum inoculant on maturity, greenhouse gas emissions and microbial community structure of manure composting.....	50
45 Generational Renewal in the Goat Farming Sector through the Andalusian Shepherds’ School (Spain).....	51
46 Non-contact body weight estimation of goats (<i>Capra hircus</i>) using lightweight PointNeXt-S segmentation and hybrid 3D point-cloud phenotyping.....	52
47 Study on the Immunocastration Efficacy of a Novel GnRH Vaccine.....	53
PART 4: Genetics, Selection, Breeds, Genome	54
48 Evaluation of coefficient of variation for different morphometric traits of goat breeds in Kerala.....	55
49 A palaeogenomics investigation of archaeological Caprinae remains from Ethiopia and Eritrea: Challenges and considerations	56
50 Study on Genetic Diversity in Changthangi Cashmere Goats of Ladakh using Microsatellite Marker.....	57
51 Phenotypic and genetic trends for productive variables on Zaraibi Goats	58
52 Association analysis of polymorphic sites in the IGFBP5 promoter region of dairy goats and their lactation traits	59
53 Developmental and Tissue-Specific DNA Methylation Dynamics of the ACSL5 Gene and Their Correlation with Expression in Fuqing Goats	60
54 Integrating genomic selection and reproductive management to Improve breeding efficiency and cashmere quality in superfine cashmere goats	61
55 Can phenotypes enlighten our understanding of goats’ origins? An Example from the Hong Kong goat population.....	62
56 The effect of doe weight on litter size at birth for goats	63
57 Differential Analysis of Reproductive Hormones, Follicle Development and Ovarian Genes in Early Estrus of Yanshan Cashmere Goats with Different Litter Sizes	64

58	Epigenetic Regulatory Mechanism of Hair Follicles in Inner Mongolia Cashmere Goat with Different Coat Types.....	65
59	Integrating Chromosome-Level Genome Assembly and Functional Genomics to Unravel the Regulatory Mechanisms of Milk Fat Synthesis in Dairy Goats.....	66
60	Combined transcriptomic and metabolomic analysis of healthy and atretic follicles in goat	67
61	Functional genomics annotation reveals critical genomic elements associated with mammary gland development in goats	68
62	Population genetic diversity and selection signal analysis of small-boned goat.....	69
63	based on specific-locus amplified fragment sequencing.....	69
64	Extracellular Lactate Promotes Secondary Hair Follicle Stem Cell Proliferation by Modulating H3K9 Lactylation and CLDN1 Expression in Cashmere Goats	70
65	Genetic diversity and signatures of selection in Russian goats (<i>Capra hircus</i>).....	71
66	Estimates of Direct and Maternal Genetic Effects on economic traits in Damascus goats...	72
67	Disruption of lysine demethylase 2A promotes intramuscular fat deposition and unsaturated fatty acids synthesis via the histone H3 lysine 36 dimethylation-peroxisome proliferator-activate	73
68	Construction of a Reference Population for Genomic Selection and Genetic Evaluation in Saanen Dairy Goats.....	74
69	Combining multiomics to analyze the molecular mechanism of underlying the formation of the colorful wool color of the Cashmere Goats	75
70	A Comparative Study on the Fineness Range and Content of Variant Cashmere Hard to Dye and Tickle in Different Breeds Ages and Body Sites of Cashmere Goat	76
71	Global Distribution, Origin and Migration of Cashmere Goat: Diversity of guard hair types and its affect on cashmere trait	77
72	GWAS analysis of lactation traits in dairy goats in the northeast farming region.....	78
73	Research on N-acetylcysteine Alleviating Growth Retardation and Rumen Microecological Disorders Induced by Heat Stress in Goats.....	79
74	An Integrated Machine Learning Framework for Genomic Breed Prediction in Goat and Sheep.....	80
75	Establishment of an inflammatory model of goat small intestinal epithelial cells induced by H ₂ O ₂	82
76	Overexpression of NOG Gene inhibits Intramuscular Adipocyte Differentiation in goat (<i>Capra hircus</i>).....	83
77	PCR Detection of Polled Intersex Syndrome.....	84
78	Integrated Single-Cell Transcriptomic Profiling of Hair Follicle Morphogenesis and Cycling in Cashmere Goats (<i>Capra hircus</i>)	85
79	FAPs-Derived LAMA2 Regulates Myogenic Differentiation and Slow Fiber Specification via DAG1-FAK Signaling in Goats.....	86

80	Revealing the RNA landscape of muscle tissue during critical developmental stages in goats using nanopore direct RNA sequencing.....	87
81	Galectin Network Dynamics Identify LGALS-11 and LGALS-14 as Genetically Relevant Markers of Seasonal Parasite Resistance in Grazing Goats.....	88
82	Deciphering the genetic basis underlying the formation of superior flavor traits in goats based on multi-omics technologies (<i>Capra hircus</i>)	89
83	Genome-Wide Association Analysis of Dorsal Black Stripe Trait in Youzhou Dark Goat .	90
84	Genomics-Assisted Marker-Assisted Breeding for Improving Fiber Quality and Yield in Pashmina Goats.....	91
85	Effects of Genetic Polymorphism of Melanocortin 4 Receptor Gene on Growth and Metabolic Traits, Rumen Microbial Community, and Signal Transduction Mechanism in Goats (<i>Capra hircus</i>)	92
86	Investigating the Regulatory Role of METTL25 in Goat Brown Adipocyte Thermogenesis	93
87	Investigation of the Secondary Follicular Cycle Patterns in Inner Mongolia Cashmere Goats Based on Skin Transcriptome Data.....	94
88	Effects of goat PINK1 gene polymorphisms on ovarian granulosa cell function.....	95
89	Design and Verification of 15K Liquid Chip for Dairy Sheep Selection	96
90	Identification of Coding Circular RNAs Potentially Involved in the Regulation of Follicular Atresia Based on RNA-Seq of Goat Follicles.....	97
91	Methylation of ELF5 gene promoter regulates β -casein synthesis in goats (<i>Capra hircus</i>)	98
92	Integrated Electronic Nose, Metabolomics and Mammary Proteomics Reveal the Metabolic Basis of Flavor Differences among Goat, Sheep and Cow Milk	99
93	Differences in Amino Acid Composition Among Skeletal Muscles from Different Anatomical Sites in Goats and the Role of Ornithine in Muscle Fiber Differentiation	100
94	Association between a novel CSN1S1-CSN2 haplotype and milk composition in the Carpathian goat breed	101
95	Effects of AAV-Mediated METTL25 Overexpression on Thermogenesis in Goat Brown Adipose Tissue.....	102
96	Multi-omics profiling of chromatin accessibility and H3K27ac reveals super-enhancer-mediated regulatory networks governing endometrial receptivity in goats	103
97	A multi-tissue atlas of allele-specific expression reveals tissue-dependent cis-regulatory variation in goats.....	104
98	Mechanism of H3K18 Lactylation Regulates Myoblast Differentiation via the ATP5H/AMPK Axis in Goat	105
99	Genome-wide association study and selection signature analysis identify genetic loci and candidate genes associated with the beard trait in goats	106

PART 5: Meat Production..... 107

- 100 Integrated metabolomic and volatilomic profiling characterizes breed-related flavor variation in indigenous goat (*Capra hircus*) meat under controlled rearing conditions 108
- 101 Characterization of Mutton Volatile Compounds in Youzhou Dark Goats and Local White Goats Using Flavoromics, Metabolomics, and Transcriptomics 109
- 102 Effects of grazing intensity and grazing method on goats (*Capra hircus*) and forage biomass 110
- 103 Chemometric and machine-learning discrimination of goat and beef meat using quality characteristics and electronic-nose responses 111
- 104 Tissue-specific volatile profiles and goaty flavor characterization in Chengdu grey goat . 112
- 105 Role and Molecular Mechanism of BTF3 in Regulating Lipid Deposition in Intramuscular and Subcutaneous Preadipocytes of Meat Goats 113
- 106 From surplus to table_ exploiting the growth potential of male Tenerife Sur goat kids through targeted feeding strategies 114

PART 6: Milk Production..... 115

- 107 Prevalence, patterns, association with biofilm formation, effects on milk quality, and risk factors for antibiotic resistance of staphylococci from bulk-tank milk of goat herds..... 116
- 108 The Impact of Polymerized Whey Protein on the Physicochemical Properties, Microstructure, Probiotic Survivability, and Sensory Properties of Hemp Extract-Infused Goat Milk Yogurt..... 117
- 109 Assessment of Non-Genetic Factors Affecting Milk Yield and Composition in the Beni Aarous Goat Breed..... 118
- 110 Differential milk cytology in goats: impact of dietary stress and comparison of analytical methods in an experimental setting..... 119
- 111 Differential Cytology of Goat Milk using Fossomatic 7DC: Infectious and Non-Infectious Factors of Variation 120
- 112 Differential expression analysis of milk fat globule membrane proteins in colostrum and mature milk of Wanlin White goats based on DIA proteomics 122
- 113 Drivers of Preference for Goat Milk: Perception and Observed Milk Quality in a Traditional Management Setting 123
- 114 Astral-DIA proteomics: Identification of differential proteins in sheep, goat, and cow milk 124
- 115 Udder Conformation and Thermal Imaging as Indicators of Udder Health in Saanen Dairy Goats 125
- 116 Identification of metabolite biomarkers for lactation stage classification in Saanen dairy goats using untargeted and targeted metabolomics..... 126
- 117 Metabolomics reveals environmental impacts on regional milk composition in dairy goats 127
- 118 Rapeseed as a dual-purpose strategy for methane mitigation and milk quality in dairy goats:

Bridging experimental evidence and farm practice	128
PART 7: Nutrition.....	129
119 Effect season and host on the nutritive value of <i>Plicosepalus kalachariensis</i> parasitic browse attached to different trees in semi-arid areas.....	130
120 The effects of the proportion of forage in the diet on daily weight gain, nutrient digestibility, rumen parameters and greenhouse gases emission of growing goats	131
121 Effect of forage feeding frequency on intake, milk production and behaviour in dairy goats	132
122 Effect of feeding order of two forages on intake, milk production and behaviour in dairy goats	133
123 Prediction of the chemical composition of the forage selected by dairy goats	134
124 Effects of diets with different concentrate-to-roughage ratios on the growth rate, serum biochemical indexes, and rumen fermentation of Guangfeng goats	135
125 Early Supplementary Feeding Improves Hair Follicle Development in Northwest Xizang White Cashmere Goats: An Analysis Based on Skin Multi-Omics	136
126 Effects of level and type of fiber sources on feed intake, milk production and composition and nutrient utilization in Alpine dairy goats.....	137
127 Influence of <i>Asparagopsis taxiformis</i> on Methane Emissions and Rumen Antimicrobial Resistance Gene Profiles in Goats	138
128 MicroRNA profiles in colostrum and transition milk of non-dairy goats fed with or without resveratrol	139
129 Integrated multi-omics reveals <i>Enterococcus faecalis</i> JM263 alleviates high-concentrate diet-induced hepatic injury via the gut-liver axis in goats	140
130 Effect of Feeding Level on Growth and Slaughter Performance, and Allometric Growth of Tissues and Organs in Female Growing Saanen Dairy Goats	141
131 Analysis of Energy and Protein Requirements of Growing Saanen Dairy Goats	142
132 <i>Bacillus pumilus</i> 315 improves intestinal microbiota and barrier function to alleviate diarrhea of neonatal goats	143
133 Effects of Rumen-Protected Methionine on cashmere fibre fineness and Hair Follicle Development in Yanshan Cashmere Goats.....	144
134 Goat gut microbiome as a reservoir for microorganism-encoded short peptides: regulation by host development age and nematode challenge	145
135 Effects of dietary lignin polyphenol on growth performance, serum biochemical indices and intestinal microbiota in weaned Huanghuai goats	146
136 Dynamic miRNA Profiles in Hulunbuir Sheep Muscle and Their Associations with Growth and Metabolic Traits	147
137 Effects of Different Melatonin Supplementation Regimens on Cashmere Production Performance in Cashmere Goat Kids (<i>Capra hircus</i>)	148

138	The Effects of Yucca Extract on Serum Immunological Parameters, Rumen Microbial Flora and Metabolism in Fattening Sheep.....	149
139	Mechanisms of melatonin in promoting intramuscular fat deposition and optimizing fatty acid profiles in fattened cashmere goats	150
140	Effect of Vitex negundo cell powder byproduct on high-concentrate diet-induced oxidative stress in lactating dairy goats	151
141	Rumen microbiome differences between goat breeds impact feed efficiency.....	152
142	Effects of Precision Nutrition Supplementation Based on Nutrient Requirements of Cashmere Goats on Production Performance of Inner Mongolia Cashmere Goats.....	153
143	Advances in Energy and Protein Requirements of Meat-type Goats.....	154
144	Effect of Database Choice on Taxonomic Classification of Rumen Prokaryotes in Goats	155
145	Milk fatty acid profile response to quebracho condensed tannin supplementation in lactating goats	156
146	Molecular mechanism of glucose regulating hepatic lipid metabolism in goats	157
147	Meat Quality Analysis of Different Muscle Parts of 6-Month-Old Wanlin White Goats ..	158
148	Multi-omics research reveals the effects of dandelion extract on oxidative stress and lactation performance in dairy goats induced by high concentrate diets	159
149	Effects of Compound Microbial Inoculants with Different Ratios on Nutrient Transformation and Maturity of Goat Manure Aerobic Composting	160
150	Harnessing native Cynanchum chinense supplementation to improve sheep performance and environmental outcomes in saline-alkali grazing systems	161
151	Goat milk feeding promotes growth and health of sucking goat kids by regulating hepatic NF- κ B pathway through gut-liver axis	162
152	Effects of Milk Replacer Feeding on Growth Performance and Gastrointestinal Microbiota of Saanen Dairy Goat Kids	163
153	Goat milk exosomes alleviate metabolic dysfunction-associated steatotic liver disease by enhancing hepatic fatty acid metabolism	164
154	Effect of Methionine on Secondary Hair Follicle Growth and Hair Dermal Papilla Cell Proliferation in Cashmere Goats.....	165
155	Growth performance, ruminal fermentation and bacterial profile of indigenous goat kids supplemented with barley fodder sprouts	166
156	<i>Asparagus Cochinchinensis</i> Polysaccharide Ameliorates D-Lactate-Induced Injury of Dazu Black Goat Ruminal Epithelial Cells via Autophagy-Mediated Suppression of the NLRP3 Inflammasome.....	167
157	Effects of Rumen-Derived Bio-Nano-Selenium and Graphene Oxide Nano-Selenium on the Structure, Function and Antibiotic Resistance of the Gut Microbiome in Lambs.....	168
158	Gram Positive Polysaccharide Utilization Loci of Active Cecal Oscillibacter Mediate Compensatory Utilization of Rumen Escaped Fiber in Goats	169
159	Enhancing the quality of mixed ration with cassava foliage by optimization fermentation	

time	170
160 Sodium Butyrate Improves Growth Performance of Dazhu Black Goat Kids and Modulates Rumen Epithelial Cell Function In Vitro: A Preliminary Investigation	171
161 Effect of Curcumin Supplementation on Feed Intake, Nutrient Digestibility, Rumen Fermentation and Growth Performance in Meat Goats	172
162 Precision animal feed management to promote quality fattening goat production in small holder farmer.....	173
163 Effects of Dietary Lycopene Supplementation on Growth Performance and Antioxidant Capacity in Goats.....	174
164 Fermentation Characteristics and In Vitro Gas production of LAB-Treated Sorghum Silage in Tropical Conditions	175
165 Betaine as a mitigation supplement for stress in small ruminants: Impact on performance, blood parameters, milk and meat production and quality: A meta-analysis	176
PART 8: Reproduction	177
166 Integrated miRNA-mRNA profiling reveals a regulatory network associated with follicular atresia in goats (<i>Capra hircus</i>).....	178
167 Analysis of the characteristics of microRNA expression profiles and reproductive regulation-mediated signalling pathways in testicular sertoli derived sEVs from Leizhou goats	179
168 Determinants of community based participatory small ruminant breeding program: evidence from smallholder goat producers in pastoral areas of Southern Ethiopia	180
169 Effect of different gonadotropins on estrus induction in Yanshan cashmere goats during the non-breeding season.....	181
170 Chromatin opening and expression pattern of LMBRD1 in Dazu Black Goat (<i>Capra hircus</i>) ovary associated with reproductive traits.....	182
171 Isolation, Identification and Adipogenic and Myogenic Differentiation Mechanism Analysis of Goat Bone Marrow Mesenchymal Stem Cells (<i>Capra hircus</i>).....	183
172 Aronia berry extract supplementation improves the quality of cryopreserved dairy goat spermatozoa	184
173 Analysis of the differences of dermal papilla cells of hair follicles in Liaoning cashmere goats at different developmental stages	185
174 <i>CDK1</i> Promotes Proliferation and Mitochondrial Respiratory Function in Goat Placental Trophoblast Cells	186
175 Single-nucleus transcriptomics reveals cellular dynamics and signaling networks orchestrating maternal-fetal interface formation during goat embryo implantation.....	187
176 Study on the Technology of Laparoscopic Ovum Pick-Up and InVitro Embryo Production in Chongming Goats	188
177 Proteomic profiling reveals the synergistic effects of astaxanthin and melatonin on the	

inhibition of cryoinjuries in ram sperm.....	189
178 Based on metabolomics and proteomics to study the effect of Poria Cocos Polysaccharide on frozen semen of Dazu black goats	190
179 <i>CSF1</i> Positively Regulates Endometrial Function via the P38-MAPK Pathways during Early Pregnancy in Goats (<i>Capra hircus</i>).....	191
180 Heat Stress Induced Differential Expression of Reproductive Genes and the Modulatory Role of Herbal Supplementation in Indigenous Goats.....	192
181 AI-Enabled 2D-3D Fusion for Automated Body Measurement in Goats	193
182 Regularized Canonical Correlation Analysis as the Preference Tool to Evaluate Multidimensional Breeding Linear Traits Underlying Fertility Phenotypes in Murciano-Granadina Does.....	194
183 Relationships of short photoperiod and male effects with faecal 16S rRNA, metabolomic analysis, serum metabolites, and reproduction performance of dairy goats in non-breeding season.....	196
184 <i>STC1</i> Gene Polymorphism and Its Effect on Ovarian Granulosa Cell Function in Dazu Black Goats.....	197
185 Ubiquitination properties of skin tissue in Inner Mongolia cashmere goats based on 4D label-free quantitative ubiquitinomics	198
186 Overview of breeding and reproduction of dairy goats in China.....	199
187 Dietary Quercetin Enhances Ovulation and Corpus Luteum Formation in Ewes via Improving Antioxidant Capacity and Follicular Development.....	200
188 <i>CRTC2</i> Promotes Goat Intramuscular Preadipocyte Differentiation and Lipid Metabolism via Interaction with <i>CLTC</i>	201
189 Integrated Single-Cell Transcriptomics and Multi-Omics Analyses Identify <i>EGR1</i> as a Master Regulator of Androgen Biosynthesis in Goat Theca Cells	202
PART 9: Other Products	203
190 Traditional Value-Added Products of the Changthang Pastoralist of Ladakh – A Way Forward	204
191 Melatonin alleviates skin aging and improves cashmere production performance in aged cashmere goats via the gut-skin axis.....	205
192 Effects of <i>Artemisia annua</i> polysaccharide and different zinc sources on antioxidant capacity, immune function, intestinal tissue morphology and fecal trace element content in cashmere kids goats	206
193 Insights into goat milk exosomes: endogenous loading and roles in alleviating colitis.....	207
194 Multivariate authentication of chevon (<i>Capra hircus</i>) against beef, buffalo and chicken using physicochemical, textural and electronic-nose fingerprinting.....	208

PART 1: Anatomy, Physiology, Welfare

Feeding and high ambient temperature effects on carbon dioxide and methane emissions in crossbred dairy goats under tropical conditions

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Objective: Goats are important dairy ruminants. The present investigation aimed to demonstrate the natural pattern of methane (CH₄) and carbon dioxide (CO₂) emissions under high ambient temperature (HTa) dairy goat as an animal ruminant model.

Methods: Twelve crossbred female Saanen goats were recruited for both winter and summer (n = 6 each). During the six weeks of experimental period, goats were offered a TMR twice daily, with free access to the water. The CH₄ and CO₂ emissions were measured via an infrared analyzer connected with respiratory chamber. Winter and summer were determined according to the Meteorological Department of Vietnam. Daily gas emission was measured in 2 chamber conditions, the ambient conditions (Amb) and the 25 °C air-conditioned conditions (25°C).

Results: Significant ambient temperature (Ta; winter, 29.8 °C; summer, 33.6 °C) was recorded with the afternoon temperature difference (Δ Ta) approximately 3.6 °C. Under chamber conditions, respiratory rate and water intake (WI) from 25°C differed significantly from those Amb, whereas dry matter intake and rectal temperature showed no significant difference. Daily CO₂ and CH₄ emissions (Fig 1 A and B) revealed the feeding related gas emissions. The peak analysis revealed the significant feeding related CH₄ emission (Fig 1B). The significant chamber effect was demonstrated via nighttime CO₂ emission. Likewise, nighttime CO₂ emission from summer was lower than winter. However, there was no effect of seasonal HTa on daily CO₂ and CH₄ emissions.

Conclusion: The present study revealed the natural pattern of gas emission from goats. We demonstrated the feeding effect on both CO₂ and CH₄ gas emissions. The short term HTa effect was on nighttime CO₂ emission and probably related in part with lower WI. Finally, there was no effect of long-term or seasonal HTa (at least at Δ Ta = 3.6 °C) effect on both CH₄ and CO₂ emission patterns.

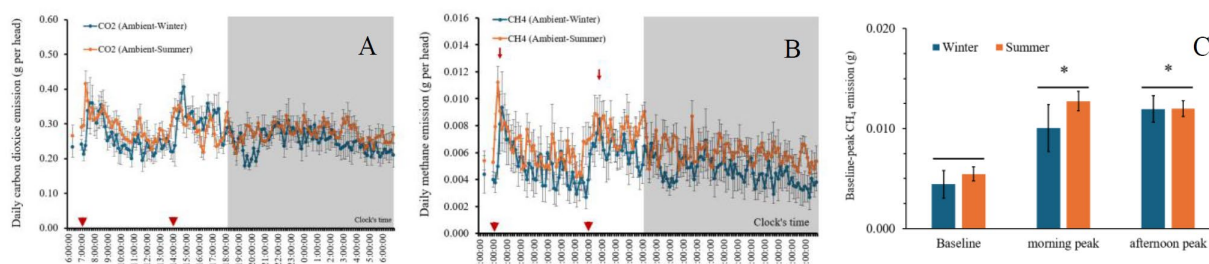


Figure 1. (A) Daily CO₂ and (B) CH₄ emission patterns. (C) Methane peak analysis. Arrows in (B) corresponds with peak analysis in (C).

Keywords: Animal welfare, Global warming, HTa, Methane, Ruminants, Water intake

Impact of Human Presence on the Cardiac Autonomic Profile of Periparturient Goats: A Biologging Approach

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Abstract: The physiological state of dairy goats during the peripartum period is highly sensitive to environmental stimuli. While human presence is often categorized as a potential stressor in livestock management, its objective impact on the caprine cardiac profile during the transition period remains insufficiently characterized. This study aimed to evaluate the influence of human presence on Heart Rate (HR) and Heart Rate Variability, specifically the Standard Deviation of Normal-to-Normal intervals (SDNN), using long-term internal monitoring. Nine goats were implanted with subcutaneous biologgers (Star-Oddi, Iceland) to record cardiac activity from 30 days prior to parturition until two months post-partum. The dataset was categorized into two conditions: periods of human presence and periods of no human presence. A total of 7,348 observations were analysed using a Mann-Whitney U test to account for unequal sample sizes and non-normal distribution. The results demonstrated a significant effect of human presence on all cardiac parameters. Contrary to the typical stress response, human presence was associated with a significant decrease in Heart Rate, with a mean of 101.3 bpm compared to 105.3 bpm during periods of absence. Concurrently, SDNN was significantly higher in the presence of humans (Median: 15.8 ms) than in their absence (Median: 11.5 ms). The significant reduction in HR and the increase in SDNN suggest a shift toward parasympathetic dominance and a reduction in sympathetic tone when humans are present. These findings could indicate that in well-managed herds, familiar human presence may act as a stabilizing or positive environmental stimulus rather than a stressor during the critical window from late gestation to peak lactation. This study highlights the value of biollogger technology in providing objective physiological metrics for animal welfare assessment in goats. Funded by Fundación CajaCanarias and Fundación Bancaria La Caixa (Ref. 2023DIG29).

Keywords: Caprine, Biologger, SDNN, Human-animal interaction, Animal Welfare.

Significant Shifts in Autonomic Nervous System Activity During Parturition in Dairy Goats

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Abstract: The peripartum period in ruminants represents a critical physiological transition involving significant metabolic and emotional stress, yet the precise dynamics of cardiac autonomic regulation during this window remain under-researched in caprines. This study aimed to characterize the changes in Heart Rate (HR) and Heart Rate Variability, specifically the Standard Deviation of Normal-to-Normal intervals (SDNN), in goats from 10 days pre-partum to 10 days post-partum. Nine animals were monitored using subcutaneous biologgers (Star-Oddi, Iceland), which allowed for continuous, minimally invasive data collection. Eleven daily electrocardiogram samples were obtained per animal to ensure representative sampling of cardiac activity. Data were analyzed using a non-parametric Friedman Test for repeated measures, followed by Durbin-Conover post-hoc pairwise comparisons. Results reveal a significant biphasic shift in cardiac activity associated with the transition from gestation to lactation. HR remained stable and significantly higher during the pre-partum phase (days -10 to 0), peaking at day -3 (123.00 bpm). Immediately following parturition (day 1), a progressive and significant decline in HR was observed, reaching its lower value on day 10 post-partum (99.00 bpm). Conversely, SDNN values followed an inverse trend; autonomic variability was lowest during the pre-partum period (e.g., 6.44 ms on day -9), indicating higher sympathetic dominance. Post-partum, SDNN significantly increased, reaching its maximum on day 10 (15.97 ms), suggesting a gradual restoration of parasympathetic tone and physiological stabilization. In conclusion, the use of Star-Oddi biologgers provided high-resolution insights into the caprine peripartum. The observed decrease in HR and concomitant increase in SDNN post-partum suggest that the metabolic and physical demands of late gestation exert a higher sympathetic load than early lactation in goats. Funded by Fundación CajaCanarias and Fundación Bancaria La Caixa (Ref. 2023DIG29).

Keywords: Caprine, Biologger, Heart Rate Variability, Parturition, Animal Welfare.

Evaluation of Cardiac Autonomic Response and Welfare in Dairy Goats During Milking via Subcutaneous Biologgers

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Abstract: The assessment of autonomic nervous system activity through heart rate (HR) and the standard deviation of NN intervals (SDNN) is a recognized non-invasive method for monitoring physiological states and welfare in livestock. This study evaluated changes in cardiac parameters in dairy goats across three distinct phases: pre-milking, during milking, and post-milking. Data were collected from nine goats implanted with subcutaneous biologgers (Star-Oddi, Iceland), and HR and SDNN were analysed using non-parametric methods. Descriptive statistics revealed a median HR of 99.0 bpm during the pre-milking phase, which shifted to 95.0 bpm during and after the milking. Regarding Heart Rate Variability, the median SDNN showed a slight increase during the milking phase (18.5 ms) compared to the basal pre-milking phase (17.7 ms), followed by a decrease in the post-milking period (16.5 ms). Data were analyzed using a non-parametric Friedman Test for repeated measures, followed by Durbin-Conover post-hoc pairwise comparisons. Results indicated that differences across the three phases were not statistically significant for either parameter. In conclusion, the milking process under the studied conditions did not induce significant autonomic disruption in the goats. The stability of HR and SDNN values suggests that the animals were well-adapted to the milking routine, indicating a high level of animal welfare and a minimal acute stress response. These findings provide a physiological baseline for future studies focusing on the impact of management practices on goat welfare. Funded by Fundación CajaCanarias and Fundación Bancaria La Caixa (Ref. 2023DIG29).

Keywords: Caprine, Biologger, SDNN, milking, Animal Welfare.

Effects of different housing conditions on behaviour and stress in Shiba goats

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Objective: There has been growing interest in animal welfare in recent years. Blood cortisol levels as a marker of stress have been reported in goats. The Shiba goat is a Japanese indigenous breed that is used in various experiments. The standards for breeding, housing and alleviation of pain were promulgated in 2006 for laboratory animals, requiring the reduction of stress. However, the effects of housing environments on the behavior and stress of goats remain unclear. Therefore, this study investigated the effects of housing conditions on behavior and stress in Shiba goats.

Methods: Four Shiba goats (W, X, Y and Z) were used as experimental animals. To simulate different housing environments, an exercise period involving outdoor exercise, a barn-housing period involving housing in the barn, and a cage-housing period involving housing in metabolic cages were established. During the exercise period, all goats were allowed to exercise outdoors in a 2,500 m² area from 10:00 a.m. to 3:00 p.m. on days without rain; at other times, they were housed in the barn. During the barn-housing period, they were kept at all times in a barn with a floor area of 6.0 m². During the cage-housing period, they were housed individually at all times in metabolic cages with a floor area of 0.7 m². Each period consisted of an 11-day acclimatization term and a 3-day sample and data collection term. The behavior of each goat was recorded for 10 minutes at 2:00 p.m. daily, followed by the collection of blood from the jugular vein. Blood samples were used to measure general composition, cortisol and oxidative stress levels.

Results: Oxidative stress levels were higher during the barn-housing period for Y than during the cage-housing period, and higher during the cage period for Z than during the barn period. Within the herd, there is a hierarchy of social rank among the goats, and Y was the lowest-ranking individual. It was observed that Y was frequently attacked by socially dominant individuals during the barn-housing period, and it is considered that this led to an increase in oxidative stress levels. However, Z was a socially dominant individual and might have experienced stress due to the confined space during the cage-housing period. W exhibited more foraging activity during the exercise period than during the cage period. It is supposed that W could not intake sufficiently during feeding times, leading to increased foraging in the exercise yard. Hostile behavior between W and X tended to be more frequent during the barn-housing period. Y showed no significant differences in any of the behaviors, while Z tended to forage more during the barn-housing period than during the cage-housing period.

Conclusion: This study revealed that different housing conditions affect the behavior and stress of goats. It was shown that low-ranking individuals are prone to stress due to competition with high-ranking individuals, while high-ranking individuals tend to stress caused by confined spaces. Social hierarchy among goats influences behavior and stress, and it is important to manage them while considering the interactions between individuals.

Keywords: Blood, Behavior, Housing, Stress, Goat

Metabolic and productive responses to heat stress in heat-sensitive and heat-tolerant Murciano-Granadina dairy goats

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Abstract: Heat-tolerant animals are identified by their ability to maintain homeothermy and to sustain productive and reproductive performance under high heat load conditions. This study studied whether heat stress causes different metabolic and productive responses in heat-sensitive and heat-tolerant dairy does. Heat conditions were assessed by the Mader et al. (2006)'s expression: $THI = 0.8 \cdot T + RH/100 \cdot (T - 14.41) + 46.4$; where T = temperature ($^{\circ}C$) and RH = relative humidity (%). A total of 33 Murciano-Granadina does in mid-lactation (40.9 ± 1 kg body weight; 2.45 ± 0.14 kg/d milk yield) were submitted to a 2-h heat challenge by shifting from thermoneutral (TN; $THI = 65$) to heat stress (HS; $THI = 86$) conditions in sawdust bedded pens of 5 inside a temperature-controlled barn. Rectal temperature (RT) and respiratory rate (RR) of each doe was measured at both conditions, and used to calculate the change ratio [$CR = (RTHS/RTTN) + (RRHS/RRTN)$], which served to classify the does as heat-tolerant (TOL, $n = 9$) or heat-sensitive (SEN, $n = 10$; $P < 0.01$). Does were then assigned to a 2-period crossover design (12 d per period) under TN ($THI = 63\text{--}65$) and HS ($THI = 79\text{--}88$) conditions in a climatic chamber. Milk yield, water intake, dry matter intake, RT, and RR were recorded daily on the last 5 d of each period and milk and jugular blood samples, for main components, metabolites and hormones, were collected weekly. At the end of each period, a glucose tolerance test (GTT) was performed (0.15 g glucose/kg) and blood samples collected from -15 to 120 min in all does. Compared with TN conditions, HS increased RT by $0.82^{\circ}C$ ($P < 0.001$), RR by 164% in the morning and 285% in the afternoon ($P < 0.001$), and water intake by 74% ($P < 0.001$), while reduced feed intake by 10% ($P < 0.001$). Milk yield increased by 5% ($P < 0.005$) but energy-corrected milk yield (2.0 ± 0.1 kg/d) was not affected by HS. On the other hand, milk fat, protein, and lactose contents decreased under HS by 16%, 14% and 4%, respectively ($P < 0.01$). Plasmatic glucose, insulin, and urea concentrations were unchanged, whereas prolactin and creatinine concentrations were 819% and 14% higher under HS, respectively ($P < 0.01$). When TOL and SEN does' phenotypes were compared, no differences were detected in RR, whereas afternoon's RT was lower in SEN than TOL does. No differences in SEN and TOL does were observed in feed and water intakes, milk yield, milk composition, or basal plasmatic metabolites. During GTT the area under the curve of glucose at 60 min tended to be lower in SEN than in TOL does ($P < 0.07$). In conclusion, Spanish Murciano-Granadina does in mid lactation were moderately affected by HS in terms of thermophysiological responses, lactation traits, and blood metabolites. Responses to the GTT suggested that HS increased the insulin resistance in all does and that heat-tolerant and heat-sensitive does employed different mechanisms to maintain blood glucose homeostasis under severe HS conditions.

Keywords: Goats, Heat stress, Heat-tolerant, Heat-sensitive

Effects of microplastics of varying particle sizes on testicular injury in goats (*Capra hircus*)

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Abstract: Microplastics (MPs), as emerging environmental contaminants, are ubiquitous in natural environments. Ingestion of MP-contaminated feed leads to the bioaccumulation of MPs in animals, and the testis, a critical reproductive organ, is particularly vulnerable to MP exposure. The present study demonstrated that dietary supplementation with polyethylene microplastics (PE-MPs) significantly reduced feed intake in goats. Compared with the control group, the small-sized PE-MPs group (S group: particle size 5-10 μm) exhibited significantly decreased testicular index and sperm motility, along with severe testicular histological damage, whereas the large-sized PE-MPs group (L group: particle size 50-100 μm) showed only mild injury. Blood PE concentrations were significantly elevated in both MP-exposed groups; notably, particles smaller than 5 μm accounted for the highest proportion of microplastics in the small-sized group. Integrated transcriptomic and metabolomic analyses revealed that PE-MPs significantly enriched pathways associated with cytoskeletal organization, immunotoxicity, lipid metabolism, antioxidant defense, and ferroptosis. In conclusion, PE-MPs can induce testicular damage and impair sperm quality in goats, with small-sized particles exerting greater reproductive toxicity. The underlying mechanism likely involves the disruption of multiple metabolic pathways, ultimately compromising testicular structure and function. These findings provide a scientific reference for healthy goat farming and animal welfare.

Keywords: Microplastics, Goats, Testicular Damage, Transcriptomics, Metabolomics

Table 1. Effects of microplastics on feed intake and testicular index in goats

	NC	S (5-10 μm)	L (50-100 μm)
Feed Intake (kg/d)	1.00 $\pm$ 0.02 ^a	0.87 $\pm$ 0.047 ^b	0.90 $\pm$ 0.04 ^b
Average Daily Gain (kg)	0.20 $\pm$ 0.09	0.28 $\pm$ 0.03	0.21 $\pm$ 0.10
Testicular Weight (g)	216.40 $\pm$ 19.08 ^a	145.05 $\pm$ 22.14 ^b	191.17 $\pm$ 25.85 ^a
Testicular Index (%)	6.10 $\pm$ 0.57 ^a	4.31 $\pm$ 0.58 ^b	5.10 $\pm$ 0.41 ^b

Note: Different letters indicate statistically significant differences ($P < 0.05$)

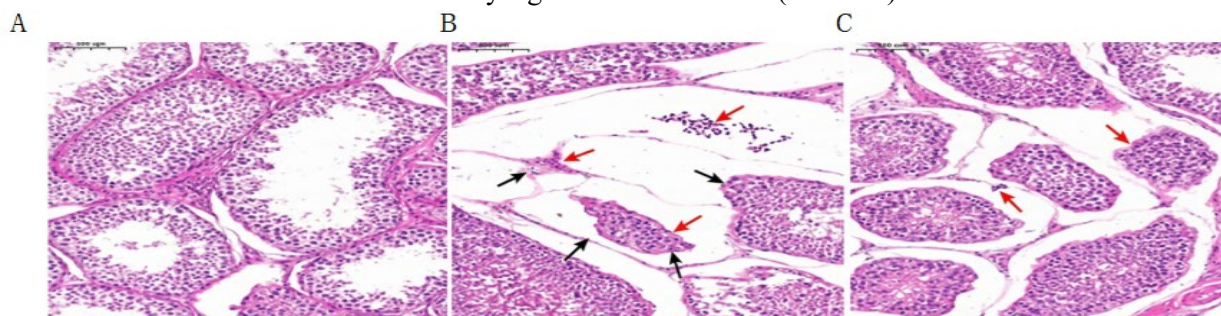


Figure 1. H&E staining of testicular tissue

Note: A, negative control B, the small-sized PE-MPs group. C, the large-sized PE-MPs group. Black arrows: structural damage of seminiferous tubules; red arrows: seminiferous epithelial damage.

Rumen Microbiome Responses to Heat Stress and their Association with Thermotolerance in Indigenous Goats

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Objective: Among the various livestock species, Goats are considered as the most ideal climate-resilient animals due to their tolerance to extreme climatic conditions. Despite their superior thermo-tolerant potential, there is limited research pertaining to heat stress and its effect on the rumen microbiota. Thus, the current study aimed at evaluating the heat stress response in two goat breeds, namely, Nandidurga and Bidri, by determining their rumen fermentation characteristics and rumen microbial diversity.

Materials and Methods: A total of 24 adult goats were randomly selected and assigned to four different treatment groups namely, NC (Nandidurga control), NHS (Nandidurga heat stress), BC (Bidri control), and BHS (Bidri heat stress). Each group consisted of six animals and were housed in climate-controlled chambers for 45 days. During the study period, the NC and BC groups were kept under thermoneutral conditions and the NHS and BHS groups were exposed to simulated heat stress.

Results: Heat stress significantly reduced rumen ammonia levels, extracellular, intracellular and total carboxymethyl cellulase (CMCase) activity in both breeds. Additionally, Nandidurga goats showed a significant decline in acetate, propionate, and total volatile fatty acid (VFA) concentrations under heat stress conditions. Further, V3-V4 16S rRNA sequencing analysis revealed considerable alterations in the rumen microbe populations of the Bidri and Nandidurga goats under heat stress. Although both breeds displayed broadly similar microbial responses, certain breed-specific differences were also evident. LEfSe analysis revealed Significant variations in the abundance of various microbial taxa, with Bidri goats exhibiting greater alterations than Nandidurga goats. These microbial changes in turn, were predicted to negatively affect important metabolic pathways.

Conclusion: The results from the study provide valuable insights on the rumen microbial responses of indigenous goats under heat stress conditions. The two goat breeds were found to possess excellent thermo-tolerant potential under heat stress. However, Nandidurga goats had fewer rumen changes than Bidri goats indicating their superior heat tolerance potential than Nandidurga goats.

Keywords: Climate resilience; Goats; Heat stress; Rumen microbiota; Thermotolerance

Effect of intramammary infections and dry-off treatment on whole blood

haematological profile and leukocytes differential of Alpine dairy goats

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Abstract: Eighty-eight Alpine goats were enrolled 7 days before dry-off in a 2 × 2 experimental design. Milk samples were analysed by bacterial culture and isolates identified by MALDI-TOF. Goats were classified according to udder health status (UH) as healthy (HEAL: sterile samples in both halves; n = 50) or infected (INFE: at least one positive half; n = 38). Goats were blocked by previous lactation milk yield, SCC and body condition score (BCS); in INFE goats, the number of positive halves and bacterial species were also considered. At -61 days from real kidding (DFK), goats were abruptly dried off without treatment (control group, CG; n = 44) or treated with an intramammary rifaximin tube in each half udder (Fatroximin, Fatro, Bologna, Italy; treatment group, TG; n = 44). Blood samples were collected at -61, -54 DFK, -9 and at 7 DFK to assess haematological profile and leukocytes differential. Data were analysed using a mixed model for repeated measures including UH, antibiotic treatment, time and their interactions as fixed effects, with parity as a covariate. Compared to CG, TG had a tendency towards higher eosinophils (0.08 vs 0.06 K/ μ L, p = 0.06) and eosinophils relative abundance throughout the experimental period (0.90 vs 0.70 %, p = 0.09), possibly reflecting the activation of the immune system against intramammary treatment.

Compared to HEAL, INFE goats had a lower mean cell volume at -9 DFK (p < 0.01) and lower white blood cells at 7 DFK (p < 0.01), possibly reflecting a greater recruitment of leukocytes in the mammary gland at the onset of lactation. Compared to HEAL-CG, INFE-TG goats had lower neutrophils at 7 DFK (p < 0.05) while, compared to HEAL-TG, INFE-TG goats had lower white blood cells, neutrophils and lymphocytes at 7 DFK (p < 0.01), suggesting that adverse effects of intramammary infections at the onset of the new lactation were especially evident in INFE goats receiving antibiotic treatment, that had the most marked infiltration of leukocytes within the mammary gland. Furthermore, INFE-TG goats had lower neutrophils/monocytes at 7 DFK than both INFE-CG and HEAL-TG (p < 0.01) and had higher monocytes/lymphocytes at 7 DFK than both HEAL-CG and HEAL-TG (p < 0.01), possibly reflecting a chronic inflammatory status in these animals.

Keywords: Peripartum, Transition period, Immunity, Leukocytes, Inflammation.

Assessing the role of horns in the short-term thermoregulation of lactating dairy goats submitted to heat stress

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Abstract: The role of permanent horns in *Bovidae spp.* has been long debated. In the wild, horns are a useful tool (e.g. feeding, grooming, defence) but, in farm animals, horns are unproductive and dangerous (i.e. animals, humans, farm facilities), which had led to the recommendation for their removal. In goats, horns are inherited as a single recessive trait linked to sex and the poll homozygote genotype is hermaphrodite. Consequently, the use of polled bucks is avoided, making dehorning a common practice. Nevertheless, evidence supports the thermoregulatory function of horns and their role in evolutionary adaptations. Thus, species from cold regions tend to have small horn-cores, which help conserve heat, whereas desert species have larger horn-cores that facilitate blood flow and heat dissipation. With this aim, the short-term function of horns in lactating dairy does was studied under thermoneutral (TN) and heat stress (HS) conditions. Heat conditions were assessed by the Mader et al. (2006)'s expression: $THI = 0.8 \cdot T + RH/100 \cdot (T - 14.41) + 46.4$; where T = temperature ($^{\circ}C$) and RH = relative humidity (%). Multiparous Murciano-Granadina dairy goats ($n = 14$; 44.6 ± 1.7 kg body weight), short black hair and in mid-lactation (124 ± 1 d; 1.92 ± 0.13 kg/d), were used. All does had medium-size scimitar-shaped horns (21.9 ± 1.3 cm) and were kept in individual sawdust bedded pens in a climatic chamber. Daily day-night length was 12-12 h. Horns of half of the does were covered by thermo-insulating plastic tubes filled with polyurethane foam, to simulate the absence of horns as a polled treatment (POLL), whereas the remained animals served as control (HORN). After a 5-day adaptation period under TN ($THI = 65$) conditions, does were exposed to HS (day, $THI = 87$; night, $THI = 78$) for 10 d, with a 2-day ramp for temperature increase. Horn isolation treatment (POLL) was removed after d 4 to assess the effect of alleviation. Thermophysiological traits (rectal temperature, respiratory rate) and water consumption dramatically increased after 2 d of HS ($P < 0.001$), whereas feed intake and milk yield steadied ($P > 0.05$), agreeing previous experiments in our goats under HS in mid and late lactation. No differences between POLL and HORN treatments ($P > 0.05$) were found at the short-term in any variable evaluated, although qualitative differences between HS and TN infrared images of the goat's heads and horns were observed. Moreover, milk yield tended to increase by 6% in the POLL does during HS ($P = 0.12$). Experimental day had effects on rectal temperature, respiratory rate, feed intake and milk yield, indicating progressive adaptation of the does to HS. Further analysis is needed to assess the role of the horns in the mid-term responses to HS.

Boosting PRRSV-Specific Cellular Immunity Development of an Fc-fused Multi-CTL Epitope Vaccine

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Objective: The constantly evolving PRRSV has been plaguing pig farms worldwide for over 30 years, with conventional vaccines suffering from insufficient protection and biosecurity risks. To address these challenges, we aim to develop an Fc-fused multi-CTL epitope vaccine for specifically boosting cellular immunity against PRRSV.

Methods: Twenty-two reported PRRSV-specific CTL epitopes were predicted for their binding affinity to the SLA alleles, and then their immunostimulatory activity was evaluated via IFN- γ ELISPOT. A recombinant protein, pFc-PTE, was constructed based on the 10 screened CTL epitopes and fused with a modified porcine Fc molecule. The immunogenicity of pFc-PTE was evaluated by stimulating PRRSV-specific splenic lymphocytes and immunization in mice.

Results: 10 screened CTL epitopes significantly stimulated PBMCs of PRRSV-challenged pigs to release IFN- γ . The pFc-PTE induced a robust cellular immune response, characterized by high levels of IFN- γ secretion. The fusion with Fc extended the duration of the immune response for at least 10 weeks post-immunization and induced a Th1-biased immune response.

Conclusions and Discussion: pFc-PTE holds promise as a novel, safe, and potent candidate vaccine in enhancing PRRSV-specific cellular immunity, and may also provide new perspectives for vaccine design against other viral diseases. Future studies will focus on *in vivo* experiments in pigs and assessing cross-protective capabilities against different PRRSV variants. pFc-PTE holds promise as a novel, safe, and potent candidate vaccine in enhancing PRRSV-specific cellular immunity, and may also provide new perspectives for vaccine design against other viral diseases. Future studies will focus on *in vivo* experiments in pigs and assessing cross-protective capabilities against different PRRSV variants. And potent candidate vaccine in enhancing PRRSV-specific cellular immunity, and may also provide new perspectives for vaccine design against other viral diseases. Future studies will focus on *in vivo* experiments in pigs and assessing cross-protective capabilities against different PRRSV variants. PRRSV variants.

Keywords: PRRSV, CTL epitope, Fc fusion, cellular immunity, vaccine development

Metabolic and sensor-based stress assessment of milk-fed goat kids transported by road at short-distances and two different densities

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Abstract: Despite the large number of young goat kids transported by road, no conditions have been specified in the EU. We studied (TechCare, EU-H2020 program, contract#862050) the effects of transportation densities, inferred from regulation EC 1/2005 for lambs <20 kg BW (0.2 m²/head or 0.010 m²/kg), aiming to monitor the stress of kids at high (0.013 m²/kg), equivalent to 8.2 kids/m², and low (0.018 m²/kg), equivalent to 5.9 kids/m², stocking rates using sensors for physical (speed, acceleration, sound, temperature-humidity) and biological (body weight and temperature, plasmatic values) monitoring. Suckling kids (36 male, 39 female) of Murciano-Granadina breed were used. Kids were fed colostrum and reared with milk replacer until reaching the Spanish “cabrito lechal” features. Kids were transported in 3 trips under morning and autumn conditions (26 ± 1°C and 47 ± 2% humidity). An homologated 2-floor and 1-axle trailer (750 kg, 1.8×1.0×1.3 m), divided in 4 compartments (0.9 m² each), was used. Trailer was towed by a van driven by a certified operator, and equipped with sensors (temperature, humidity, sound and acceleration) placed in the internal face of the trailer’s frontal side. Journeys consisted of 119±2 km (1 h and 56 min; 62±1 km/h). Animal stress responses were assessed through individual measurements taken before (h0), after (h2) and following a 22-h recovery period (h24). At each time, BW (kg) and body temperatures (rectal, lacrimal, iris) were recorded, and blood samples collected for muscle damage markers (CK and LDH), cortisol (COR) and serum metabolites (NEFA, glucose and urea) analyses. Sensor’s data were continuously recorded. Data were analysed by MIXED procedure for repeated measurements (SAS v.9.4). Small differences between trips were observed in our study, the BW of kids of the trip 1 tending to be greater than in trip 3 (9.70 vs. 9.05 kg; $P = 0.13$). Although not significant, heavier kids showed lower values of COR, LDH and NEFA, stressing the critical age and BW at which they were transported. Marked increases in most variables resulted by transportation ($P = 0.12$ to 0.001), indicating a dramatic stress event, although no differences by density were detected ($P = 0.74$ to 0.045). The exceptions were lacrimal’s temperatures (0.38 °C; $P = 0.045$) and NEFA concentrations (0.063 mmol/L; $P = 0.008$) which increased by density, agreeing with lipolytic effects. Because most indicators increased, the lower numerical values observed for the low stocking density were considered as more favourable. No differences in BW were observed by the effect of density ($P = 0.74$). The accelerations measured on the trailer were much higher than those reported in the driver’s cabin, with extreme vertical changes (z-axis acceleration reaching 11.8 g compared to 1.5 g; $P < 0.001$), and excessive noise (>800 dB and >1400 Hz) surpassing regulatory limits for human occupational environments and suggesting that they were relevant stressors. In practice, no differences should be expected when kids are transported at stocking rates varying between 6-8 kids/m². No densities ≥ 9 kids/m² should be used. Challenges such acceleration, noise and low temperatures persisted as kid stressors.

Tolerance and Adaptive Responses of Goats to Saline Drinking Water: Evidence from a Systematic Review

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Abstract: Freshwater scarcity is increasingly limiting livestock production in arid and semi-arid regions, increasing the interest in saline and brackish water as alternative drinking sources. This study synthesized the available evidence on the responses of goats to saline drinking water, focusing on water and feed intake, nutrient utilization, rumen function, metabolic responses, and productive performance. Goat studies have included a wide range of breeds, salinity concentrations, and exposure periods, resulting in considerable variability in responses. Overall, the goats showed substantial tolerance to saline drinking water and generally maintained their dry matter intake under moderate-to-high salinity. Their greater tolerance is associated with efficient renal water conservation, lower water turnover, adaptation to arid environments, and behavioral flexibility. Drinking-water intake commonly increased as salinity increased, although responses at high concentrations were breed- and time-dependent. Gradual adaptation was particularly important; Boer goats exposed progressively to saline water tolerated concentrations of up to 15,000 mg/L total dissolved solids (TDS) without adverse effects. The digestive responses were also relatively resilient. Several studies have reported no significant changes in nutrient digestibility or rumen fermentation even at elevated salinity, although ruminal pH and fermentation patterns varied with salinity, breed, and physiological status. Productive responses were similarly robust; saline water up to 8,326 mg/L TDS did not affect body weight gain or milk yield in crossbred goats, whereas milk yield and major physicochemical and sensory characteristics were maintained in Alpine goats. Collectively, the evidence indicates that goats have a considerable capacity to utilize saline drinking water, but a single universal tolerance threshold cannot be defined because responses depend on breed, ionic composition, exposure duration, diet, and adaptation strategy. These findings support the strategic use of goats in water-limited production systems and highlight the need for long-term, breed-specific studies using naturally saline water to establish practical drinking water guidelines.

Keywords: goats; saline drinking water; total dissolved solids; salinity tolerance; osmoregulation; rumen function; arid environments

PART 2: Diseases

Nationwide investigation of respiratory problems in goat kids in Greece

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Objective: The objectives of the study were (a) the assessment of the presence of respiratory problems in goat kids and (b) the identification of variables associated with the presence of the problems in the farms.

Methods: The work was part of a wider study performed in farms with the participation of farmers, by means of an in-person questionnaire investigation. Data were collected from 119 goat herds. Data were collected through on-site visits to farms and collection of information by using a detailed, structured questionnaire.

Results: Annual incidence rate for respiratory problems in goat kids was 1.1% (1.0–1.2%). Annual incidence rate was significantly lower in farms with semi-extensive or extensive management system (1.0%) than in farms with intensive or semi-intensive or extensive (1.3%) management system. In multivariable analysis, the proximity to industrial sites and the administration of antibiotics to newborns routinely emerged as significant predictors for respiratory problems in goat kids. Among goat farmers, 22.7% considered ‘pneumonia’ as the second most important health problem of goat kids. Respiratory problems were more often declared an important problem by farmers in proximity to industrial sites: 21.6% *versus* 12.5%.

Conclusion: Overall, the study contributes information regarding the presence of respiratory problems in goat kids in Greece. A notable finding has been the association of proximity to industrial sites with a higher incidence rate of respiratory problems of lambs and kids in the farms. This has similarities to the results of relevant studies on people and potentially reflects that air pollution in the farm environment might be a factor to take into account in health management. One may also postulate that, possibly, data from farms can be employed to indicate potential risk from air pollution for humans, although further and more detailed work will be necessary to draw relevant conclusions.

Lameness in adult goats in Greece: prevalence, predictors, treatment, importance for farmers

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Objective: The present study refers to an extensive investigation of lameness performed countrywide in Greece, on 119 goat farms. The specific objectives of this work were to present data on the occurrence of lameness on goat farms and to identify variables (including variables related to climatic factors) associated with the disorder.

Methods: Farms were visited and animals on the farm were assessed clinically for the presence of lameness; further, an interview was carried out with the farmer to obtain information regarding practices applied on the farm. Climatic variables at the location of each farm were derived from NASA research.

Results: The within farm prevalence rate varied from 0.0% to 30.0% in goat herds. The mean $\pm$ standard error (median (interquartile range)) within farm prevalence rate among goat farms was 2.6% $\pm$ 0.5% (0.0% (0.0%)). Multivariable analysis for within farm prevalence of lameness revealed one significant predictor in goat farms: increased precipitation at the farm location. Treatment of lameness involved mostly administration of antibiotics; the antibiotics administered most often were lincomycin and oxytetracycline. There was a tendency for higher median within farm prevalence of lameness among farms where no antibiotic administration was practiced. Finally, 4.2% of goat farmers considered lameness as an important health problem for the animals, specifically the fifth most important problem on the respective farms.

Conclusion: The study has provided information regarding the presence of lameness in goats in Greece. The results also indicate the importance of increased precipitation at the farm location for the presence of the problem on farms. These findings can be useful in the health management of goat farms. Whilst farmers recognize the importance of lameness for adult animals, mastitis is still considered the most important health problem on farms due to the financial significance for milk production.

Healthcare Management Practices Adopted by goat Farmers in the Rif region of Northern Morocco

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Abstract

A study on health management practices in goat farming was conducted among 150 farmers in northern Morocco. Data regarding animal health were collected through random sampling. Enterotoxemia and internal parasitism were the most frequently reported health issues, affecting 75% of flocks, while respiratory diseases showed a high prevalence (56%), likely influenced by climatic and seasonal variations. These, health disorders were closely related to husbandry practices, feeding systems, and sanitary conditions. The present study showed that nearly 60% of farmers administered treatments without veterinary supervision, while only 14.5% consulted veterinarians, primarily during emergencies due to high costs. Antiparasitic drugs were the most commonly used, followed by antibiotics and vaccinations. Overall, goat health management in the region is predominantly curative rather than preventive, highlighting an urgent need for strengthened preventive strategies and improved access to veterinary support.

Inter-scorer reliability of animal-based welfare indicators in subtropical goats

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Abstract: In 2015, the first Animal Welfare Indicators (AWIN) assessment protocol for goats was published. These indicators are validated for lactating adult dairy goats in intensive or semi-intensive production systems in Europe. However, evidence of their validity and applicability in other systems is scarce, including across East and Southeast Asia, where goat farming is well established. This study aimed to assess the inter-scorer reliability of 7 animal-based welfare indicators (AWINs) in non-dairy goats reared under an extensive-to-semi-intensive production system. Between January and March 2025, 2 independent scorers recorded 7 AWINs (body condition score, hair coat condition, fecal soiling, nasal discharge, ocular discharge, overgrown claws, and udder asymmetry) in 309 goats selected among 17 Hong Kong goat farms using a stratified random sampling design. Indicator descriptions were extracted from the AWIN assessment protocol for goats. Inter-scorer reliability was analyzed using Cohen's Kappa. The protocol has been approved by the Animal Research Ethics Sub-Committee of the City University of Hong Kong. Most goats assessed were younger than 1 year (49.2%; 152/309) and female (74.1%; 229/309). Nasal discharge and fecal soiling demonstrated moderate agreement ($\kappa = 0.45\text{--}0.51$). Body condition score and udder asymmetry achieved fair reliability ($\kappa = 0.28\text{--}0.33$). Hair coat condition and ocular discharge exhibited the lowest reliability ($\kappa = 0.10\text{--}0.14$). Overgrown claws were never recorded. The overall poor interscorer reliability of AWINs reveals critical gaps in their use for non-dairy goats. Further refinement and validation are required to support their use across management systems.

Keywords: Animal Welfare, Hong Kong, *Capra hircus*, Goat

Development of Nanopore sequencing Nemabiome and mixed amplicon metabarcoding for anthelmintic resistance detection and gastrointestinal nematode species identification in European goat herds

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Objective: Treatment of helminths relies on regular administration of broad-spectrum anthelmintics from a limited number of classes. Reports of resistance are now widespread, although resistance to levamisole (LEV) remains less so. Accurate diagnostics are essential to managing resistance and ensuring sustainability of drugs. Here we present findings from an initial pilot study examining the use of on-site Nanopore sequencing for Nemabiome and anthelmintic resistance monitoring in goats in Greece and Poland.

Methods: We developed a rapid mixed amplicon nanopore sequencing approach to identify isolates to the species level, and to survey anthelmintic resistance associated SNPs for LEV. We amplified the ITS2 region, and exon 4 of the *acr-8* gene, for species identification and levamisole resistance marker detection respectively.

Results: Pooled samples at the regional level in Northern Greece, showed *H. contortus* was the dominant species (>95%), but no evidence of LEV resistance in Greece. We then examined 84 goat herds in Poland at the farm level. We found *H. contortus* was the dominant species in the majority of herds, and *Trichostrongylus* spp dominant in the remaining herds. We further noted widespread emergence of LEV resistance in *H. contortus*, *Teladorsagia circumcincta*, and *Trichostrongylus* spp. We further found LEV resistance at >40% in several herds with a treatment history of extensive LEV use.

Conclusion: Nanopore sequencing presents a valuable opportunity for improving epidemiological monitoring of anthelmintic resistance, particularly in Central and Southern Europe. Here we successfully demonstrate its use for simultaneous Nemabiome and anthelmintic resistance marker detection in multiple species.

Keywords: Anthelmintic, resistance, nematode, helminth, sequencing, diagnostic

Prevalence of helminth infections in the goat population in Poland

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Background: A wide range of parasitic genera and species affecting the gastrointestinal and respiratory tracts occur in small ruminants worldwide, leading to substantial economic losses and reduced farm productivity. Despite their veterinary importance, data on the occurrence of these parasites in Polish small ruminants remain scarce. Poland, one of the largest countries in Europe, covers 312,696 km² and is administratively divided into 16 voivodeships. The national goat population currently comprises around 70,000 animals and has shown a steady increase in recent years. Therefore, the aim of this study was to assess the prevalence of gastrointestinal and pulmonary parasites in goats in Poland.

Materials and methods: Faecal samples were collected from 218 goat herds (including 3071 individual animals) scattered over the entire country. All samples were examined using modified McMaster method, centrifugal sedimentation, and Baermann technique. Additionally, coproculture of the gastrointestinal nematodes (GIN) was prepared from all samples by mixing collected faeces and pooling in a single sample. After 7-day incubation the larvae were extracted by Baermannization, and 100 subsequent strongyle larvae of the third type (L3) were identified based on their morphological features in the light microscope (400× magnification). The genera or species of L3 were identified at the herd level.

Results and discussion: The most prevalent parasites were GINs of the strongyle type present in 213 herds (98%) and 2,556 individual animals (83%). Among the GINs, *H. contortus* (203 herds; 93%) and *Trichostrongylus* spp. (192 herds; 88%) were most common, followed by *Teladorsagia circumcincta* (101 herds; 46%), *Oesophagostomum* spp. (98 herds; 45%), and *Nematodirus* spp. (15 herds; 7%). Furthermore, *Strongyloides papillosus* was found in 196 animals (6%) from 49 herds (24%), *Moniezia* spp. in 24 animals (0.8%) from 16 herds (7%), *Skrjabinema* spp. in 17 goats (0.6%) from 14 herds (7%), and *Trichuris* spp. in 36 animals (1%) from 26 herds (12%). The only parasite of respiratory tract found in the study was the nematode *Muellerius capillaris*, present in 172 herds (79%) and 1,382 goats (45%). The least common parasite found in our study was *F. hepatica*, confirmed only in 1 goat (0.03%).

Conclusion: Goats in Poland are most commonly infected with gastrointestinal nematodes (GINs) from the superfamily Trichostrongyloidea, particularly *Haemonchus contortus*, *Trichostrongylus* spp., and

Teladorsagia circumcincta. These parasites account for the majority of helminth-related health problems observed in Polish goat herds. Among respiratory parasites, *Muellerius capillaris* appears to be the predominant species. In contrast, *Fasciola hepatica* is detected only rarely in goats in Poland, indicating that its overall impact on goat health is minimal.

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Application of nanopore sequencing mixed amplicon metabarcoding for surveillance of benzimidazole resistance in Polish goat herds

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Objective: Ruminant livestock, including goats, are central to global agriculture but face productivity losses and increased greenhouse gas emissions due to gastrointestinal nematode (GIN) infections and growing anthelmintic resistance (AR). Conventional diagnostics have limitations, while molecular approaches such as deep-amplicon sequencing and Nemabiome metabarcoding improve species and resistance detection. This study applies mixed amplicon nanopore metabarcoding to surveil benzimidazole resistance in gastrointestinal nematodes of Polish goats.

Methods: PCR amplicons for ITS2 and benzimidazole beta-tubulin isotype-1 from 36 samples (herds) were purified, pooled per sample and sequenced on an R10.4.1 Oxford Nanopore flow cell with high-accuracy base calling. Demultiplexed reads were quality-filtered; ITS2 reads were classified with Minimap2 to estimate species abundance. Beta-tubulin reads were mapped to species-specific references, and key codons analysed to classify susceptible and mutant variants and estimate their frequencies.

Results: We validated our nanopore protocol by characterising GIN L3s from 36 Polish goat herds, detecting 15 ITS2 ASVs and applying sheep-derived correction factors to estimate species abundance. *H. contortus* and *T. colubriformis* predominated in all herds, with *T. circumcincta* and several other GINs generally at lower abundance; three samples yielded insufficient ITS2 reads. We then quantified benzimidazole-associated SNPs, finding F200Y highly prevalent in *H. contortus* and common in *T. colubriformis*, but less frequent in *T. circumcincta*. Other mutations were mostly low frequency and often associated with poor sequencing depth.

Conclusions: Nanopore mixed amplicon metabarcoding effectively profiled GIN species and confirmed high F200Ybenzimidazole resistance prevalence in *H. contortus* from Polish goat herds, supporting sustainable parasite control. This portable approach advances AR surveillance in goats.

Acknowledgments: This work was supported by the ERA-NET ICRAD, 3rd Call, under the project METABOL-AR (An application of metabolomics to the detection of anthelmintic resistance of gastrointestinal nematodes to benzimidazoles in goats) the grant no. ICRAD/III/28/METABOL-AR/2025. This ERA-NET has received funding from the European Union's Horizon 2020 research and innovation programme under Grant Agreement No 862605. This research is based upon work from COST Action ENVIRANT, Environmental impact of anthelmintics in livestock and alternatives to minimize their use (CA23154), supported by COST (European Cooperation in Science and Technology).

Keywords: Anthelmintic, resistance, nematode, helminth, sequencing, diagnostic

Protective Effects of *Lactobacillus Reuteri* Isolated from Goats in a Murine Model of *Salmonella* Infection

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Abstract: Probiotics possess the potential to enhance gastrointestinal health and inhibit the colonization of pathogenic microorganisms. However, the role and mechanism of *Lactobacillus reuteri* in inhibiting *Salmonella enteritidis* colonization is unknown. In this study, we isolated and characterized *L. reuteri* strain DY25 from goat feces and evaluated its probiotic properties and protective effects against *Salmonella* infection in a mouse model. The strain demonstrates elevated survival rates in simulated gastrointestinal fluids, exhibits significant hydrophobicity and self-aggregation properties, and shows robust adhesion to intestinal epithelial cells. Additionally, *L. reuteri* DY25 demonstrated significant antibacterial activity against *S. enteritidis* and other pathogenic bacteria. *In vivo* experiments revealed that the administration of *L. reuteri* DY25 resulted in enhanced daily weight gain, increased jejunal villus length, and an elevated villus height-to-crypt depth (V/C) ratio in mice. *L. reuteri* also modulated the gut microbiota by increasing the *Firmicutes*-to-*Bacteroidota* (F/B) ratio and enhancing the abundance of beneficial *Lactobacillus* species. Furthermore, *L. reuteri* DY25 mitigated *Salmonella*-induced intestinal inflammation by downregulating the expression of pro-inflammatory cytokines, including IL-6, IL-1 β , TNF- α , and IFN- γ , and by attenuating histopathological damage in both the jejunum and colon. These findings highlight the excellent probiotic properties of *L. reuteri* DY25, underscoring its potential as a probiotic supplement for preventing and treating animal diseases such as diarrhea.

Keywords: *Lactobacillus reuteri*, Probiotic properties, Protective effect, *Salmonella enteritidis*

Heat stress induces apoptosis and ferroptosis in goat (*Capra hircus*) skeletal muscle satellite cells via oxidative stress and disruption of iron homeostasis

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Objective: Heat stress (HS), caused by sustained high temperatures, is a major constraint on livestock production, particularly in hot and humid regions. When the temperature–humidity index (THI) exceeds a critical threshold, HS induces metabolic disorders and oxidative stress, thereby impairing animal growth performance and meat quality. Although Nubian goats exhibit some heat tolerance, their productivity still declines under prolonged HS, possibly due to dysregulated programmed cell death in skeletal muscle cells; however, the underlying mechanisms remain unclear. Therefore, this study aimed to investigate the effects of HS on apoptosis and ferroptosis in goat skeletal muscle satellite cells.

Methods: Goat skeletal muscle satellite cells (GMSCs) were used as an in vitro model to establish an HS treatment system (37 °C as the control group and 41.5 °C as the HS group). Cell proliferation and apoptosis were assessed using CCK-8, EdU staining, and flow cytometry. Gene expression levels were analyzed by qRT-PCR. Intracellular malondialdehyde (MDA) content and antioxidant enzyme activities were measured, and protein expression levels were determined by Western blot. In addition, oxidative stress, iron homeostasis, and lipid peroxidation were evaluated using reactive oxygen species (ROS) probes, iron assay kits, and C11-BODIPY staining.

Results: After 3 days of HS treatment, cell viability and proliferation were significantly decreased ($P < 0.001$), while apoptosis was significantly increased ($P < 0.001$). The expression levels of apoptosis-, ferroptosis-, and pro-oxidant-related genes were significantly upregulated, whereas proliferation- and antioxidant-related genes were downregulated. HSP70 protein expression was significantly increased ($P < 0.05$). Moreover, HS significantly elevated intracellular MDA and ROS levels, Fe^{2+} content, and lipid peroxidation, while suppressing antioxidant enzyme activities.

Conclusion: HS promotes apoptosis and ferroptosis in goat skeletal muscle satellite cells by inducing oxidative stress and disrupting iron homeostasis, which may impair muscle development.

Keywords: Heat stress; Skeletal muscle satellite cells; Apoptosis; Ferroptosis; goat

Gastrointestinal strongyles epidemiology in goats in Japan

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Abstract: A longitudinal survey of gastrointestinal strongyles (GIN) in goats was conducted from 2022 to 2025 in nine regions in Japan. A total of 496 goats from 29 farms were tested for packed cell volume (PCV) and fecal egg count (FEC, epg). Blood samples were taken from the jugular vein, and fecal samples were collected from the rectum. Goats were not dosed with anthelmintics for 4 weeks before sampling. Goat breed (dairy, indigenous, and mix), age of tested day (0, 1, 2, 3, 4, 5, and 6+ year old), and management practice (grazing, confinement, and grazing-confinement combination) were recorded. Fecal egg count was logarithmically transformed as $\ln\text{FEC} = \ln(x + 2,000)$ for analysis. The average age of goats was higher ($P < 0.05$) in Chugoku, Kyushu, and Okinawa regions, where goat meat is traditionally consumed. Infection levels by GIN based on PCV and $\ln\text{FEC}$ varied ($P < 0.0001$) by region in Japan; higher in Hokkaido, Kansai, Chubu, and Kyushu, and lower in Tokai, Shikoku, and Okinawa. Two-year-old goats had lower $\ln\text{FEC}$ ($P < 0.05$) than goats in the other age groups. Dairy breed had much higher $\ln\text{FEC}$ ($P < 0.0001$) and lower PCV ($P = 0.0001$) than indigenous and mixed breeds. Management practice affected PCV ($P = 0.0003$), with higher values for confinement and lower for grazing and combination, whereas $\ln\text{FEC}$ values of confinement and combination were similar ($P = 0.0648$). Sampling season also affected PCV, with Summer < Winter < Spring ($P < 0.0001$), and $\ln\text{FEC}$, with Winter < Spring and Summer ($P < 0.0001$). There was an age $\times$ breed interaction for PCV ($P = 0.0008$) and $\ln\text{FEC}$ ($P < 0.0001$). In conclusion, this study presented the current situation of GIN infection in various regions of Japan, where goat GIN epidemiology has not been reported for decades due to the low goat population. Another longitudinal survey of anthelmintic resistance in GIN is required due to the rising goat population in Japan.

Keywords: GIN infection, goats, longitudinal survey

Predicting somatic cell count in goat milk using explainable Machine Learning and Deep Learning approaches

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Abstract: Somatic cell count (SCC) is a key indicator of udder health and milk quality in dairy goats, with direct relevance for herd management, mastitis monitoring, and product safety. However, SCC is influenced by multiple biological, physicochemical, and microbiological factors, making its prediction a complex task. This study aimed to evaluate the potential of machine learning and deep learning approaches to predict SCC in goat milk using routine milk-recording data.

The dataset was derived from official milk-recording records from dairy goat farms in the Canary Islands, Spain. The initial dataset comprised 22,797 records from 529 farms collected between 2017 and 2018. After data cleaning, duplicate removal, missing-value filtering, date consistency checks, outlier handling, and biological plausibility assessment, the final modelling dataset included 18,606 samples. Six predictors were retained: fat, protein, lactose, solids-non-fat, bacterial count, and freezing point. SCC was modelled using a $\log_{10}$ transformation to reduce skewness and stabilise variance.

Several supervised regression models were compared, including ordinary least squares regression, decision trees, Random Forest, XGBoost, Histogram-based Gradient Boosting, and a Keras multilayer perceptron. Model performance was assessed using R^2 , RMSE, and MAE. Hyperparameter tuning was performed for the best-performing machine learning models using RandomisedSearchCV and Optuna, while the neural network was tuned using Hyperband.

Tree-based ensemble models outperformed linear regression, decision trees, and the deep learning baseline. The best overall performance was obtained by Random Forest optimised with Optuna, followed by XGBoost. Deep learning showed competitive but lower predictive performance, suggesting that, for this structured tabular dataset, ensemble tree models were more suitable. Explainability analyses using feature importance, permutation importance, and SHAP consistently identified bacterial count as the dominant predictor, followed by protein and lactose.

These findings support the use of explainable machine learning as a practical tool for SCC prediction in dairy goats and highlight the relevance of microbiological and compositional milk traits in modelling udder health indicators.

Keywords: Somatic cell count, goat milk, dairy goats, Machine Learning, Deep Learning.

First detection and pathogenicity of caprine kobuvirus and caprine bocaparvovirus in diarrheic goats in Southwest China

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Objective: Diarrhea in goat kids is a major cause of economic loss in intensive farming. Viral pathogens play a critical role, yet the virome in diarrheic goats remains poorly understood. This study aimed to identify emerging viruses associated with goat diarrhea and to characterize their molecular features, epidemiology, and pathogenicity.

Methods: Fecal samples from diarrheic goats in Sichuan, Chongqing, and Hunan were analyzed by viral metagenomic sequencing. TaqMan qRT-PCR (for caprine kobuvirus, CKoV) and specific SYBR Green I qPCR (for caprine bocaparvovirus, CapBoV) were developed and validated. A total of 1076 and 410 samples were tested for CKoV and CapBoV, respectively. CKoV was isolated using goat colonic mucosal epithelial cells. Pathogenicity was assessed by oral inoculation of 7-day-old kids with CKoV isolates, and with CapBoV-positive fecal suspension. Clinical signs, necropsy, viral distribution, histopathology, and immunohistochemistry were examined.

Results: Metagenomics identified two novel viruses: CKoV and CapBoV. CapBoV prevalence was 32.2% (132/410), significantly higher in diarrheic (40.0%) than non-diarrheic samples (22.7%) ($P < 0.05$). CKoV prevalence was 23.8% (256/1076), 40% in diarrheic vs 3% in healthy samples; kids aged 3 days to 1 month showed the highest positivity (57.4%–87.7%). Two CKoV strains were isolated. Inoculation of CKoV into 7 days kids caused severe watery diarrhea within 48–54 h, intestinal distension, and shedding of mucosal epithelial cells in duodenum and jejunum. Viral RNA was detected in heart, liver, spleen, lung, kidney, lymph nodes, and entire intestinal tract (highest in jejunum, 7.68×10^6 copies/ μ L), with re-isolation. Naturally infected kids showed similar pathological changes (**Figure 1**). For CapBoV, oral inoculation caused no clinical signs, but viral RNA was detected in spleen, small intestine, and lung; histopathology revealed mucosal necrosis and splenic lesions; immunohistochemistry confirmed viral antigen, suggesting potential enteric pathogenicity.

Conclusion: This study is the first to identify CapBoV in goats and to successfully isolate CKoV in China. Both viruses are widely prevalent in Southwest China and significantly associated with kid diarrhea. CKoV causes severe systemic infection in young kids, while CapBoV exhibits subclinical infection with evidence of tissue tropism and pathological changes. The results obtained here have significant implications for the diagnosis and control of diarrhoea in goats.

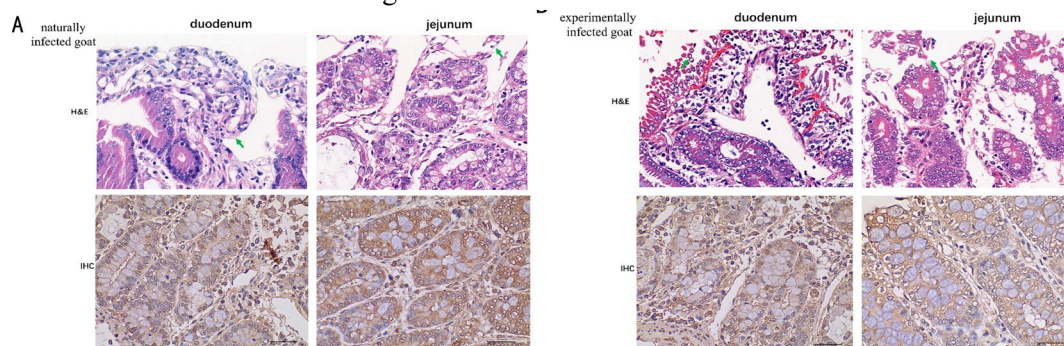


Figure 1. HE staining effects in intestine after infection with Aichivirus C (400 $\times$).

Keywords: Caprine Kobuvirus, Caprine Bocaparvovirus, Diarrhoea, Goat, Pathogenicity

Research on portable detection of subclinical mastitis in dairy goats based on Vis-NIR absorption spectroscopy

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Abstract: Subclinical mastitis has high incidence rate and insidious, which seriously endangers the health of dairy goats. However, there is a lack of effective means to detect it in time to intervene in advance. Visible Near Infrared (Vis-NIR) spectroscopy has the advantages of in-situ and rapid detection, and is widely used in pathological tissue detection. The commonly used methods for detecting mastitis in dairy goats currently include clinical observation and somatic cell count detection. Clinical observation method heavily relies on personal experience and has strong subjectivity, which can easily lead to misdiagnosis; The somatic cell count detection method requires the collection of milk samples, which is not only complex but also time-consuming, and cannot achieve timely on-site detection. In response to this issue, this study proposes an on-site detection method for subclinical mastitis in dairy goats based on Vis-NIR absorption spectroscopy (Figure 1). Using the number of somatic cells in dairy goat milk samples as a characterization of subclinical mastitis in dairy goats, a designed Vis-NIR absorption spectroscopy acquisition system suitable for dairy goat breasts was used to collect absorption spectra of dairy goat breast tissues. Machine learning technology was used to establish a mastitis prediction model based on dairy goat breast absorption spectra, providing new possibilities for the detection of subclinical mastitis in dairy goats.

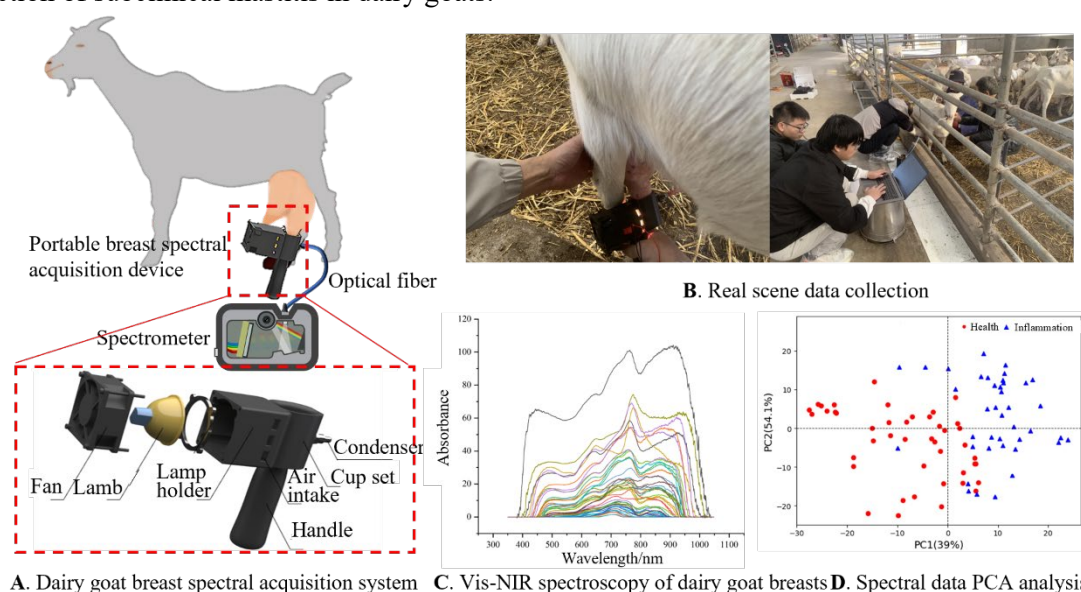


Figure 1. Schematic diagram of detecting mastitis in dairy goats based on Vis NIR spectroscopy

Keywords: Dairy goat, Mastitis, Vis-NIR spectroscopy, Non-destructive detection, Smart Farming

A type 2 immune circuit and arachidonic acid metabolism role in anti-nematode infection: evidence from transcriptome and targeted metabolome data in goat

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Abstract: The gastrointestinal nematode infection poses a covert threat to both humans and domestic animals worldwide, eliciting a type 2 immune response within the small intestine. Intestinal tuft cells detect the nematode and activated group 2 innate lymphoid cells. Tuft cell derived leukotrienes (one of the metabolites of arachidonic acid) were found to drive rapid anti-helminth immunity, but it is still poorly understood whether the tuft cell mediated type 2 immune circuit and arachidonic acid metabolism modulate anti-parasitic immunity in the gastric epithelium. This study was designed to evaluate the immunological responses of goats inoculated with or without *H. contortus*. Results showed that *H. contortus* infection induced a systemic type 2 immune response, characterised by lymphocyte proliferation and greater eosinophils both in peripheral blood and abomasal mucosa, as well as increased type 2 cytokines IL-4, IL-5, and IL-13. Infection of *H. contortus* altered the transcriptome of the abomasum epithelium, especially tuft cell mediated circuit-key genes. The infection also influenced the abomasal microbiota, arachidonic acid metabolism and related lipid metabolites, accompanying with great increases in the secretion of leukotrienes and prostaglandins. These findings demonstrate the role of tuft cells mediated circuit in sensing *H. contortus* infection and immune activation, reveal the candidate function of arachidonic acid involved in anti-helminth immunity, and suggest novel strategies for the control of parasitic diseases in livestock and humans.

Keywords: Abomasal bacteria, Abomasum transcriptome, Arachidonic acid metabolites, *Haemonchus contortus*, Type 2 cytokines

Diagnostic performance of a rapid on-farm test for detecting CNS subclinical mastitis in dairy goats

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Objective: There is limited availability of reliable, rapid diagnostic tests to detect subclinical mastitis on-farm in dairy goats in a timely manner. Thus, this study evaluated the diagnostic performance of a commercial rapid on-farm test for cows to properly detect subclinical mastitis caused by coagulase-negative staphylococci (CNS) identified by MALDI-TOF.

Methods: A total of 46 aseptically collected half-udder milk samples were obtained from clinically healthy Murciano-Granadina goats at early-, mid-, and end-lactation. Samples were frozen, thawed, and analyzed by culture, MALDI-TOF, and Mastatest. Infected samples were defined as those with ≥ 5 colonies and ≤ 2 species per sample. Mastatest is a rapid on-farm ELISA-based diagnostic test (enzyme-linked immunosorbent assay). Of the 46 samples, 15 were negative and 31 were positive. Based on MALDI-TOF, most positive samples were associated with CNS. Diagnostic performance was evaluated for i) infected versus non-infected; ii) CNS (all pathogens were CNS) vs non-CNS ("other Gram-positive", CNS-associated mixed cultures, and non-infected); iii) CNS+ (at least one CNS pathogen) vs non-CNS+ ("other Gram-positive" and non-infected). Diagnostic performance was evaluated using confusion-matrix metrics, sensitivity, specificity, balanced accuracy, the Cohen's kappa statistic (κ), and Fisher's exact test.

Results: The 96.8% of the infected samples were associated with CNS. *S. caprae* and *S. simulans* were the most frequently isolated CNS species (25.8% each), followed by *S. capitis* (12.9%) and *S. xylosus* (9.7%). Additionally, *Corynebacterium pseudotuberculosis* and *Trueperella pyogenes* (0.03% each) were also detected. The 83.9% of the infected samples presented just one CNS. Diagnostic performance results are summarized in **Table 1**. Across all scenarios, Mastatest showed better diagnostic performance for infected versus non-infected discrimination than for CNS classification, with higher balanced accuracy and greater agreement with MALDI-TOF. Agreement ranged from moderate-to-good for infected discrimination and moderate for CNS classification.

Conclusion: Mastatest may be useful as a rapid on-farm screening tool for discriminating infected from non-infected goat milk samples due to its high sensitivity, balanced accuracy, and moderate-to-good agreement with MALDI-TOF. However, its performance for CNS classification was lower, suggesting limited reliability for etiological identification of subclinical mastitis pathogens.

Table 1. Diagnostic performance of Mastatest for the discrimination of infected, CNS, or CNS+ compared to MALDI-TOF

Parameter	Infected vs. non-infected	CNS vs. non-CNS	CNS+ vs. non-CNS+
Se (%)	83.87 (66.27-94.55)	62.07 (42.26-79.31)	60.00 (40.60-77.34)
Sp (%)	80.00 (51.91-95.67)	88.24 (63.56-98.54)	87.50 (61.65-98.45)
Balanced ac (%)	81.94 (59.09-95.11)	75.16 (52.91-88.93)	73.75 (51.13-87.90)
κ	0.618 (0.380-0.856)	0.453 (0.219-0.687)	0.415 (0.181-0.648)
Fisher's exact test	$P < 0.001$	$P < 0.001$	$P = 0.002$

Se = Sensitivity, Sp = Specificity, Balanced ac = Balanced accuracy, κ = Cohen's kappa)

Keywords: Dairy goats; subclinical mastitis; Mastatest; on-farm diagnostics

Epidemiological Surveillance and Clinical Management of High rated infection in Goats under intensive Environment: A Longitudinal Analysis

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Objective: Caprine health management is a critical determinant of economic sustainability for the livestock sector in South Asia, where intensification often exacerbates disease transmission risks. This longitudinal study investigates the epidemiology, disease burden and clinical outcomes of a centralized goat population (~450 animals) under intensive management environment at the Livestock Production Research Institute, Bahadur Nagar, Okara.

Methodology: Over a 12-month period (July 2023-June 2024), 1590 Clinical cases across eight diverse breeds—including Teddy, Barbari, DDP, Nachi, and Beetal variants (Makhi Cheeni, Faisalabadi, Gujrati and Nukri) were systematically recorded and analyzed. Data was categorized by month, pathology, and breed to evaluate seasonal prevalence and the efficacy of standardized therapeutic protocol.

Results: The annual clinical burden suggested that each animal required veterinary attention approximately 3.5 times per year. **Gastrointestinal disorders, specifically diarrhea, remained the primary health challenge, comprising 34.97% of all clinical cases.** Other significant pathologies included hemoparasite/anemia (18.24%) conjunctivitis (14.15%) and various wounds and injuries (12.45%).

Seasonal analysis identified distinct temporal spikes: diarrhea peaked during the monsoon (July-Aug) and autumn (Oct-Nov) transitions, while hemoparasites—primarily *Theileria* and *Anaplasma*—showed peak prevalence during the warm, humid months of July to September. Remarkably, conjunctivitis cases surged in October (137 cases), affecting nearly 30% of the herd. Breed wise susceptibility data highlighted **Teddy and Makhi Cheeni breed as exhibiting the highest frequency of clinical records.** A standardized clinical therapeutic regimen for diarrhea, utilizing a combination of anticholinergics, adsorbents and targeted antimicrobials, achieved a 94.3 % recovery rate with a mean recovery duration of 4.02 days.

Conclusion: The study underscores the necessity of transitioning from reactive treatment to predictive prophylaxis. Strategic health management—integrating pre-emptive vector control in June and intensified deworming in September—is essential for mitigating seasonal morbidity spikes. These findings provide a statistically robust blueprint for maintaining caprine productivity in high density research and production settings.

Keywords: Goats, Seasonal pattern, morbidity, Resilience, Intensive conditions.

The Healthier Goats Project: Lessons learned after eliminating CAE, CLA and Paratuberculosis from the Norwegian dairy goat population

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The Healthier Goats Project represents one of the most comprehensive national disease control initiatives conducted for small ruminants. From 2001 to 2014, caprine arthritis encephalitis (CAE), caseous lymphadenitis (CLA), and paratuberculosis were systematically eradicated from Norway's dairy goat population. The initiative's success was attributable to robust farmer participation, integrated cooperation among industry stakeholders, veterinary authorities, veterinarians in practice and government agencies, compulsory program enrolment linked to milk delivery, and stringent biosecurity standards.

Over a decade after the project's conclusion, Norwegian dairy goats remain healthy. Few disease cases have occurred, mainly from biosecurity lapses and, for CLA live sheep contact, but there has been no widespread return of the three chronic infectious diseases. Paratuberculosis has not been detected in goats in Norway since 2010, indicating continued success of the original control measures.

Post-eradication surveillance remains fundamental to preserving disease-free status. Surveillance in dairy goat herds relies primarily on bulk milk testing, performed four to five times annually, enabling cost-efficient, population-wide monitoring and high compliance among farmers. Conversely, voluntary surveillance in suckling goat herds and sheep flocks is less standardized, which leads to inconsistent coverage and representativeness. This disparity underscores a persistent challenge in achieving comprehensive health monitoring across varied production systems, some of which may act as reservoirs for disease.

Despite favorable overall conditions, several risks threaten sustained disease freedom. Significant concerns include widespread movement of live animals, despite strict regulations in Norway, and increasing numbers of "hobby goats," whose owners may lack sufficient biosecurity knowledge. Additionally, diminishing biosecurity awareness among new farmers and those not engaged directly with milk delivery presents an ongoing challenge. As collective memory of disease diminishes, the risk increases that valuable lessons from earlier eradication efforts will be forgotten.

Norway's experience illustrates that national-scale elimination of goat diseases is feasible, yet enduring success hinges on ongoing surveillance, effective communication, and unwavering attention to biosecurity. Twelve years post-eradication, the Healthier Goats Project serves as a reminder that disease freedom is not static but requires continual diligence and commitment.

Keywords: Caprine arthritis encephalitis virus, caseous lymphadenitis, paratuberculosis, surveillance, biosecurity

An Intelligent Interpretation Method for Brucellosis Rose Bengal Plate Test Based on YOLOv8-CNN Machine Vision Machine Vision

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Objective: Brucellosis, a zoonotic infectious disease caused by *Brucella* species, poses severe threats to livestock production and public health. In China, it remains a major endemic disease in cattle and sheep, causing significant economic losses through abortion, infertility, and reduced milk yield. The Rose Bengal Plate Test (RBPT) is widely used for antibody screening due to its simplicity and speed; however, manual visual interpretation suffers from subjectivity, poor inter-operator consistency, and susceptibility to human errors during high-throughput testing. Consequently, it fails to meet the demands for efficient and standardized detection in large-scale farms and primary-level veterinary stations. This study aimed to develop an automated intelligent interpretation system for RBPT based on machine vision and deep learning, achieving objective, standardized, and high-throughput interpretation of antibody results.

Methods: Over 5,000 RBPT images were collected and annotated for model development. The workflow comprised: (1) image acquisition using industrial cameras; (2) automatic localization of reaction wells via the YOLOv8 object detection algorithm; (3) extraction of individual well images; (4) agglutination status classification using a dedicated CNN classifier; (5) intelligent determination of results (negative: uniform pink liquid; positive: presence of agglutination granules); (6) automated result output and electronic report generation; and (7) comprehensive performance evaluation against the gold standard manual interpretation, including accuracy, sensitivity, specificity, and system stability assessment.

Results: In external clinical validation using an independent set of 1,200 samples, the system achieved an overall accuracy of 96.8%, a sensitivity of 97.2%, and a specificity of 96.4%. Compared with manual interpretation, the system markedly improved consistency and efficiency, with a throughput of 430 samples per hour, meeting the requirements for large-scale batch testing.

Conclusion: This study successfully developed and validated an automated intelligent interpretation system for RBPT based on YOLOv8-CNN machine vision. The system has been integrated into a fully automated brucellosis detection workstation (ZKTH BAT4300), realizing an unmanned workflow from automatic sample loading and image acquisition to result reporting. This implementation significantly reduces human error and enhances detection standardization and repeatability. Furthermore, the technical framework is extensible to other serological agglutination tests, providing critical support for the intelligent management of livestock diseases and laboratory diagnostic automation.

Keywords: Brucellosis, Rose Bengal Plate Test (RBPT), YOLOv8, Convolutional Neural Network (CNN), Machine vision, Automated detection

Reflecting on the Journey Towards Peste des Petits Ruminants (PPR) Eradication

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Abstract: Peste des Petits Ruminants remains a major constraint to livelihoods, food security and resilience in vulnerable regions worldwide. To address this threat, FAO and WOAH have joined forces to achieve global eradication of PPR by 2030. As the target date approaches, there is growing interest in understanding the factors that facilitate or hinder progress and in identifying operational lessons that can inform future eradication efforts. This paper reviews global progress and lessons learned from recent global and regional meetings, high-level stakeholder discussions and country-submitted information on PPR eradication. Drawing on experiences from countries at different stages of the eradication pathway, it examines common challenges, successful practices, and emerging priorities to accelerate progress towards the global eradication goal.

Across regions, progress has been underpinned by sustained political commitment, domestic resource mobilisation, and strong veterinary services, including adequate workforce capacity, effective surveillance systems, reliable diagnostic capabilities and robust vaccination delivery mechanisms. Countries that have advanced in their eradication efforts have often linked PPR control and eradication activities to broader national priorities such as rural development, food security, poverty reduction, economic resilience and climate adaptation, helping to secure long-term support and investment. Cross-border collaboration remains essential in areas characterised by transboundary livestock movements and shared production systems, with regional coordination, harmonised approaches and information sharing reducing the risk of disease persistence and reintroduction. The meaningful involvement of livestock keepers, pastoralists, women and youth is essential for strengthening awareness, surveillance and acceptance of disease control measures, highlighting the value of community-centred approaches. Experiences shared by countries demonstrate the importance of adapting interventions to local epidemiological conditions and production systems, that one-size-fits-all approach is unlikely to be effective and that successful programmes are often those that tailor strategies to local realities while maintaining alignment with global objectives.

Keywords: PPR, eradication programme, small ruminants, WOAH, FAO, livelihoods

Research on Gene-Edited Goats Resistant to Prions

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Abstract: Transmissible spongiform encephalopathies (TSEs, prion diseases) are fatal zoonotic neurodegenerative diseases caused by misfolded prions, posing a serious threat to livestock production and public health. Breeding prion-resistant goats has long been a primary goal of animal breeding. Given that prion diseases have an extremely long incubation period and a 100% mortality rate once clinical symptoms appear, intervening in the *PRNP* gene via CRISPR/Cas9 gene editing technology is one of the most effective strategies for fundamentally preventing TSEs. In this study, adult Leizhou goats were used as both donors and recipients. Donor goats underwent superovulation using a controlled-release drug delivery device, progesterone, and decreasing doses of follicle-stimulating hormone (FSH) and luteinizing hormone (LH); recipient goats were synchronized using a controlled-release device (CIDR), gonadotropins from pregnant mares, and prostaglandins. Two sgRNAs targeting exon 3 of the goat *PRNP* gene were designed and complexed with the Cas9 protein to form ribonucleoprotein (RNPs). Single-cell zygotes recovered approximately 10 hours after laparoscopic artificial insemination were treated via microinjection with Cas9/sgRNA RNPs and cultured at 37°C and 5% CO₂ until the 2–4 cell stage, after which they were surgically transferred to the ampullary segment of the fallopian tubes of the synchronized recipient goats. A total of 13 microinjected zygotes were transferred into three recipient goats, resulting in one successful pregnancy and the birth of three live offspring (designated No. 11, No. 14, and No. 33). PCR amplification and Sanger sequencing confirmed that the editing efficiency was 100% in all offspring. Specifically, kid No. 11 exhibited a 591-bp deletion in the coding sequence (CDS) of exon 3 and was biallelic knockout. Continuous growth monitoring showed that these goats exhibited normal health and physical development, comparable to the wild-type control group. In this study, using CRISPR/Cas9 RNP microinjection and zygote transfer techniques, we successfully generated *PRNP*-knockout Leizhou goats with a 100% editing efficiency. The disruption of the *PRNP* coding region (CDS) did not adversely affect the goats' physiological growth or survival rate. These results establish an efficient platform for breeding prion-resistant ruminants and advance research on the prevention and control of TSEs.

Keywords: Prion resistance, *PRNP* gene, CRISPR/Cas9, Gene editing, Leizhou goat, Transmissible spongiform encephalopathies

Lactobacillus pentosus W17 alleviates intestinal inflammation and oxidative stress by regulating AEA and the intestinal microbiota

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Abstract: A newly isolated strain, *Lactobacillus pentosus* (L. pentosus) W17 from healthy goat feces, protects against *Salmonella Typhimurium* (S. Typhimurium)-induced intestinal inflammation and oxidative stress in mice. The strain showed good acid (pH 2.0, 66.3% survival) and bile salt (0.3%, 38.7% survival) tolerance, strong self-aggregation (82.1%) and co-aggregation with S. Typhimurium (77.0%), and no hemolytic activity. In infected mice, administering W17 before infection preserved intestinal barrier proteins (Occludin, Claudin-1, ZO-1), lowered pro-inflammatory cytokines (TNF- α , NF- κ B, IL-1 β , IL-18) and myeloperoxidase activity, and eased oxidative stress (reduced malondialdehyde, increased superoxide dismutase and glutathione). 16S rRNA sequencing and metabolomics further showed that W17 reshaped the gut microbiota by boosting short-chain fatty acid-producing genera including Lachnospiraceae, *Odoribacter*, and *Rikenella*. W17 restored intestinal anandamide (AEA) levels that dropped sharply after *Salmonella* infection, which in turn activated the Nrf2/HO-1 antioxidant pathway. Preventive administration of W17 was more effective than therapeutic administration or the antibiotic enrofloxacin. These results point to AEA as a key mediator of probiotic action and suggest that L. pentosus W17 could be a promising candidate for combating intestinal inflammatory diseases in goats and potentially other livestock species, as well as humans.

PART3: Economy, Sociology, Production systems, Housing

Goat farming: a viable livelihood avenue in semi-arid communal rangelands in KwaZulu-Natal, South Africa

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Abstract: Livestock production is a primary means of livelihood for communal farmers. However, production is hampered by degrading rangelands, theft, drought, diseases and mortalities, which minimise the value of livestock farming as a viable option for livelihood. However, goats are resilient and thrive even under harsh conditions. We identified and quantified constraints to communal goat farming in a semi-arid environment in KwaZulu-Natal, South Africa. We determined goat mortalities, sales, slaughters and theft varying herd sizes i.e. 17 herds in 2017-2018 and 13 in 2022-2023 in Msinga. We counted the number of live, dead, slaughtered, sold and lost goats in each herd. We sexed and aged the goats for the different category counts. We used descriptive statistics to analyse the data. We counted 2628 and 4945 goats in 2017-2018 and 2022-2023, respectively. The composition of herds was skewed towards more does (38-42%), while Billy goats were least (1-2%) in both year periods. Adult mortalities were low (< 2-3%; N = 144) in both years, with kid mortalities reaching 30% (N = 237) in the 2017-2018 period. Losses due to theft were low at 1% (N = 41) in both years. Females and castrates were disproportionately (N = 36; 89%) stolen with castrates stolen to a lesser extent. Only 375 (7%) were sold over the two-year periods, while 91 goats representing about ZAR227 500 were slaughtered for household use. Goat farming and productivity appeared to be stable, if not greater, in the latter year period despite the prevailing challenges associated with theft and mortalities. Sales and slaughters were the dominant forms of goat utilisation in Msinga. Mortalities of adult goats and theft happened less, and did not appear to constrain productivity. Supplementary feeding could reduce starvation and mortality. Ultimately, goat farming could be a lucrative and stable income avenue for small-scale farmers.

Keywords: Mortality, Production, Sale, Small-scale farming, Theft

Dynamics and Management of Extended Lactations in French Dairy Goat Herds: From Reproductive Adjustment to Strategic Choice

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Introduction Traditionally, dairy goat management relies on an annual kidding cycle with a lactation period of approximately 300 days. However, caprine physiology allows for the extension of milk production without an intervening kidding event. In France, "extended lactation" (EL) is defined as a continuous production period exceeding 485 days (approximately 16 months). This practice has rapidly expanded, evolving from a "subsided" method used to manage reproductive failures ("imposed" EL) to a "chosen" management strategy ("chosen" EL) aimed at increasing system flexibility.

Methods This study is based on longitudinal data from the French milk recording database collected between 2011 and 2024, representing over 4.4 million lactations in about 2,700 herds (between 1,196 and 1,638 herds according to the year). The evolution of productive time spent in EL, animal performances, and herd-level management factors were analyzed.

Results and Discussion. The share of productive time spent in LL remained below 5% until 2012 but surpassed 12% in 2024. In 2023, 16% of initiated lactations became EL. By 2024, nearly 70% of herds in performance testing utilized EL to some degree. The practice is particularly prevalent in larger herds, out-of-season breeding systems, and herds dominated by the Saanen breed. Furthermore, very long lactations (≥ 28 months) now constitute more than 25% of all extended lactations.

Production analysis shows that goats in EL exhibit atypical lactation curves characterized by cyclic production "rebounds" occurring roughly every 350 to 400 days (at approximately 500, 850, and 1,200 days). The comparison of the production of EL over two years with two successive lactations over the same 660-day period shows that the total quantity of milk produced is generally equivalent, or even slightly higher in favor of the EL.

Breeder motivations can be grouped into four main pillars. First, management flexibility is enhanced by synchronizing primiparous goats with the adult herd and allowing continued growth without early rebreeding. Second, economic optimization is achieved through increased winter milk production, reduced replacement costs, and improved building utilization. Third, work organization benefits from fewer kidding events (decrease of the workload associated with neonatal care and the rearing of replacement kids), leading to smoother labor distribution and more consistent milk supply, particularly for on-farm processing. Finally, EL support market adaptation by ensuring year-round milk production and reducing dependence on volatile kid meat markets. Overall, this approach contributes to improved technical efficiency, economic performance, and labor conditions. However, farmers and their advisors highlight several points of attention regarding the selection of females for extended lactations (milk performance and udder health) as well as herd management practices: forage quality, ration adjustment to avoid excessive body condition, and the use of separate groups to better meet the specific needs of the animals.

Conclusion Extended lactations have evolved into a major strategic tool for the resilience of French goat farming systems. While the technical benefits are clear for productivity and work reorganization,

ongoing research is necessary to fully understand the long-term impacts on genetic progress and herd longevity.

Keywords: goats, extended lactation, farming system

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Life on the Edge of Changthang: An Overview of Threatened Nomadic Culture of Ladakh

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Abstract: “Changthang,” a Tibetan word meaning “western plateau,” is the name given to the vast plateau of Tibet lying to the west of China and extending into the Indian side in Ladakh. The area is known for its hostile terrain, with a very low hydric index, an altitude ranging from 14000 ft to 16000 ft asl, and temperatures ranging from 30 in summer to -40 during winter. The area is full of rugged mountains, barren land, and dispersed pasture grasses, fostering world-unique germplasm such as Changthangi Cashmere goats, Changthangi Sheep, Semi-domesticated Yak, Zanskari horse, and *Bos taurus* in the form of Local cattle. It is also the habitat of the world's precious wild life germplasm like Snow leopard, Tibetan antelope, Tibetan Gazelle, Tibetan Wolf, Red Fox, Blue Sheep, Argali, Wild Yak and many wild birds etc. The native ‘Changpa’ tribal people inhabit the Changthang region, who migrate from one place to another with their livestock throughout the year. The pashmina, internationally known as cashmere, is the finest fibre of all domestic animals produced by several breeds of pashmina goat all over the world, and our Changthangi goat produces the finest pashmina fibre in the world. The livestock of the Changthang region has sustained the economy of thousands of Changpa nomads since the beginning, and they have lived in a harmonious way to date. Now, due to poor production from livestock, low market value for livestock products, limited pastures, hard life, alternative and easy source of income like tourism, these nomads are migrating towards towns, leaving their age-old practice of pastoralism. A detailed study in this regard has been conducted under AICRP on the Changthangi goat and presented in this article.

Key Words: Changthang, Changpa, Livestock, Pashmina.

Effects of grazing and adding supplementary feeding on goats (*Capra hircus*) and forage biomass

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Abstract: Overgrazing can lead to grassland degradation, reduced forage production, and lower animal performance, whereas appropriate grazing intensity combined with supplementary feeding can enhance animal productivity and economic returns while maintaining or improving pasture condition. This study aimed to evaluate the effects of different grazing intensities on goat performance and forage biomass, to assess the impact of combining grazing with supplementary feeding on grazing capacity and economic efficiency, and to identify an optimal regime for Guizhou black goats that balances productivity with grassland sustainability and supports rational grazing management. This study used Guizhou black goat ewes and wethers as experimental animals. Weighing and mowing methods were employed to measure the effects of different grazing intensities, with and without supplementary feeding, on goat body weight, serum biochemical parameters, and pasture forage biomass. The results showed that grazing intensity significantly affected grassland forage biomass and post-grazing herbage regrowth rate. Overall, weight gain in the light-grazing group was greater than in the moderate-grazing group, which in turn exceeded that of the heavy-grazing group. Within the same treatment group, ewes had a significantly higher weight gain rate than wethers ($P < 0.05$). Comprehensive analysis indicated that combining grazing with supplementary feeding can significantly improve the grazing capacity and economic returns of grassland-based goat production. Increasing grazing intensity alone did not enhance the economic benefits of goat farming. Under a concentrate supplementation level of 0.15 kg/head/day and a leas-bean dreg supplementation level of 1.0 kg/head/day, the optimal grazing system for Guizhou black goats was identified as a stocking rate of 45 head/hm² with rotational grazing over a 24-day cycle, grazing each paddock for 6 days.

Keywords: Grazing intensity, Supplementary feeding, Guizhou black goats, Economic efficiency

Development of digital tools to support decision-making processes in the dairy goat sector using collaborative methodologies

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Abstract: The dairy goat sector in Spain has undergone a process of continuous evolution in recent decades, adapting to changing circumstances and providing responses that have enabled it to establish itself as a leading economic activity. Nevertheless, the sector faces a complex set of challenges, notably the loss of competitiveness, the weakening of the value chain, and the ageing of the workforce along with a lack of generational renewal. With the aim of ensuring the continuity of these livestock systems and attracting young people to the sector—promoting its digital and technological transformation—since 2018, functional groupings of stakeholders have been established in Andalusia (Spain). Through the support of the European Innovation Partnership (EIP-Agri), these groups have developed participatory methodologies that have led to the implementation of stable innovation partnerships for data analysis and processing, as well as for the development, testing, and co-creation of technological solutions, new products, and services. The alliance among the production sector—represented by the federation of Associations of Purebred Andalusian Producers and DCOOP, Spain’s leading goat milk cooperative—cutting-edge technology companies, and the University of Seville has contributed to the development and use of innovative digital tools, RUMIA/AmalteUS. These tools enable the straightforward collection of information and the generation of indicators that support improved decision-making in the technical-economic domain, the reduction of greenhouse gas (GHG) emissions, and enhanced resilience management within livestock farming operations. The final outcome is the implementation of a new way of working and interacting within the sector, making it more sustainable, profitable, competitive, digitalized, and socially recognized, while ensuring a stronger strategic position within the food supply chain and, in particular, greater bargaining power for its production.

Keywords: Dairy goat, Digitization, Technical-Economic Indicators, Decision-making support

Integrating the concept of resilience into a decision support tool for dairy goat farming: a methodological proposal

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Abstract: Resilience, understood as the ability of farms and livestock systems to maintain their activity in the face of increasing crises and trends affecting them, is based on five principles—reserves, diversity, connectivity, interaction and modularity—according to the Resilience Alliance (2010). In order to bring these concepts closer to the realities of the livestock sector, a methodological proposal has been developed to measure and enhance the resilience of small ruminant farms. Based on this proposal, a resilience module has been incorporated into the technical-economic management software (RUMIA/AmalteUS) used by dairy goat farmers associated with Cabrandalucía. This process involved: (i) the design of a questionnaire; (ii) the linkage of this new module with technical and economic indicators already calculated in RUMIA/AmalteUS; (iii) the design of an annual output report for technicians, compiling the results of 59 resilience indicators, 21 attributes and 5 principles; and (iv) the design of an annual output report for farmers, which, in addition to presenting the results obtained for their farm, includes a qualitative assessment of their level of resilience and potential areas for improvement. Sustained use of this tool over time will make it possible to relate management practices to changes in farm resilience and, thereby, contribute to the overall sustainability of livestock systems.

Keywords: Resilience, Indicators, Goat Farming, Sustainability.

The China's goat milk way: Opportunities and limitations in a growing market

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Abstract: Milk production and consumption steadied in China for many years because the lack of tradition and poor market and industry development. This changed dramatically with the modernization impulse of the dairy goat industry. A key step was initiated in the 1940's by Prof. Liu Yinwu at the Northwest A&F University (NWA&FU) in the Shaanxi province by improving the production systems and milk yields of 2 local goats breeds: the High Yielding Xinong Dairy Goat and the Guanzhong Dairy Goat. In the 1980's the breeds and the production systems proposed by Prof. Yinwu, including an ecological grass-goat-grain model, spread across China as a high-quality animal protein food resource. The goat's dairy products have currently gained relevant attention in China as popular food sources due to their nutritional properties, low allergenicity and functional components. The expansion of goat's dairy products was continued by Prof. Cao of the NWA&FU and firmly supported by the Chinese Dairy Industry. The Chinese Dairy Industry is nowadays shifting toward high quality standards and greater diversification by developing many improved dairy products based in fermentation (e.g. yogurt), essential mineral fortification (e.g. Se) and boosting immunity system using goat's milk, milk whey and colostrum. The increase in dairy consumption is also creating new opportunities for other small ruminant dairy products (i.e. sheep). Goat's milk has established recognition in China and international markets especially in milk dry powder of immediate dissolution addressed to family daily consumption. National statistics indicate that goat population is the world's largest, but milk production remains limited compared to cow's milk, suggesting that greater specialization is needed. Global comparisons show that, despite having high yielding Chinese farms and having implemented high reproductive and genetic technology, European systems achieve, on average, higher productivity through specialized breeds and high throughput processing chains. Consumer studies reveal interest in health benefits, but barriers remain related to taste, familiarity, and product availability. Production constraints include limited breeding systems, low processing capacity, and fragmented supply chains. In conclusion, China presents yet significant opportunities for goat's dairy development due to resource availability and growing demand. However, improving productivity, product diversification, and market acceptance are essential. Future research should integrate production efficiency, consumer behaviour, and supply chain development.

Keywords: Dairy products, Industry, History, Milk, Goat

Effects of Compound Microbial Inoculants on Bacterial Community Succession and Functional Association During Goat Manure Aerobic Composting

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Objective: Aerobic composting represents a key waste management strategy in goat production systems, where microbial communities serve as the primary driving force behind organic matter transformation and humification. While compound microbial inoculants have been shown to enhance composting efficiency, the mechanisms by which exogenous inoculants reshape indigenous bacterial communities and their functional correlation with composting progress remain poorly understood in goat manure systems. This study employed 16S rDNA sequencing to investigate the effects of compound microbial inoculants (*Bacillus subtilis*, *Trichoderma viride*, and *Aspergillus niger*) at different ratios on bacterial community structure, diversity, and functional associations during goat manure aerobic composting.

Methods: Goat manure and rice straw (10:1 dry weight ratio) were composted for 60 days with four treatments: a control group (CK, no inoculant), and three experimental groups supplemented with compound inoculants at 0.2% of dry weight, with *Bacillus subtilis*:*Trichoderma viride*:*Aspergillus niger* ratios of 1:1:1 (T1), 1:2:2 (T2), and 2:1:1 (T3). Samples at days 7, 31, and 60 were subjected to 16S rDNA sequencing (36 samples total). Analysis included alpha and beta diversity, phylum- and genus-level taxonomic profiling, linear discriminant analysis effect size (LEfSe), and Spearman correlation between differential taxa and physicochemical parameters.

Results: A total of 22,483 operational taxonomic units (OTUs) were detected. Partial least squares discriminant analysis confirmed that inoculant addition significantly altered bacterial community structure ($P < 0.05$). Firmicutes dominated during the thermophilic phase (76–85%) but declined sharply, while Bacteroidota, Proteobacteria, and Actinobacteriota increased significantly during maturation. T2 exhibited significantly higher Deinococcota abundance at days 7 and 60 ($P < 0.05$). LEfSe revealed that *Glycomyces*, *Planktosalinus*, and *Parapedobacter* were significantly enriched in T2 at day 31; *Truepera* and *Membranicola* were significantly enriched in T2 at day 60. Spearman correlation analysis showed *Truepera*, *Longispora*, and *Aequorivita* significantly positively correlated with nitrogen content, and *Paenibacillus* positively correlated with temperature.

Conclusion: The 1:2:2 compound inoculant reshaped the bacterial community by selectively enriching functionally relevant taxa (*Truepera*, *Membranicola*) positively associated with nitrogen retention during the maturation phase, revealing an "inoculant–community–function" regulatory pathway that enhances both biological efficiency and environmental safety of goat manure management in goat production systems.

Keywords: goat manure composting, 16S rDNA sequencing, Bacterial community succession, Microbial inoculants, Spearman correlation

The Role of Climate-Induced Hazards in Farmers' Knowledge and Adoption of Risk-Mitigating Technologies_ Evidence from Low- and High-Risk Goat Farming Areas in India

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Abstract: Our understanding on knowledge and adoption of climate risk-mitigating technologies in livestock/agriculture farming remains minimal. Existing research highlights socio-cultural, farming and innovation attributes as drivers of adoption leaving behind the role of climate-induced hazards. To address the research gap, researchers conducted random-effects meta-analysis of published literature. Pooling the results of studies showed that farmers in high and low hazardous states had similar knowledge levels and overall extent of adoption of risk mitigating technologies. In high incidence states, the extent of adoption vaccination, deworming, ectoparasite control, healthcare and breeding practices was higher by 29.44, 8.14, 29.94, 11.23 and 9.93 percentage points, except feeding. The extent of vaccine adoption was only significantly higher with absolute difference. The extent of vaccine adoption had a significant difference of 29% percentage points ($p < 0.001$) and hazard classification explained 82% between study variance (Figure 1). While in case of deworming, breeding and healthcare showed higher adoption but high statistical uncertainties and high heterogeneity limits interpretation. Added studies on ectoparasite suggest large adoption gap, but limits inference on account of few studies. The overall adoption of goat farming technologies in low and high incidence states was 46.75% and 40.56% respectively with -6.19 percentage point difference. Further, adoption of feeding practices and knowledge on risk mitigating technologies has low percentage point difference among hazard levels and confidence interval overlapped with zero indicating no relationship between hazard and adoption. This study also found women farmers had lower knowledge (28–37%) and adoption (35%) compared to pooled averages of 49% and 42%, respectively, reflecting gender disparities. This suggests that adoption of technologies addressing explicit threats in goat rearing is shaped by hazard level leaving less perceptible or indirect technologies.

Keywords: Climate Adaptation, Natural Hazards, Goat farming, Extension system, Adoption

Effects of compound lactobacillus plantarum inoculant on maturity, greenhouse gas emissions and microbial community structure of manure composting

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Abstract: To address the problems of environmental pollution, high greenhouse gas emissions and low maturity quality existing in manure composting, sheep manure was used as the sole raw material in this study. Two treatments were established: a control group without inoculant addition and an experimental group supplemented with 0.1% compound Lactobacillus plantarum inoculant (p326: p002 = 1:1). The compost temperature, carbon dioxide (CO₂) emission, maturity indices, nutrient contents, transformation characteristics of calcium and zinc, and microbial community were continuously monitored during composting. The results showed that compared with the control group, the compound inoculant prolonged the high-temperature period by 1 day and significantly reduced the cumulative CO₂ emission flux by 46.52% ($P = 0.05$). It significantly increased the electrical conductivity at the end of composting and decreased the E4/E6 value ($P < 0.05$), which promoted the rapid maturity of compost. Meanwhile, the compound inoculant remarkably improved the transformation efficiency of total phosphorus, total nitrogen and organic matter, and enhanced calcium stability and zinc passivation rate ($P < 0.05$). In addition, it significantly reduced the relative abundances of *Chloroflexota*, *CU05-9* and *Fodinicurvata* ($P < 0.05$) and optimized the microbial community structure. In conclusion, the compound Lactobacillus plantarum inoculant can effectively reduce greenhouse gas emissions, improve compost maturity and optimize microbial community structure, which provides theoretical basis and technical support for the efficient resource utilization of livestock and poultry manure.

Keywords: Manure composting, Compound Lactobacillus plantarum inoculant, Greenhouse gas emission reduction, Compost maturity, Microbial community structure

Generational Renewal in the Goat Farming Sector through the Andalusian Shepherds' School (Spain)

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Abstract:

The Andalusian Shepherds' School, coordinated by the Andalusian Institute for Agricultural and Fisheries Research and Training (IFAPA), is an innovative initiative aimed at promoting generational renewal in extensive livestock farming, particularly within the goat sector in southern Spain. The programme combines traditional pastoral knowledge with modern technical and managerial skills adapted to current farming challenges.

Spanish goat sector faces important structural problems, including an ageing farming population, low incorporation of young farmers, labour shortages, and rural depopulation. In response, the Shepherds' School offers specialized theoretical and practical training in animal management, animal welfare, farm economics, sustainability, and digital technologies applied to extensive production systems.

A key component of the programme is its mentoring-based approach, in which experienced shepherds and goat farmers supervise trainees during practical placements on commercial farms. This system facilitates the transfer of practical knowledge and encourages the continuity of family farming systems. Since its creation, the School has trained more than 200 students and 200 farmers, with a high percentage subsequently entering livestock-related activities.

Beyond its socioeconomic impact, the initiative contributes to environmental sustainability, as extensive goat farming plays a significant role in biodiversity conservation, wildfire prevention, and maintenance of Mediterranean ecosystems. The programme also promotes entrepreneurship and the participation of women and young people in rural areas.

In conclusion, the Andalusian Shepherds' School represents a successful model of professional training, knowledge transfer, and rural development that supports generational renewal and long-term sustainability in the Andalusian goat farming sector.

Keywords: young people, grazing systems, training, promotion

Non-contact body weight estimation of goats (*Capra hircus*) using lightweight PointNeXt-S segmentation and hybrid 3D point-cloud phenotyping

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Objective: Accurate, low-stress body weight monitoring is essential for precision feeding, growth assessment, health management and intelligent goat production. This study aimed to develop a non-contact goat body weight estimation framework by integrating lightweight 3D point-cloud segmentation, anatomical-region feature extraction and grid-filling volumetric modelling.

Methods: Multi-view goat point clouds were acquired using three structured-light depth cameras arranged in a top-and-bilateral configuration and stored in PLY format. Raw point clouds were processed by voxel downsampling, RANSAC-based ground removal, preliminary segmentation and normalization. A lightweight PointNeXt-S network was used to divide the goat body into the back, chest, hip and other regions. To improve suitability for limited livestock samples and on-farm deployment, the encoder width, residual-block number and expansion ratio were reduced, and online rotation augmentation was applied. After semantic segmentation, three categories of predictors were extracted. The first comprised linear morphometric traits, including body length, body width, body height, chest width, chest depth, hip width, back length and other body-size descriptors. The second comprised area-related descriptors from segmented regions, such as back area, chest area, hip area and projected surface areas. The third comprised grid-filling volume features. For volumetric estimation, a 3D bounding box was expanded around the cleaned goat point cloud, a regular grid was generated, and KD-Tree nearest-neighbor searching was used to classify occupied grid nodes. Body volume was then calculated from the occupied grid cells. Final body weight was estimated using a hybrid regression model combining dimension-based, area-based and volume-based predictions.

Result: Preliminary livestock point-cloud segmentation experiments showed that PointNeXt-S with online augmentation achieved an overall accuracy of 92.4% and a mean intersection over union of 81.1%, using only approximately 0.81 million parameters. The IoU values for the back, chest, hip and other regions were 89.6%, 79.2%, 75.5% and 79.9%, respectively. The lightweight model achieved accuracy comparable to PointNet2 MSG while requiring substantially fewer parameters and shorter training time. For goat body weight estimation, grid-filled point-cloud volume showed a strong linear relationship with actual live weight, with an R^2 greater than 0.95, and reduced prediction error to approximately 4%. The hybrid model further improved interpretability by linking body weight to segmented body dimensions, regional areas and volumetric features.

Conclusion: This study provides a deployable 3D point-cloud phenotyping workflow for non-contact goat body weight estimation. The combination of PointNeXt-S segmentation and hybrid feature fusion supports automated weighing, precision feeding, body condition monitoring and intelligent goat production management. Future work will expand goat-specific annotations, optimize PointNeXt-S with KAN and attention mechanisms, and validate the model under complex farm conditions.

Keywords: Goat, Body weight estimation, 3D point cloud, PointNeXt-S, Semantic segmentation, Grid-filling volume, Precision livestock farming

Study on the Immunocastration Efficacy of a Novel GnRH Vaccine

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Objective: Surgical castration can improve meat quality but raises animal welfare concerns. Our group previously developed a tandem repeat GnRH(30) recombinant vaccine that successfully induced immunocastration in Leizhou black goats, significantly suppressing reproductive function and improving meat quality. However, its cross-species applicability in pigs remained unclear. To address this, we established three models—intact control (IC), surgical castration (SC), and immunocastration (IM)—in Guangdong-Guangxi small-ear spotted pigs to compare reproductive suppression and meat quality, thereby validating cross-species feasibility.

Methods: Nine male Guangdong-Guangxi small-ear spotted pigs (77 d, 12±2 kg) were randomized into IC (untreated), SC (surgical castration at 3–7 d), and IM (subcutaneous GnRH vaccine at 11 and 20 wk, 4 mL). Slaughtered at 43 wk. Serum testosterone and anti-GnRH antibodies (ELISA); testicular histology (HE); qPCR for HPG axis, spermatogenesis, apoptosis, and inflammation-related genes; meat quality traits. One-way ANOVA with Tukey HSD.

Results: IM group: anti-GnRH Ab peak ~0.9–1.0 at 16 wk ($P < 0.01$ vs IC/SC) (**Figure 1A**); serum T dropped from ~10 to <2 ng/mL by wk 30 (comparable to SC, $P < 0.001$ vs IC) (**Figure 1B**); testis (~30 g) and epididymis (~7 g) lower than IC (~88 g, 21 g) ($P < 0.001$); histology showed tubular atrophy and spermatogenic cell loss; hypothalamic Kiss1, pituitary Gnhrh, testicular Cyp17a1 ↓ ($P < 0.01$ –0.0001); spermatogenic genes SYCP3, PRM1 ↓; apoptosis imbalance. Meat: FCR ~3.4 (vs SC ~4.8, $P < 0.01$); glutamate in longissimus dorsi ~900 vs SC ~150 µg/100g ($P < 0.0001$); carnosine in semimembranosus ~14,000 vs IC/SC ($P < 0.01$).

Conclusion: The novel GnRH(30) vaccine successfully achieved immunocastration in Guangdong-Guangxi small-ear spotted pigs, effectively suppressing reproductive function, inducing testicular atrophy, blocking spermatogenesis, and significantly improving meat flavor. These findings are highly consistent with previous results in Leizhou black goats, demonstrating reliable cross-species applicability of this vaccine.

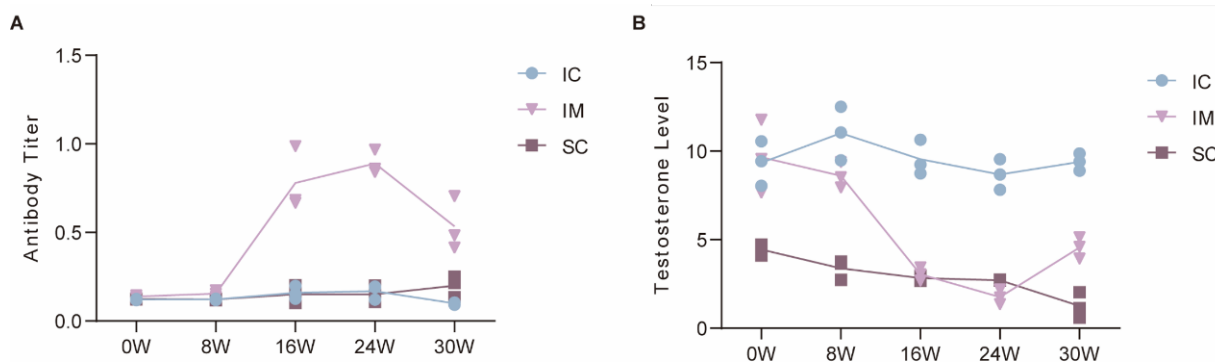


Figure 1. Anti-GnRH antibody and testosterone dynamics in immunized pigs.

Keywords: GnRH ; immunocastration; Leizhou goat; small-ear pig; reproduction; animal welfare

PART 4: Genetics, Selection, Breeds, Genome

Evaluation of coefficient of variation for different morphometric traits of goat breeds in Kerala

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Abstract: Within a breed there are variations in morphometric traits which helps them to adapt better to the local micro climatic conditions and topography of a particular region where they are reared. By studying the phenotypic characterization of the same breed in different regions we can understand their evolutionary changes better. However, it is difficult to compare different morphometric traits together and for this reason coefficient of variation (CV) can be used. Measurements were recorded with the help of a measuring tape and the live body weight was obtained using a digital weighing balance. The mean and standard deviation for each trait was calculated using SPSS V.26. The coefficient of variation for each trait from each centre was calculated using the standard formula. The current study was undertaken on 403 Malabari and Attappady Black goats from four distinct regions spread across central and north Kerala districts. Malabari does, two years of age were selected from organized farms at Mannuthy (178), Pookode (61), Thiruvizhamkunnu (29) and Kottakkal (35). It was reported that the animals from Pookode had the highest CV% for bodyweight (37.24) followed by the animals from Mannuthy (23.63) with animals from Kottakkal having the least CV% with a value of 22.79%. The highest variation in body length was reported in animals from Mannuthy (17.12) and the least from Kottakkal (7.27). Least variation in body height was reported for animals from Thiruvizhamkunnu and the highest was for animals from Pookode. The coefficient of variation for chest circumference was observed to be 13.66% for animals residing in Pookode while the animals from Mannuthy had a CV% of 7.9. The Attappady Black does were selected from Mannuthy (48), Attappadi region (31) and Thiruvizhamkunnu (21). It was found that the animals from Mannuthy exhibited maximum variation for body weight (23.16%) compared to the animals from Attappadi region which exhibited the least variation (8.66%). Similar results were reported for body length and body height. Higher CV% was reported from Mannuthy goats for chest circumference (9.15%) and cannon bone circumference (9.32%). For both breeds it was reported that the CV% for morphometric traits was less than 10% although body length, chest circumference and cannon bone circumference in Malabari goat had a CV% of greater than 10%. The CV% for body weight in both breeds was over 20%. While morphometric traits in adult animals does not change significantly over a short period of time, body weight is affected by different factors on a daily basis. The current study highlights the variation in different morphometric traits within a breed based on their geographical location and could shed insight on local adaptations of a breed.

Keywords: Coefficient of variation, Malabari, Attappady Black goats, India, Morphometric traits

A palaeogenomics investigation of archaeological *Caprinae* remains from Ethiopia and Eritrea: Challenges and considerations

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Abstract: Despite ancient DNA (aDNA) research revealing valuable bio-cultural insights into livestock domestication, it faces major challenges due to poor preservation, degradation, and contamination, which hinder species identification, data analysis, and interpretation. This study aimed to assess endogenous DNA content, evaluate taxonomic species screening pipelines and discuss the technical challenges encountered in aDNA analysis. Fourteen *Caprinae* specimens from four sites in Ethiopia and Eritrea (curated at the Ethiopian Museum) were shotgun sequenced following DNA extraction, library construction, and amplification. Four samples (ST01, ST02, ST09, and ST11) were identified as domestic goats using HAYSTAC, BLAST, and phylogenetic approaches. These samples had been previously identified as goats using osteological criteria. The PALEOMIX pipeline was also used to visualise and quantify post-mortem DNA damage patterns and confirm the authenticity of endogenous DNA. Nuclear and mitochondrial genome coverage was low throughout all 14 samples (~0.005% and 0.25%, respectively). The four goat samples showed a relatively higher mapping rate when aligned to the goat reference genome assembly (ARS1) using the PALEOMIX pipeline compared to the sheep reference genome (ARS-UI_Ramb_v2.0). Our aDNA samples were significantly degraded due to exogenous and endogenous DNA-damaging factors. As a result, it was difficult to further assess the genetic comparison between ancient and modern goat populations. However, the pipelines, procedures, and approaches used to screen ancient goats from other ancient caprine species, along with the visualization and quantification of post-mortem DNA damage patterns, are critically important, all of which can open doors for further research on ancient goats and other livestock species.

Keywords: Ancient DNA; *Caprinae* species; East Africa; Species identification

Study on Genetic Diversity in Changthangi Cashmere Goats of Ladakh using Microsatellite Marker

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Abstract: The genetic diversity in a population is the backbone for future breeding plan and improvement. In a remote Tibetan plain of Changthang the only way to study the diversity among Cashmere goat is using the molecular genetics tools like Microsatellite. The present study was undertaken to study the genetic diversity among different subpopulations of Changthangi Cashmere goats of Ladakh India in which 15 highly polymorphic microsatellite markers from the list suggested by ISAG-FAO were used. The maximum no of alleles (15) was observed for locus ILSTS-087 and minimum (4) observed for ILSTS-005. The overall mean observed number of alleles across all loci was 9. The average observed homozygosity and heterozygosity was 0.25 and 0.75 respectively indicating selection process favoring heterozygosity over a period of time. The overall mean of Shanon's Information Index for the whole population and polymorphism information content value (PIC) observed was 1.66 and 0.7117 respectively, indicating presence of wide diversity among Changthangi Goats of Ladakh. The mean FIS, FIT and FST values for the whole population are found to be -0.0433, 0.0121 and 0.0531, respectively with a gene flow rate of 4.4601. The low FIS and FIT values indicate low level of inbreeding within the population and also point towards low genetic differentiation within the populations. Multilocus FST values indicated that around 5.31% of the total genetic variation was explained by a population difference, the remaining 94.69% corresponding to differences among individuals. Estimation of genetic distance using Nei's genetic distance method between different clusters shows that the Changthangi goat has a diverse population with great scope for improvement. Deviations from Hardy-Weinberg equilibrium were noted for most of the locus. Bottleneck analysis revealed no bottleneck for Changthangi Goat population under all the three mutation models for sign test, the standardized difference test and Wilcoxon rank test. The overall result of the study indicates a highly diverse Changthangi Cashmere goat population and the genetic distance computed from the present study can be utilized for implementing a sound future breeding programme for the genetic improvement of this goat for pashmina production.

Key words: Allele, Changthangi goat, Cashmere, Genetic diversity, Microsatellite markers, Pashmina.

Phenotypic and genetic trends for productive variables on Zaraibi Goats

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Objectives: Estimated genetic parameters beside phenotypic and genetic trends for growth traits on Zaraibi goats.

Methods: The dataset included measurements on 673 kids, the progeny of 15 bucks and 213 does gathered between 2018 to 2020. Variables studied are birth weight (BW), weaning weight (WW) and average daily gain from birth to weaning (ADG). All variables were analysis using animal model implemented in the MTDFREML. The model includes the fixed effects of month and year of birth, sex and type of birth and random effects of animal, permanent environmental factors and error.

Results: The overall mean was 2.03 ± 0.01 kg for BW, 10.18 ± 0.08 kg for WW and 0.90 ± 0.001 g/day for ADG. Statistical analyses indicated that, year of birth sex and type of birth had significant ($p < 0.01$) effects on all traits, while the month of birth had no significant effect ($p > 0.05$) on all traits genetic correlation among all traits studied were positive and highly significant and ranged from 0.76 to 0.95. Annual phenotypic trends for BW, WW and ADG were 0.14 ± 0.02 kg/year, 0.37 ± 0.10 kg/year and 35 ± 0.001 g/year for ADG. Annual genetic trends for BW, WW and ADG were 0.009 ± 0.003 kg/year, 0.0195 ± 0.004 kg/year and 23.10 ± 0.002 g/year, respectively.

Conclusion: The present results suggested that breeding programs should therefore prioritize direct selection for growth performance. Positive phenotypic and genetic trends for BW, WW and ADG could be due to plan of selection of bucks for increase birth and weaning weights of kids.

Key words: Phenotypic Genetic Trends Zaraibi Goats

Association analysis of polymorphic sites in the *IGFBP5* promoter region of dairy goats and their lactation traits

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Objective: The dynamic balance between the proliferation and apoptosis of mammary epithelial cells (MECs) is a key factor determining milk yield and lactation duration. Insulin-like growth factor binding protein 5 (*IGFBP5*) exhibits cyclical variation in goat mammary tissue and functions to promote MEC apoptosis. This study aimed to identify the core promoter region and key transcription factors of the *IGFBP5* gene in Laoshan dairy goats, and to analyze the association between single nucleotide polymorphisms (SNPs) in the promoter region and lactation traits.

Methods: We analyzed the upstream sequence of the *IGFBP5* transcription start site and constructed six luciferase reporter plasmids (P1-P6) containing 5' end deletion fragments. These were transfected into HEK293T cells to detect dual-luciferase activity to identify the core promoter. Potential transcription factor binding sites were predicted using online tools like Jaspar, and site-directed mutagenesis was performed to validate the regulatory effects of candidate transcription factors. Furthermore, KASP high-throughput genotyping technology was utilized to genotype a key SNP in 368 Laoshan dairy goats, and a general linear model (GLM) was applied for association analysis with lactation traits.

Results: The P6 fragment (-253 bp to +265 bp) exhibited significantly higher transcriptional activity ($P < 0.05$), identifying it as the core promoter region of *IGFBP5*. Mutations at the Sp1 and Zeb1 binding sites had no significant effect ($P > 0.05$). However, the CEBPA binding site mutation led to a significant decrease in relative luciferase activity ($P < 0.05$), preliminarily confirming CEBPA as an important positive regulator driving *IGFBP5* transcription. Population genetic analysis revealed a moderately polymorphic SNP (g.31118538G>T) in the promoter region. Association analysis demonstrated that this locus was significantly associated with total solids, non-fat milk solids, and milk fat content. Notably, the heterozygous TG genotype showed highly significant heterosis for total solids and non-fat milk solids ($P < 0.01$), while the TT genotype exhibited the optimal phenotype for milk fat content ($P < 0.05$).

Conclusion: This study successfully cloned the core promoter sequence of the *IGFBP5* gene in dairy goats and elucidated the molecular mechanism by which the CEBPA transcription factor targets the core region to positively drive transcription. The identified key SNP (g.31118538G>T) has significant regulatory potential on core lactation traits. These findings provide a solid theoretical basis and critical molecular markers for marker-assisted selection and the efficient propagation breeding of high-quality milk components in Laoshan dairy goats.

Keywords: Laoshan dairy goats, *IGFBP5* gene, core promoter, CEBPA transcription factor, SNP association analysis

Developmental and Tissue-Specific DNA Methylation Dynamics of the ACSL5 Gene and Their Correlation with Expression in Fuqing Goats

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Objective: Lipid metabolism is a key determinant of growth and meat quality in goats. The *acyl-CoA synthetase long-chain family member 5 (ACSL5)* gene is essential in lipid metabolism, but the epigenetic mechanisms regulating its expression, especially CpG island methylation, remain largely unclear in goats. This study aimed to explore whether intronic CpG-rich methylation regions are involved in regulating *ACSL5* gene expression in goats.

Methods: A CpG-rich methylation region (MR) at 947–1192 bp in the first intron of the *ACSL5* gene was identified. Bisulfite sequencing PCR was used to detect methylation levels in multiple tissues of Fuqing goats at different developmental stages. The mRNA expression of the *ACSL5* gene was measured by quantitative real-time PCR. Spearman's correlation was analyzed the relationship between MR methylation and transcript abundance of the *ACSL5* gene.

Results: The MR showed distinct tissue-specific methylation patterns: the highest levels appeared in kidney and adipose (75%–100%), and the lowest in liver (35%–73%). Hypermethylation in brain increased with age (Figure 1A). The mRNA level of the *ACSL5* gene was most abundant in liver, followed by skeletal muscle, and was significantly lower in adipose after birth (Figure 1B). A weak negative correlation was detected overall, with stronger negative correlations in kidney ($\rho = -0.624$, $P = 0.001$) and biceps femoris ($\rho = -0.441$, $P = 0.001$).

Conclusion: The study suggests that intronic methylation of the *ACSL5* gene may serve as a key epigenetic mechanism regulating its expression in goats. This finding provides insights into potential genetic selection strategies for livestock improvement based on methylation patterns.

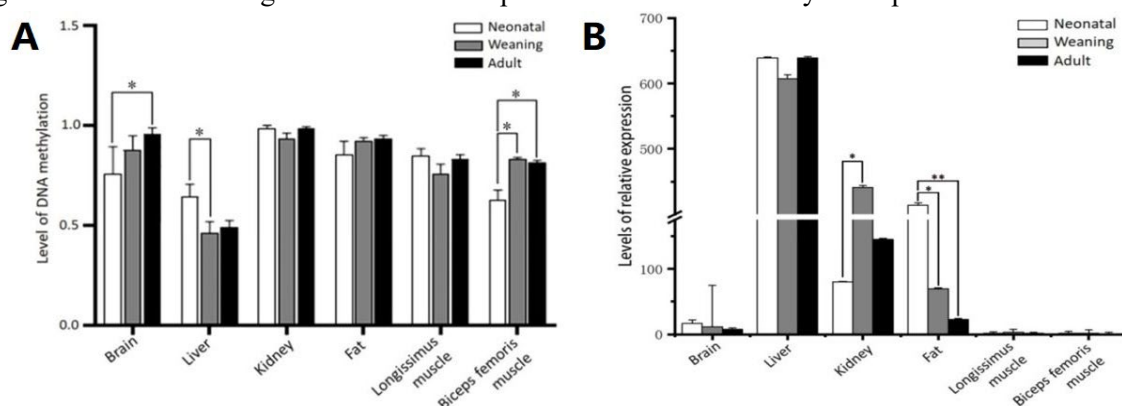


Figure 1. Methylation patterns of the IVS1 MR across tissues (a) and across stages (b)

Keywords: Goat; *ACSL5* gene; Developmental stage; DNA methylation; Correlation analysis

Integrating genomic selection and reproductive management to Improve breeding efficiency and cashmere quality in superfine cashmere goats

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Abstract: The cashmere goat industry is confronted with dual challenges: the degradation of cashmere quality caused by extensive crossbreeding and the long cycle of conventional breeding programs. To address these issues, this study established an efficient breeding system for superfine cashmere goats by integrating advanced genomic technologies and optimized reproductive management. First, a breed-specific genomic reference panel for Alashan cashmere goats was constructed, with an imputation accuracy of 0.979; the single-step GBLUP (ssGBLUP) model was identified as the optimal approach for genomic selection, with a prediction accuracy ranging from 0.347 to 0.375, enabling efficient early-generation selection. Second, an open nucleus breeding system combined with multiple ovulation and embryo transfer (MOET) and customized management software was implemented to accelerate genetic gain. Third, the application of traditional Chinese medicine-induced estrus synchronization successfully achieved three lambings in two years per ewe, increasing the annual reproductive rate by more than 40%. Through continuous selective breeding, the nucleus flock ($n = 2465$) reduced the average cashmere fiber diameter to 14.48 μm while maintaining high cashmere yield (726.62 g). Over the past five years, 1315 superior breeding rams have been disseminated, improving 263,000 local goats. This integrated system effectively breaks the negative genetic correlation between fiber diameter and cashmere yield, providing solid technical support for the high-quality and sustainable development of the global cashmere industry.

Keywords: Superfine cashmere goat, Genomic selection, Single-step GBLUP, Population reproductive efficiency, Quality improvement and efficiency enhancement

Can phenotypes enlighten our understanding of goats' origins? An Example from the Hong Kong goat population

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Abstract: While commercial goat breeds are well characterized globally, goat populations not subjected to selective breeding often lack phenotypic descriptions. This knowledge gap is particularly significant in regions such as Hong Kong, where import histories and breeding records are sparse. This study aimed to describe and compare the phenotypes of Hong Kong goats with those of other breeds. In winter 2026, 187 healthy adult female goats were randomly selected from 17 farms across Hong Kong. Five morphological traits and six morphometric measurements were recorded according to the Food and Agriculture Organization's guidelines and compared with published goat phenotypes, using Hierarchical Clustering on Principal Components, and t-distributed Stochastic Neighbor Embedding. Hong Kong female goats were predominantly black (34.2%, 64/187), bearded (62.2%, 117/187), with curved horns (70.1%, 131/187) and erect ears (74.9%, 130/187). All females had long hair. On average, wither height, chest girth, and body, ear, horn, and head lengths were 59.91 cm ($\pm$ 4.96), 74.58 cm ($\pm$ 7.18), 64.06 cm ($\pm$ 6.61), 13.34 cm ($\pm$ 1.73), 14.94 cm ($\pm$ 4.83), and 19.88 cm ($\pm$ 2.19), respectively. Overall, Hong Kong goats showed the greatest similarity to Makatia goats, likely due to phenotypic heterogeneity in both populations. Divided into 3 clusters, one of them showed similarities to both South Asian and African breeds, while the other two aligned with Chinese, South Asian, and African breeds. The similarities of Hong Kong goats with various breeds suggest a history of gene flow from multiple regions, likely related to Hong Kong's colonial past.

Keywords: Morphology, Breed, Hong Kong, *Capra hircus*, Goat

The effect of doe weight on litter size at birth for goats

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Objectives: Estimated some non genetic factors affecting litter size at birth on Damascus, Zariabi and Balad herds of goats.

Methods: The dataset included measurements on 473 kids, the progeny of 50 bucks and 114 does gathered between 2011 to 2017. Litter size at birth (LSB) was analyzed using linear mixed model, which includes the fixed effects of breed, month and year of birth, sex and covariate of body weight of doe and random effects of bucks, does with bucks and errors. In addition genetic parameter for LSB was analyzed using animal model implemented in the MTDFREML. The model includes the fixed effects of breed, month and year of birth, sex, covariance of body weight of doe and random effects of animal, permanent environmental factors and error.

Results: The overall mean of LSB was 1.54, 1.42 and 1.15 for Damascus, Zariabi and Balad, respectively. Statistical analyses indicated that, Bucks, breed, Month and year of birth and weight of doe had significant ($p < 0.01$) effects on LSB, while does within bucks and sex had no significant effect ($p > 0.05$). Estimates of partial linear and quadratic regression coefficients of LSB on weight of doe were significant and being 0.069 ± 0.027 no/kg and -0.0010 ± 0.0004 no/kg², respectively. The prediction equations of LSB on body weight of doe (x), where: $y = a + b_1x + b_2x^2$ was constructed. The maximum LSB was attained when body weight of doe had 34.5kg. Estimate of direct heritability for LSB was 0.18 ± 0.08 .

Conclusion: The present results suggested that heavy body weight of does generally produce larger litter size at birth due to better nutritional status and body capacity.

Keywords: Body weight, doe, Egyptian goats

Differential Analysis of Reproductive Hormones, Follicle Development and Ovarian Genes in Early Estrus of Yanshan Cashmere Goats with Different Litter Sizes

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Objective: Litter size is an important economic trait in goats with low heritability, controlled by multiple genes and epigenetic regulation. Reproductive hormone secretion and ovarian gene expression in early estrus directly determine follicle development and ovulation efficiency, which are key factors affecting litter size. The aim of this study was to investigate the differences in serum reproductive hormone levels, follicle development and ovarian gene expression during early estrus in Yanshan Cashmere Goats with different litter sizes, and to reveal the molecular mechanism underlying high prolificacy.

Methods: Yanshan Cashmere Goats (3-4 years old) with three consecutive single or twin litters were divided into high-yield (twin) and low-yield (single) groups (n=5 each). Serum reproductive hormones were measured by ELISA. Follicle numbers were counted after slaughter. Ovarian tissues were used for histological observation and RNA-Seq. Differentially expressed genes (DE mRNAs, DE lncRNAs, DE circRNAs, DE miRNAs) were screened and verified by RT-qPCR. GO and KEGG enrichment and ceRNA regulatory networks were constructed.

Results: Serum FSH, E₂ and the number of medium follicles in the high-yield group were significantly higher ($P < 0.05$) than that of the low-yield group, while T and LH were significantly lower ($P < 0.05$) in the high-yield group. A total of 1182 DE mRNAs, 235 DE lncRNAs, 737 DE circRNAs and 180 DE miRNAs were identified. These RNAs were mainly enriched in ovarian steroidogenesis, PPAR, PI3K-Akt and cAMP signaling pathways. Key genes including CYP11A1, STAR, 3BHSD, PPARG, SPARC, STC1, SRGN and JAK3 were involved. Two ceRNA networks (lncRNA-miRNA-mRNA and circRNA-miRNA-mRNA) were established and three core regulatory axes were predicted: MSTRG.6432.1-novel-m0133-3p-HEY2, novel_circ_030939-novel-m0133-3p-HEY2, and MSTRG.21574.1-miR-144-y-CDH2. Key regulators including HEY2, CDH2, novel-m0133-3p and miR-144-y were identified.

Conclusion: Differences in FSH, E₂ and key ovarian genes may regulate hormone secretion, follicle development and ovulation, leading to different litter sizes in Yanshan Cashmere Goats.

Keywords: Cashmere goat; Litter size; Reproductive hormone; Follicle development; Gene expression

Epigenetic Regulatory Mechanism of Hair Follicles in Inner Mongolia Cashmere Goat with Different Coat Types

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Abstract: Inner Mongolia Albas cashmere goat is famous for its excellent cashmere quality, and is a famous cashmere and meat goat breed in China. The coat types are mainly divided into long hair type and short hair type. There are significant differences between the two in pile fineness and pile quality. As the basic unit of villi growth, hair follicles are closely related to different coat types. However, the mechanism of how epigenetics regulates hair follicle growth in different coat types is not fully understood. In this study, Inner Mongolia cashmere goat was selected as the research object. Through comprehensive analysis of ATAC-seq, CUT&Tag and WGBS data of skin tissue, the potential regulatory relationship between differentially expressed genes and chromatin accessibility, histone modification and DNA methylation status was explored. Transcriptome data suggest that the two coat types differ the most in the hair follicle resting period, so the apparent mechanism of this period is analyzed. The results of ATAC-seq and CUT&Tag showed that the open chromatin region was more abundant in the skin tissue of long-haired individuals. There were 3096 peaks in the upper and 1388 peaks in the lower chromatin accessibility. Histone H3K4me3 and H3K27ac modifications were mainly concentrated in the transcription start site (TSS) region of genes, and there were 1917 different H3K4me3 modification genes and 1699 different H3K27ac modification genes between different hair coat types. The results showed that PDGFC, ITGA5, PAK1, BCL2 and VAV3 had significant differences in open chromatin region and histone modification of H3K4me3 and H3K27ac. During the growth of long hair follicles, PDGFC showed more open chromatin areas, and the degree of modification of histone H3K27ac was relatively high. H3K4me3 modification of VAV3 was also highly enriched in long-hair follicles. These differential genes were significantly enriched in PI3K-Akt, Ras, Rap1 and other signaling pathways. When WGBS was integrated, it was found that the VAV3 gene was hypermethylated and the PDGFC gene was hypomethylated during the growth of long hair follicles. These differential genes PDGFC and VAV3 are enriched in Rap1, MAPK and cAMP signaling pathways. Therefore, the results of this study suggest that PDGFC and other genes may be regulated by open chromatin status, histone modification, and DNA methylation, and affect hair follicle growth of different coat types through Rap1 and MAPK signaling pathways. This study provides a new perspective on the transcriptional regulation mechanism of hair follicle growth differences in cashmere goats with different coat types, and provides a theoretical basis for improving the quality and production of cashmere goats in China.

Keywords: Inner Mongolia cashmere goat; coat types; epigenetic regulation; chromatin accessibility

Integrating Chromosome-Level Genome Assembly and Functional Genomics to Unravel the Regulatory Mechanisms of Milk Fat Synthesis in Dairy Goats

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Objective: Dairy goats, as one of the earliest domesticated domestic animals, have become widely raised economic animals around the world. As we know, goat milk contains an abundant variety of nutrients, including proteins, vitamins, and, especially, unsaturated fatty acids (UFAs), which are beneficial to human health. Prospero homeobox 1 (PROX1) is a highly conserved transcription factor that regulates various biological processes during vertebrate growth and development. Previous data showed that PROX1 could upregulate the carnitine palmitoyltransferase 1A (*CPT1A*) expression, leading to increased production of acetyl-CoA dependent on fatty acid β -oxidation, thus promoting lymphangiogenesis, indicating that *PROX1* is strongly involved in lipid metabolism. In this study, we aimed to elucidate the mechanism whereby *PROX1* regulates lipid metabolism during lactation in dairy goats. We observed that PROX1 negatively regulating lipid synthesis and TAG accumulation in GMECs. Moreover, PROX1 enhanced PPARGC1A transcription by binding to the PPARGC1A promoter.

Methods: A 3-year-old male Xinong Saanen dairy goat from the farm of Northwest A&F University in Shaanxi province of China was chosen for collecting blood and qualified DNA were used for sequencing. RT-qPCR and WB were used to explore the function of PROX1 in fatty acid metabolism. RNA-seq technology will be used to screen the downstream target genes of PROX1 and verify the role of them to reveal the molecular mechanism of PROX1 regulating fatty acid metabolism through downstream target genes. PROX1 knockout mice are produced by Cre-loxP system.

Results: we generated a 2.63 Gb chromosome-level genome assembly for dairy goats. ChIP-seq and RNA-seq analyses of goat mammary glands at different lactation stages revealed a novel lactation regulatory factor, Prospero homeobox 1 (PROX1). We found that PROX1 exhibits the highest expression level during peak lactation period. PROX1 knockdown enhanced the expression of genes related to de novo fatty acid synthesis and triacylglycerol (TAG) synthesis in goat mammary epithelial cells (GMECs). Consistently, intracellular TAG and lipid droplet contents were significantly increased in PROX1 knockdown cells and reduced in PROX1 overexpression cells, and we observed similar results in PROX1 knockout mice. Following PROX1 overexpression, RNA-seq showed a significant upregulation of PPARGC1A expression. Further, PPARGC1A knockdown attenuated the inhibitory effects of PROX1 on TAG contents and lipid-droplet formation in GMECs. Moreover, we found that PROX1 promoted PPARGC1A transcription via the PROX1 binding sites (PBSs) located in the PPARGC1A promoter.

Conclusion: we generated a high-quality de novo genome assembly of Xinong Saanen dairy goat. This genome has greatly enhanced our understanding of genomic diversity and amplification in ruminants. PROX1 negatively influenced the synthesis of fatty acid, triacylglycerol, and lipid droplets by modulating the triacylglycerol expression of genes involved in lipid metabolism in GMECs. In addition, PROX1 regulated PPARGC1A transcription by binding to its promoter region, indicating that alterations in PROX1-mediated PPARG expression are important mechanisms by which PROX1 regulates lipid synthesis in GMECs.

Keywords: Dairy goat, genome, PROX1, transcriptional regulation, fatty acid

Combined transcriptomic and metabolomic analysis of healthy and atretic follicles in goat

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Abstract: As the reproductive organs of female livestock, the development, maturation, and atresia of follicles are critical factors affecting reproductive performance. Follicular atresia is a key factor influencing reproductive efficiency in animals, and the death of granulosa cells is central to the induction of follicular atresia. To provide a theoretical basis for improving breeding efficiency, healthy follicles (HF), early atretic follicles (EAF), and late atretic follicles (PAF) were collected from 11 superovulated Chengdu Ma goats. Through transcriptomic sequencing analysis, a total of 2,177 differentially expressed genes (DEGs) were identified between the HF group and the EAF group, of which 1,768 were upregulated and 409 were downregulated, a total of 3,482 DEGs were identified between the HF group and the PAF group, of which 3,067 were upregulated and 415 were downregulated ($P < 0.05$). Metabolomic analysis identified 107 differentially expressed metabolites (DEMs), which were enriched in amino acid metabolism, lipid metabolism, nucleotide metabolism, membrane transport, and the digestive system ($P < 0.05$). A KEGG pathway analysis was performed by combining DEGs with DEMs. The results revealed 33 commonly enriched pathways, comprising 136 DEGs and 60 DEMs, primarily involving metabolic pathways and cAMP signaling pathways, as well as neuroactive ligand-receptor interaction. Significantly correlated DEGs and DEMs were identified in metabolic pathways associated with follicular atresia. For example, in the nucleotide metabolism pathway, thymidine showed a significant positive correlation with ADAMTS4 gene expression; in the arginine metabolism pathway, L-arginine ethyl ester showed a significant positive correlation with OST4 and TUBB4B gene expression; In the unsaturated fatty acid synthesis pathway, the metabolite 20-carboxyarachidonic acid showed a significant positive correlation with TUBA1C gene expression. In summary, this study contributes to the identification of candidate genes and metabolites associated with follicular atresia in goats, and the integrated analysis of transcriptomic and metabolomic data provides insights into the study of follicular atresia in goats.

Keywords: Transcriptome, Metabolomics, Follicles, Goat

Functional genomics annotation reveals critical genomic elements associated with mammary gland development in goats

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Objective: Functional genomics annotation is crucial for understanding the molecular mechanisms of economical traits in livestock, particularly in non-coding regions. However, cis-regulatory elements in the dairy goat mammary gland across developmental stages remain poorly characterized. This study aims to define their dynamic features and construct a mammary gland functional element atlas, providing a key resource for elucidating regulatory mechanisms underlying mammary development and complex traits.

Methods: Mammary gland tissue from Saanen dairy goats was collected at four key developmental time points: puberty, pregnancy, lactation, and involution, to generate 20 transcriptomic and 34 epigenomic datasets. These were integrated to conduct multi-omics integrated analyses focusing on the dynamic changes of cis-regulatory elements during mammary gland development. ChromHMM was used to annotate chromatin states. K-means clustering algorithm was employed to identify period-specific regulatory elements. The nearest-association method based on genomic coordinates was used to identify target genes associated with elements.

Results: A total of 534,043 non-redundant regulatory elements were annotated, covering five chromatin states. K-means clustering grouped the cross-period dynamic changes of these chromatin states into three categories: 1) the puberty maintenance program; 2) the pregnancy remodeling program; 3) the lactation-specific differentiation program, revealing the biological functions corresponding to different dynamic regulatory patterns. Among these, lactation-specific strong enhancers are highly associated with functions such as mammary gland development and fatty acid metabolism. Further, a regulatory element-target gene network was constructed to elucidate the molecular regulatory mechanisms underlying the complex morphology of the mammary gland. For example, the lactation-specific enhancer at chr6:8590944-85919600, which regulates the casein synthesis gene CSN2, provides a molecular basis for elucidating the regulatory network of mammary gland development.

Conclusion: This study systematically constructed a functional annotation atlas of regulatory elements involved in mammary gland development in dairy goats. It provides a basis for screening crucial regulatory elements that govern mammary gland development and lactation traits, thereby offering important theoretical support for molecular breeding in dairy goats and for elucidating the regulatory mechanisms of complex traits.

Keywords: Dairy goat, Mammary gland, Regulatory elements, Chromatin states, Multi-omics

Population genetic diversity and selection signal analysis of small-boned goat based on specific-locus amplified fragment sequencing

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Objective: This study aimed to use simplified-locus amplified fragment sequencing (SLAF-seq) technology to detect single nucleotide polymorphisms (SNPs) across the entire genome of small-bone goats, Hexi cashmere goats and Inner Mongolian cashmere goats (Alba). By assessing their genetic diversity, this research provided a theoretical foundation for characterizing the genetic background of small-boned goats and identifying novel molecular genetic markers.

Methods: A total of 60 healthy adult ewes, comprising 20 individuals each from the small-boned goats, Hexi cashmere goats and Inner Mongolia cashmere goats (Albas) populations, were selected for this study. Genetic diversity was calculated using Perl editing, including minor allele frequency (MAF), observed heterozygosity (H_o), expected heterozygosity (H_e), gene diversity index (Nei), polymorphism information content (PIC), and Shannon-Wiener index (SHI); population differentiation index (F_{ST}) was calculated using VCF tools. Run of homozygosity (ROH) were identified, and the genomic inbreeding coefficient F_{ROH} was calculated to evaluate the degree of inbreeding. Intersection was used to identify selection signatures. Candidate genes within these regions were subsequently subjected to Kyoto Encyclopedia of Genes and Genomes (KEGG) and Gene Ontology (GO) enrichment analyses.

Results: A total of 5,253,776 SNPs were identified, predominantly located in intergenic regions. With the exception of H_o (0.197), the small-boned goat population exhibited the highest values across all genetic diversity metrics. Specifically, the average MAF, H_e , Nei , PIC, and SHI for small-boned goats were 0.216, 0.302, 0.312, 0.247, and 0.466, respectively. F_{ST} analysis showed that the differentiation level of the small bone goat was low compared with that of the Hexi cashmere goats (0.043), and moderate compared with that of the Inner Mongolia cashmere goats (Alba) (0.052). The small-boned goat had the fewest ROH fragments, the highest proportion of 0-1Mb fragments, and F_{ROH} of 0.10. Selection signature analysis successfully identified key candidate genes associated with economically important traits, including *PPP3CA* and *KDM2B*.

Conclusion: The small-boned goat is less differentiated from the Hexi cashmere goat, and moderately differentiated from the Inner Mongolia cashmere goat (Albas). The identification of candidate genes associated with skeletal development provides a robust theoretical foundation for the rational conservation, breeding, and utilization of small-boned goats, as well as a valuable reference for the future excavation of molecular genetic markers.

Keywords: Small-boned goat; Simplified genome sequencing; Genetic diversity; Selection signal analysis

Extracellular Lactate Promotes Secondary Hair Follicle Stem Cell Proliferation by Modulating H3K9 Lactylation and CLDN1 Expression in Cashmere Goats

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Objective: Paracrine signals derived from dermal papilla cells (DPCs) of secondary hair follicles in cashmere goats mediate the regulation of hair follicle stem cell (HFSC) fate, representing one of the key determinants controlling cyclic follicle regeneration and cashmere fiber growth, ultimately influencing cashmere yield and quality. Histone lysine lactylation has emerged as a crucial link bridging cellular metabolism and epigenetic regulation; however, whether and how it contributes to DPC-mediated regulation of HFSC proliferation remain poorly understood. This study aims to elucidate how DPC-derived signals drive lactate accumulation in HFSCs and subsequently regulate their proliferation, and to explore the role of histone lactylation in the secondary hair follicle cycle.

Methods: A transwell co-culture model was established using proliferating secondary DPCs and HFSCs derived from growing cashmere goats. HFSCs cultured alone (Control) and HFSCs in co-culture with DPCs (Co-culture) were subjected to CUT&Tag, transcriptomic, and proteomic sequencing (n=3), followed by integrative multi-omics analysis. For functional validation, Within the co-culture model, HFSCs were divided into three groups: Blank (untreated control), 15 mM lactate, and 5 mM 2-deoxy-D-glucose (2-DG). Flow cytometry was employed to assess differential expression of H3K9 lactylation (H3K9la) and CLDN1.

Results: Glycolysis-related genes were upregulated in hair follicle stem cells (**Figure 1A**), accompanied by an elevated extracellular acidification rate (**Figure 1C**). Treatment with 5 mM 2-DG suppressed the proliferation of hair follicle stem cells (**Figure 1B**), whereas 15 mM lactate promoted their proliferation (**Figure 1D**). Multi-omics integration revealed a single overlapping protein, Claudin-1 (CLDN1) (**Figure 2A**), and a significant H3K9la enrichment peak was detected within the CLDN1 promoter region (**Figure 2B**). Compared with the control group, 2-DG treatment induced a leftward shift in the H3K9la fluorescence histogram, corresponding to a 22.9% reduction in modification levels, whereas the lactate group exhibited a rightward shift (**Figure 2C**) and an approximate 21.4% increase in mean fluorescence intensity (MFI) (**Figure 2E**). Similarly, for CLDN1 protein expression, 2-DG treatment caused a leftward shift in the fluorescence histogram and a 31.9% decrease in expression levels, while the lactate group showed a rightward shift (**Figure 2D**) and an approximate 22.4% increase in MFI (**Figure 2F**).

Conclusion: In summary, these findings establish that lactate acts as a key metabolic signal orchestrating hair follicle stem cell fate during the anagen phase via the H3K9la/CLDN1 axis. This study provides new insight into how the metabolic microenvironment governs stem cell fate decisions during the hair follicle cycle through histone lactylation.

Keywords: Histone lactylation, Stem cell regulation, Secondary hair follicle, Cashmere goat

Genetic diversity and signatures of selection in Russian goats (*Capra hircus*)

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Abstract: Domestic goats (*Capra hircus*) combine unique biological, ecological, and economically significant traits. They are undemanding in terms of feeding and housing conditions. Domestication of goats occurred approximately 10,000 years ago in the Fertile Crescent, from where they spread across the globe and populated diverse habitats, leading to the creation of numerous local breeds well adapted to specific environmental conditions (steppe zones, deserts, semi-deserts, valleys, mountains, and highlands). However, many local goat breeds are vulnerable or critically endangered due to their inability to withstand intensive production and are bred only in small herds. Therefore, assessing the level of genetic diversity in local breed populations is essential for developing *ex situ* conservation programs. The rapid advancement of molecular genetics techniques over the past two decades, particularly next-generation sequencing (NGS), has enabled the sequencing of the entire genome of the domestic goat. The aim of this study was to identify authentic genomic variants underlying the development of adaptive and economically significant traits in Russian goat breeds. Tissue samples from Orenburg ($n = 19$), Altai Mountain, Soviet Mohair, and Karachai goats ($n = 20$ each) were collected for this study. Paired-end libraries (150 bp reads) were constructed for each animal. NGS was performed using a NovaSeq 6000 sequencer (Illumina, Inc., San Diego, CA, USA), with ~20X genome coverage. Alignment to the reference goat genome assembly ARS1.2 was performed using bwa-mem2 tools (version 2.2.1) and SAMtools (version 1.21). We used three approaches to search for traces of selection using ROH island indicators, calculating F_{ST} values, and cross-population extended haplotype homozygosity (XP-EHH). At the first stage, using a sliding F_{ST} window, regions with the highest average F_{ST} value in each window were identified. Next, SNPs with the highest F_{ST} values were selected within these regions, for which allele and genotype frequencies were calculated in each breed. Comparative analysis revealed both known candidates and genes with poorly studied or unknown functions in small ruminants (*APIAR*, *FICD*, and *TRPC4AP*). Among the candidates were genes associated with milk production and lipid metabolism (*ACSS2* and *TOMIL2*), immunity (*ALPK1*, *TIFA*, and *CCDC88C*), reproductive functions (*ALKBH5*, *MADIL1*, and *DRC3*), growth and development (*MYH7B*), and stress resistance (*ATPAF2*). In addition, 14 SNPs were identified that showed the greatest differences between the studied goat breeds. Our findings shed light on the features of genetic diversity and signatures of selection in Russian goat breeds and will be used in further breeding and genetic work with these breeds.

Keywords: Goat, Local breeds, WGS, SNP, Genes, Signatures of Selection

Estimates of Direct and Maternal Genetic Effects on economic traits in Damascus goats

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Objectives: The aims of the present study were determined the phenotypic and genetic characteristics for litter size at birth (LSB), birth weight (BW) and weaning weight (WW) in Damascus goats.

Methods: Data used in the present study were collected from Damascus goats kept at Sakha Farm, belonging to Animal production Research Institute, Ministry of Agric., Dokki, Cairo, Egypt. The MTDFREML software was used to evaluate data from 664 kids, the progeny of 138 and 233 Does, gathered between 2010 to 2018. Three models were compared: Model 1 (direct genetic effects only), Model 2 (adding permanent environmental effects), and Model 3 (adding maternal genetic effects and direct–maternal covariance).

Results: The overall mean was 1.39 ± 0.02 for LSB, 3.61 ± 0.03 kg for BW and 12.90 ± 0.15 kg for WW. Least squares analysis of variance showed the significant effect of bucks, does within bucks, month, year of birth and sex in most variables studied. The direct heritability estimates for LSB, BW and WW were 0.29 – 0.34, 0.16 – 0.34 and 0.09 – 0.27 across models, respectively, whereas maternal heritability ranged from 0.09 to 0.39. The study revealed maternal genetic effects on litter size at birth and birth weight but their total contribution to growth trait variation is modest, and model parsimony suggests that maternal effects on weaning weight be excluded.

Conclusion: Breeding programs should therefore prioritize direct selection for growth performance, whereas management strategies such as enhanced nutrition, targeted kidding, and support for first-parity do provide more rapid and effective avenues to improve pre-weaning developmental outcomes.

Key words: Direct maternal, Economic traits, Damascus

Disruption of lysine demethylase 2A promotes intramuscular fat deposition and unsaturated fatty acids synthesis via the histone H3 lysine 36 dimethylation-peroxisome proliferator-activate

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Abstract: Identifying key candidate genes regulation on content and composition of intramuscular fat (IMF) deposition is critical for enhancing meat quality traits. As a specific demethylase for histone H3 lysine 36 dimethylation(H3K36me2), lysine demethylase 2 A (KDM2A) epigenetically modulates cellular processes including proliferation and differentiation by modifying chromatin architecture. Nevertheless, the regulatory role and precise molecular mechanism of this macromolecular interaction during intramuscular adipogenesis requires further investigation. In vitro goat intramuscular adipogenesis assays indicated that KDM2A ablation promotes IMF deposition and polyunsaturated fatty acid (PUFA) synthesis, whereas KDM2A overexpression has the opposite effect. Consistently, adipocyte-specific KDM2A knockout mice models under high-fat diet/glycerol induction all revealed its genetically deletion specifically increased IMF accumulation and PUFA content in vivo. Furthermore, we mechanistically demonstrated that disruption of KDM2A promotes intramuscular adipogenesis through structural modification of the chromatin landscape, specifically via the elevation of H3K36me2 at the peroxisome proliferatoractivated receptor gamma (PPAR γ) locus and subsequently activating its transcription. Collectively, our work uncovers KDM2A as an epigenetic modulator of IMF deposition, offering novel insights for meat quality enhancement via heritable epigenetic regulation. The demonstrable efficacy of targeting this pathway underscores its epigenetic potential in livestock improvement programs.

Construction of a Reference Population for Genomic Selection and Genetic Evaluation in Saanen Dairy Goats

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Abstract: Genomic selection (GS) can significantly improve breeding efficiency for low-heritability traits, but its effectiveness depends on a high-quality reference population. In this study, a large-scale reference population for genomic selection was constructed to meet the demands of the dairy goat industry. A total of 2,788 Saanen dairy goats in peak lactation (average lactation days: 102.3 ± 0.9 days) from the Qingshuihe Youran Dairy Goat Farm in Inner Mongolia were genotyped using the DGS25K liquid-phase chip. Simultaneously, 20 economically important traits across five categories were systematically measured: body conformation (6 traits, including body height and body length), udder traits (3 traits, including teat length, udder circumference, and udder structure), milk production performance (300-day average milk yield), milk composition (8 traits, including milk fat percentage and milk protein percentage), and reproductive traits (2 traits, including litter size and litter weight). A reference population for genomic selection in Saanen dairy goats was thus established. Phenotypic quality control was performed on 10 core traits: body height (BH), body length (BL), body oblique length (BOL), heart girth (HG), rump width (RW), milk protein percentage (PP), milk fat percentage (FP), average milk yield (AMY), litter size (LN), and litter weight (LW). After quality control, data robustness improved significantly, with standard deviations notably reduced (e.g., SD of BH decreased from 4.50 to 3.96). Using the GBLUP model, heritability (h^2) estimates for each trait were obtained: BH (0.569), PP (0.534), and AMY (0.426) were high heritability traits; HG (0.276) and BOL (0.226) were moderate heritability traits; RW (0.081), LN (0.081), and LW (0.052) were low heritability traits. A 5-fold cross-validation strategy repeated 20 times was employed to evaluate the genomic prediction accuracy of the GBLUP model for the 10 economic traits in Saanen dairy goats. The results showed significant differences in prediction accuracy across traits. BH (0.131) achieved the highest accuracy, indicating the best predictive performance, followed by PP (0.122) and HG (0.111). In contrast, LN (−0.024) and LW (−0.070) showed negative prediction accuracies, the lowest among all traits, significantly inferior to those of body conformation and production traits, reflecting the limited efficacy of the current reference population for genetic evaluation of reproductive traits. This study successfully constructed a genomic selection reference population covering multiple economic traits in Saanen dairy goats, elucidated the genetic parameters and predictive potential of each trait, and provided a scientific basis for early (pre-weaning) precise selection of dairy goats, thereby offering a scientific approach to improving the coverage of elite germplasm and accelerating genetic progress in dairy goats.

Keywords: Saanen dairy goat; Genomic selection; Reference population; Genetic evaluation

Combining multiomics to analyze the molecular mechanism of underlying the formation of the colorful wool color of the Cashmere Goats

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Abstract: Colored cashmere goats are highly valued in the market due to their eco-friendly nature, as they do not require dyeing. This study aimed to investigate the genetic determinants regulating fleece color formation and hair growth through an integrated analysis of transcriptomic, proteomic, and metabolomic datasets from the growing-phase skin of Inner Mongolian white, black, and reddish-brown cashmere goats. The results showed that 749, 521, and 219 proteins were specifically expressed in the growing-phase skin of reddish-brown and white, black and white, and reddish-brown and black goats, respectively. Functional enrichment analysis revealed that differentially expressed proteins (DEPs) across the different cashmere color groups were predominantly enriched in GO terms related to metabolism, cellular processes, and protein processing. Enrichment results from the Kyoto Encyclopedia of Genes and Genomes (KEGG) indicated that lysosomes, ECM receptor interactions, and mitochondrial autophagy were significantly enriched across multiple comparisons, suggesting that these pathways are core mechanisms influencing the functional properties of cashmere goat skin and, consequently, regulating fleece color and hair follicle growth. Integrated transcriptomic and proteomic analysis identified 10 overlapping DEGs and DEPs, among which TYRP1 and TYR play crucial roles in regulating protein and gene expression levels. Integrated transcriptomic and metabolomic analysis revealed that DEMs and DEGs were jointly enriched in ABC transporters and neuroactive ligand-receptor interactions. Combined proteomics and metabolomics analysis identified 89 DEMs highly correlated with the genes RAB32 and YY1. This study is the first to reveal the molecular basis of color variation in Cashmere goats through a multi-omics approach, providing a theoretical foundation for molecular breeding.

Keywords: Cashmere goats, Multi-omics, Coat color, Molecular breeding, Hair follicle

A Comparative Study on the Fineness Range and Content of Variant Cashmere Hard to Dye and Tickle in Different Breeds Ages and Body Sites of Cashmere Goat

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Abstract: This study aimed to investigate the fineness range of variant cashmere hard to dye and tickle (secondary fine cashmere fibers) in different breeds, ages and body sites of cashmere goats and analyze the variation in its content. The findings provide a reference for the classified collection of cashmere, promote the optimization of carding processes, and improve the quality of commercial cashmere products. Four cashmere goat breeds (Liaoning Cashmere Goat, Albas Cashmere Goat, Hanshan White Cashmere Goat, and Shaanbei White Cashmere Goat) were selected, with six female goats aged 1–5 years per breed. A total of 600 cashmere samples were collected from five body sites: rump, neck, abdomen, back, and shoulder. Fiber types, fineness, and their variation characteristics were analyzed to define the fineness range of secondary fine cashmere fibers and calculate their relative content. The results showed that raw cashmere could be classified into four types: guard hair, heterotypical hair, secondary fine cashmere fibers, and primary fine cashmere fibers. Breed, age, and body site significantly influenced cashmere fiber diameter. The ranking of mean fiber diameter (MFD), fiber diameter standard deviation (FDSD), and coefficient of variation of fiber diameter (CVFD) among breeds was as follows: Shaanbei White Cashmere Goat > Liaoning Cashmere Goat > Hanshan White Cashmere Goat > Albas Cashmere Goat. MFD initially increased and then decreased with age, while both FDSD and CVFD showed a continuous increasing trend with age. The MFD of neck cashmere (16.15 μm) was significantly higher than that of other sites, whereas the shoulder had the lowest MFD (15.38 μm) and the back exhibited the highest fiber uniformity. The fineness range of secondary fine cashmere fibers in all breeds was from mean fiber diameter + one standard deviation ($\mu + \sigma$) μm to 25 μm . The content of secondary fine cashmere fibers in Shaanbei White Cashmere Goats was approximately 15%, compared to around 10% in the other three breeds. Their content increased then decreased with age, peaking at 3–4 years old. The highest proportion was found in the neck (15.63%) and the lowest in the shoulder (10.31%). A significant positive correlation was observed between secondary fine cashmere fiber content and MFD. Accordingly, it is recommended that cashmere be collected separately by body sites, with cashmere from 3–4-year-old goats and the neck site can be packaged separately as needed.

Keywords: Cashmere goat, Cashmere fineness, Variant cashmere hard to dye and tickle, Raw cashmere grading, Industrial application

Global Distribution, Origin and Migration of Cashmere Goat: Diversity of guard hair types and its affect on cashmere trait

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Abstract: Cashmere goats are globally important economic livestock that produce high-quality cashmere fiber. Their origin, migration history, germplasm distribution and genetic basis of cashmere traits are core supports for the sustainable development of cashmere industry. Based on systematic collection, collation and mining of literatures in recent years, we summarized the origin, East Asian migration routes, global distribution pattern of cashmere goat germplasm resources, and discuss the research progress of multi-omics (genomics, transcriptomics, proteomics, epigenomics) in revealing the genetic regulation mechanisms of cashmere yield, fineness, length and other quality traits. Archaeological and genomic evidence showed that domestic goats were initially domesticated in western Iran (near the Fertile Crescent) about 6,000–7,000 years ago. Accompanied by human nomadic activities, the ancestors of cashmere goats migrated eastward along the steppe route: Western Iran → Central Asia → Pamir Plateau → Xinjiang → Mongolian Plateau → North China, and gradually formed the main distribution belt of cashmere goats in East Asia. At present, cashmere goats are mainly distributed in arid and semi-arid regions of Asia, Europe, Oceania and North America, among which China has the most abundant germplasm resources, including Inner Mongolia cashmere goat, Liaoning cashmere goat, Tibetan cashmere goat and other excellent local breeds. Genomic studies based on T2T-goat1.0 assembly have identified a batch of selection signals and candidate genes (such as *FGF5*, *EDA2R*, *ABCC4*) related to cashmere traits. Transcriptomics, proteomics and epigenomics jointly revealed that *KRT* family, *KAP* family genes, Wnt, BMP signaling pathways and non-coding RNAs play key regulatory roles in hair follicle development and cashmere growth. This review systematically sorted out the origin, East Asian migration routes, global distribution characteristics of cashmere goat resources and the multi-omics regulation network of cashmere quality traits, and pointed out the future research directions such as precise molecular breeding and germplasm innovation. It provides theoretical reference for the protection, utilization and genetic improvement of Cashmere goat germplasm resources worldwide.

Keywords: Cashmere goat; Germplasm resources; Origin; East Asian migration; Global distribution; Multi-omics; Genetic regulation

GWAS analysis of lactation traits in dairy goats in the northeast farming region

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Abstract: The dry matter, fat, and vitamin content in the milk secreted by dairy goats (*Capra hircus*) are all higher than those in cow's milk. In particular, the fat globules are smaller and the casein content is lower, making it easier to digest and absorb for humans compared to cow's milk. Moreover, the northeastern agricultural regions have abundant feed resources. This study focuses on the dairy goat breeds currently being continuously selected and bred in the agricultural areas of Jilin Province, conducting a genome-wide association analysis on the lactation traits of 300 dairy goats. The results are as follows: Annotation of the GWAS results for lactation traits in dairy goats revealed that genes such as *API5* and *TTC17* on chromosome 15 are associated with udder circumference traits in dairy goats. Genes such as *EGR3*, *CCAR2*, and *BIN3* on chromosome 8, *EPCAM*, *MSH2*, and *KCNK12* on chromosome 11, *FHIT* on chromosome 22, and *XPO6* and *SBK1* on chromosome 25 are associated with teat length traits in dairy goats. Genes such as *TRNAC-GCA-216* and *TMEM132E* on chromosome 19, *TRNAS-GGA-105* and *CTIF* on chromosome 24 are associated with milk yield traits. Genes such as *SNAIL* and *SLC9A8* on chromosome 13, and *VPS26A* and *SRGN* on chromosome 28 are associated with lactose traits. Genes such as *HES2* and *ACOT7* on chromosome 16 are associated with milk fat traits in dairy goats. The expression of *ACOT7*, *EGR3*, *EPCAM*, and *SNAIL* genes in the mammary gland tissues of high- and low-milk-yielding dairy goats was detected using immunohistochemistry, quantitative fluorescent PCR, and Western blot. The results showed that all four genes, *ACOT7*, *EGR3*, *EPCAM*, and *SNAIL*, were expressed in mammary gland tissues. The expression levels of *ACOT7*, *EGR3*, and *EPCAM* genes were significantly higher in the mammary glands of high-milk-yielding goats compared to low-yielding goats ($P < 0.05$), while the expression of the *SNAIL* gene was significantly lower in the mammary glands of high-milk-yielding goats than in low-yielding goats ($P < 0.01$).

Keywords: Dairy goat; Lactation traits; GWAS; Mammary gland tissue

Research on N-acetylcysteine Alleviating Growth Retardation and Rumen Microecological Disorders Induced by Heat Stress in Goats

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Objective: Heat stress triggers rumen microbiota dysbiosis and metabolic disorders, leading to a decline in growth performance and severely compromising the welfare and productivity of goat farming. As an acetylated precursor for glutathione (GSH) synthesis, N-acetylcysteine (NAC) possesses a dual antioxidant mechanism attributed to the active thiol group (-SH) in its molecular structure. Currently, NAC has been proven effective in alleviating heat stress-induced intestinal damage and oxidative stress in monogastric animals. However, it remains unclear whether NAC can mitigate the decline in goat performance caused by heat stress by reshaping the rumen microbial structure and regulating metabolic profiles in ruminants. Consequently, this study focused on Wanlin White goats and integrated physiological and biochemical parameters, 16S rRNA gene sequencing, and non-targeted metabolomics to systematically investigate the regulatory effects of NAC on the rumen microbes and metabolites of goats under heat stress.

Methods: At a goat farm in Fuyang, Anhui, three-month-old Wanlin White goats with similar age and body weight (n=42) were selected as the research subjects. The animals were divided into three groups: the thermo-neutral control group (CON; n=12; THI=69.44±0.37), the heat stress group (HS; n=12; THI=83.05±3.07), and the heat stress with oral N-acetylcysteine treatment group (HS+NAC; n=12; THI=81.39±2.91). During the experimental period, the body weight of the goats in each group was measured every 10 days. Serum and rumen fluid were collected at the end of the experiment. Serum metabolites were detected using ELISA kits. Rumen microbiota and metabolites were sequenced using PacBio Sequel and UPLC-Q/TOF-MS/MS, respectively. The microbiota and metabolites were analyzed via the BMKCloud platform. Furthermore, the potential correlations between oral NAC supplementation and physiological indicators, serum biochemical parameters, microbes, and metabolites in heat-stressed goats were evaluated.

Results: HS significantly reduced goat ADG and elevated inflammatory/damage markers (LPS, CRP, iFABP) while disrupting rumen microecology and lowering *Prevotella* abundance and antioxidant metabolites (L-citrulline, lipoamide). NAC supplementation effectively reversed these effects, restoring growth performance, microbial balance, and metabolite levels. Correlation analysis confirmed that key metabolites were significantly negatively associated with inflammation and intestinal injury.

Conclusion: Dietary NAC alleviates heat stress in goats by improving the ruminal redox microenvironment, which reshapes the damaged core microbiota (*Prevotella*) and boosts key metabolic precursors (lipoamide, L-citrulline). This dual “microbiota-metabolite” restoration preserves intestinal barrier integrity, blocks endotoxin-triggered systemic inflammation, and thereby reduces inflammation-driven energy expenditure, restoring normal growth performance.

Keywords: N-acetylcysteine; Rumen microbiota; Metabolomics; Heat stress in goats

An Integrated Machine Learning Framework for Genomic Breed Prediction in Goat and Sheep

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Objective: At present, more than 1,000 sheep and goat breeds have been documented worldwide. These breeds are widely distributed across the globe and possess distinct genetic characteristics as well as valuable production traits. Accurate prediction of sheep and goat breeds is of great significance for the conservation and utilization of germplasm resources, molecular breeding, and meat traceability. Machine learning algorithms have been widely applied to predict breed information and estimate breeding values using genomic information. Therefore, in this study, we used sheep and goat data provided by the Farm-GTEx project and applied machine learning methods to accurately predict sheep and goat breeds separately based on genomic variation information, providing a reference for the construction of molecular identification systems for these species.

Methods: The technical workflow of this study is shown in Figure 1. This study used data from the Farm-GTEx project, including whole-genome data from 8,171 sheep samples representing 118 breeds, comprising a total of 3,427,511 SNP loci, and whole-genome data from 4,701 goat samples representing 79 breeds, comprising a total of 5,156,589 SNP loci. Principal component analysis was performed separately for all sheep and goat breeds using PLINK software, and outlier samples within each breed were removed according to breed-based clustering patterns. Breed-informative SNPs were selected using the fixation index (FST) and average Euclidean distance (AED). Different numbers of SNP features, including 2,000, 5,000, 10,000, 20,000, 50,000, 100,000, and 200,000 SNPs, were extracted to compare prediction performance. Genotype files were encoded using two strategies: label encoding and one-hot encoding. Four machine learning methods, namely random forest (RF), K-nearest neighbors (KNN), support vector machine (SVM), and extreme gradient boosting (XGBoost), were used to predict sheep and goat breeds separately. In addition, hybrid status prediction was performed for sheep individuals. Classification performance was evaluated using accuracy as the assessment metric. Meanwhile, genomic breed composition analysis (GBC) was incorporated to establish an analytical strategy of “continuous ancestry component estimation followed by supervised classification prediction,” aiming to distinguish purebred individuals from potentially admixed individuals. Finally, functional annotation and eQTL overlap analysis were performed on the optimized SNP marker set, and the final pipeline was deployed as an online breed prediction platform.

Results: The SNP loci selected using FST achieved higher prediction accuracy than those selected using AED across all five methods. When the number of SNPs was 50,000, the average prediction accuracy of the FST method reached 94.7%, which was 0.91% higher than that of the AED method. When the number of SNPs was below 2,000, the accuracy of breed classification prediction was lower than 85%. As the number of SNPs increased, breed prediction accuracy gradually improved. When the number reached 20,000, the average accuracy exceeded 90%, and when the number of SNPs reached 50,000, the accuracy reached 93.71%. Based on the 50,000 SNP loci selected by FST and encoded using one-hot encoding, the SVM model achieved higher classification accuracy than the other models, with a

prediction accuracy of 96.79%. The prediction accuracies of the other three models were 92.35% for XGBoost, 91.96% for KNN, and 90.84% for RF. The confusion matrix results indicated that Merino sheep were the most likely to be confused with other breeds among sheep. Among goats, cashmere goats were the most likely to be confused with other breeds. Compared with supervised classification alone, the analytical pipeline in which GBC analysis is performed first followed by machine learning classification can first evaluate the continuous genetic composition of individuals and then predict breed labels, thereby reducing the risk of incorrectly assigning admixed individuals to a single breed with overly high confidence. Functional annotation and eQTL overlap analysis further indicated that the optimized SNP marker set not only had strong breed-discriminating power, but may also be associated with important biological functional regions. The developed online prediction platform can output predicted breed labels, candidate breed probabilities, GBC-based genetic composition results, and the classification of individuals as purebred or admixed.

Conclusion: Machine learning methods provide efficient and interpretable technical approaches for breed identification and genetic resource management in small ruminants. The integrated machine learning framework developed in this study can not only predict sheep and goat breeds using genomic variation information, but also incorporate GBC analysis to continuously estimate the genetic composition of individuals, thereby improving the ability to distinguish purebred from admixed individuals. The optimized 50K SNP panel achieves a balance among prediction accuracy, marker number, and efficiency for online deployment, showing potential applications in breed identification, germplasm resource conservation, product authentication, and livestock genomic management. In conclusion, this study established a practical, interpretable, and online-applicable AI-assisted framework for sheep and goat breed identification, providing an important reference for the construction of molecular identification systems and the precise utilization of genetic resources in small ruminants. In the future, more population samples, multi-omics data, and deep learning methods could be further integrated to improve the stability and accuracy of the model in complex population structures and admixed individual identification.

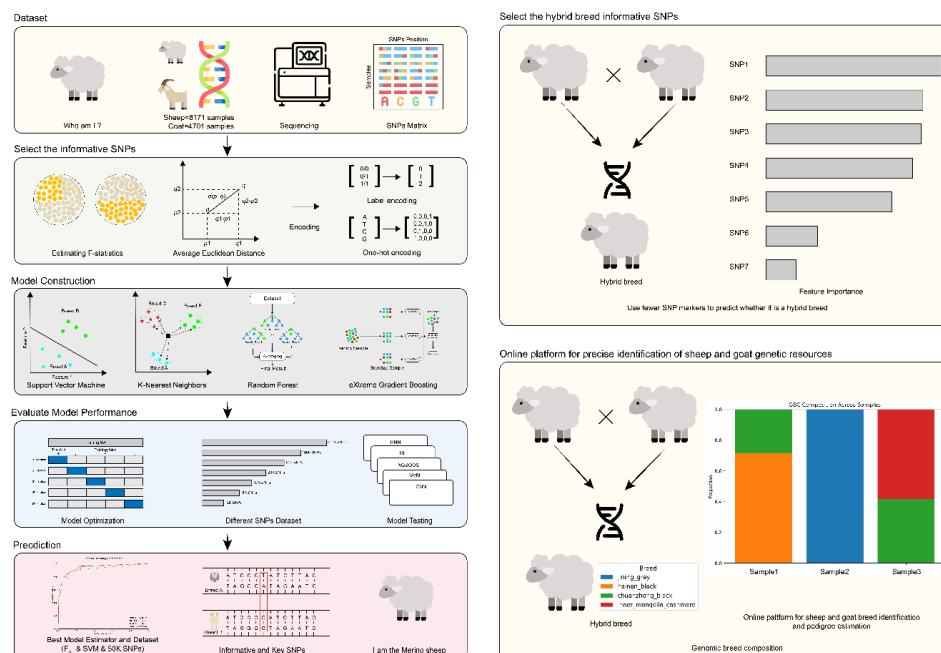


Figure1 Overview of the machine-learning framework for sheep and goat breed identification and genomic composition prediction

Keywords: Breed prediction, machine learning, SNP, GBC, eQTL

Establishment of an inflammatory model of goat small intestinal epithelial cells induced by H₂O₂

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Objective: The intestine, as the main site for nutrient absorption and immune cell aggregation in animals, serves as the body's first line of defense. Hydrogen peroxide (H₂O₂) can increase the level of reactive oxygen species (ROS) in goat small intestinal epithelial cells, activate the NF-κB signaling pathway to drive inflammatory responses, thereby disrupting the intestinal barrier and further weakening the protective function of the intestine. Therefore, in this study, using goat immortalized small intestinal epithelial cells as a model, we established a hydrogen peroxide-induced inflammatory model of small intestinal epithelial cells by adding different concentration gradients of H₂O₂ and using the CCK-8 method, aiming to investigate the effect of hydrogen peroxide on the expression of inflammatory markers in these cells.

Methods: Cells were seeded into T-25 culture flasks, and the culture medium was replaced every two days. When the cell confluence reached approximately 80%, the cells were seeded into 96-well plates at a density of 5×10⁴ cells per well and incubated for 24 h. Subsequently, the medium was replaced with fresh DMEM/F12 medium containing different concentrations of H₂O₂, with final concentrations of 100, 200, 300, 400 and 500 μmol/L. After incubation for 12 h, 10 μL of CCK-8 solution was added to each well, and the plates were incubated at 37 °C for 2 h in a humidified atmosphere with 5% CO₂. The absorbance (OD value) of each well was measured at 450 nm using a microplate reader. The cell viability percentage was calculated to establish the oxidative damage model. Total cellular RNA was extracted and reverse-transcribed into cDNA, and real-time quantitative polymerase chain reaction (qPCR) was applied to perform relative quantitative analysis on the expression levels of target genes.

Results: According to the results of CCK-8 cell proliferation and viability assay, cell viability showed a concentration-dependent gradient correlation with hydrogen peroxide concentration; cell proliferation was significantly decreased at the concentration of 300 μmol/L H₂O₂ ($P < 0.001$), and the cells maintained an appropriate survival rate, which was suitable for the establishment of the oxidative damage model. The expression levels of TLR4, IL-1β and TNF-α in intestinal epithelial cells were detected by qPCR, and one-way analysis of variance (ANOVA) was performed using SPSS 26 statistical software. The results indicated that the expression levels of TLR4, IL-1β and TNF-α in the H₂O₂ treatment group were significantly up-regulated compared with the control group.

Conclusion: Studies have shown that ROS acts as a central link in the inflammatory signaling pathway, activates the NF-κB signaling pathway, and markedly upregulates the expression of pro-inflammatory genes such as IL-6, IL-1β and TNF-α, thereby further amplifying inflammatory signals. Moderate ROS can serve as signaling molecules to protect the inflammatory response, while excessive ROS breaks the redox balance, induces harmful inflammation, causes severe cellular dysfunction, and even drives cells toward death.

Keywords: H₂O₂, Intestinal epithelial cells, Reactive oxygen species

Overexpression of NOG Gene inhibits Intramuscular Adipocyte Differentiation in goat (*Capra hircus*)

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Abstract: Intramuscular fat (IMF) in goats is a key factor affecting mutton quality such as flavor and juiciness. It is also one of the indicators for evaluating animal meat quality. Either excessively high or low intramuscular fat content exerts a great impact on meat quality and sensory flavor. Studies have confirmed that the formation of intramuscular fat is closely associated with the differentiation of preadipocytes, a process involving the mutual regulation of numerous gene expression and protein secretion. To clarify the regulatory role of the *NOG* gene in the differentiation of goat intramuscular preadipocytes, *NOG* gene was first cloned, and bioinformatics analysis was performed on the sequence to obtain its relevant biological characteristics. Subsequently, the overexpression plasmid of goat *NOG* was transfected into cells, followed by induced differentiation. Morphological observation, quantitative real-time PCR (qPCR) and other experiments were conducted to determine the effect of *NOG* gene overexpression on this differentiation process. The results showed that the full-length sequence of the goat *NOG* gene is 1269 bp, containing a 698 bp coding sequence (CDS). The *NOG* gene was widely expressed in eight goat tissues, including the liver, heart and adipose tissue, with the highest expression level detected in the testis. After detecting the overexpression efficiency, *NOG* was successfully overexpressed in goat intramuscular preadipocytes (**Figure 1A**). Oil Red O staining (**Figure 1B**) and Bodipy staining (**Figure 1C**) results revealed that *NOG* overexpression reduced the number and size of lipid droplets in goat intramuscular preadipocytes. Meanwhile, qRT-PCR results showed that the expression levels of *FASN* (fatty acid synthase), *PPAR γ* (peroxisome proliferator-activated receptor γ) and *C/EBP α* (CCAAT/enhancer binding protein α) were significantly downregulated. In conclusion, *NOG* inhibits the differentiation of goat intramuscular preadipocytes, and this inhibitory effect may be achieved by downregulating the expression of adipogenic differentiation marker genes including *PPAR γ* , *C/EBP α* and *FASN*.

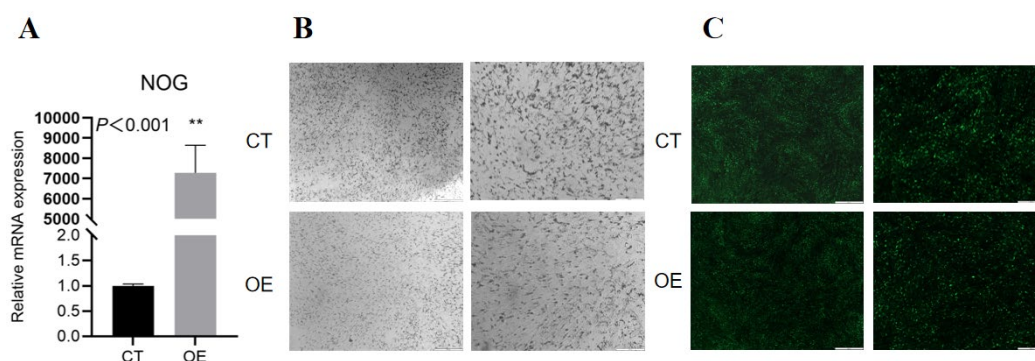


Figure 1. Overexpression efficiency(A), Oil Red O staining (B) and Bodipy staining (C)

Keywords: Goat; *NOG*; Intramuscular fat cells; Overexpression; Cell differentiation

PCR Detection of Polled Intersex Syndrome

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Abstract: In modern intensive goat farming systems, the presence of the horned phenotype brings a series of significant negative effects, including increased intraspecific aggression leading to mechanical injuries, damage to housing facilities, and potential safety hazards for farm personnel. Although physical and chemical disbudding can be applied in practice, this process not only increases labor costs but also induces severe physiological stress, immune suppression, and secondary infections in young animals, seriously violating the increasingly valued principles of animal welfare. Therefore, breeding polled (hornless) goats is regarded as the fundamental solution to the above problems. However, intersexuality and infertility have emerged as major constraints in the breeding of polled goats, causing substantial economic losses in production. Hence, accurately identifying intersex goats using available scientific methods is of great significance for ensuring the orderly selection of polled goats and reducing production losses. In this study, a total of 74 goat whole blood samples were collected and stored at -20°C for subsequent use. Although molecular detection methods for intersex goats have been reported earlier, the low sequence conservation of the PIS locus across different goat breeds, and the fact that some detection methods were established before the discovery of the inverted repeat insertion mutation at the PIS locus, mean that traditional methods using PCR primers flanking the PIS locus to detect fragment deletions cannot accurately identify intersex goats. To detect the sex characteristics and PIS locus mutations of intersex goats at the genomic level, we designed primers targeting the Y chromosome-specific SRY gene sequence and performed PCR amplification for sex identification. The results showed that all male samples amplified a specific 272bp band, while female samples did not. This is consistent with previous findings that "intersex goats are genetically female". However, two samples with male external phenotypes failed to amplify the 272bp band. Subsequently, we designed a pair of specific primers targeting the central region of the PIS deletion fragment (producing a 369bp PCR amplicon) and performed PCR on all samples. The results showed that all normal goat samples amplified the expected 369bp band, whereas the two phenotypically male samples did not, indicating that intersex goats carry a deletion at the PIS locus, while normal goats have at least one intact PIS allele. Combined with the above molecular results and subsequent slaughter examination, the two phenotypically male samples were confirmed to be intersex goats. Thus, the identification method established in this study can rapidly and accurately detect intersex goats, providing a reliable technical support for the precise screening of intersex individuals during the breeding of polled goats.

Keywords: Polled Intersex Syndrome, Horned phenotype, PCR

Integrated Single-Cell Transcriptomic Profiling of Hair Follicle Morphogenesis and Cycling in Cashmere Goats (*Capra hircus*)

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Objective: The secondary hair follicle (SHF) of the cashmere goat (*Capra hircus*) is a specialized skin structure essential for the production of high-value cashmere fibers. While the embryonic cytodifferentiation stage (E120) and the adult anagen phase both exhibit robust follicular growth, a systematic characterization of their shared molecular programs remains to be established. This study aimed to construct an integrated single-cell atlas to identify conserved cellular features and lineage dynamics governing hair follicle (HF) morphogenesis and cycling.

Methods: We performed an integrated analysis of single-cell RNA sequencing (scRNA-seq) datasets from cashmere goat skin at the embryonic E120 stage and adult phases (anagen and telogen). hdWGCNA, Slingshot, and *scVelo* were employed to delineate core cell populations and transcriptional kinetics. To characterize regulatory hubs, transcription factors (TFs) were identified using the *AnimalTFDB 4.0* database, and their target genes were predicted based on homologous targeting relationships within the *GTRD* database. Lineage-specific TF-target gene regulatory networks were constructed for each unique cell branch. Key expression patterns were spatially validated via immunofluorescence staining.

Results: Integrated analysis revealed significant transcriptional convergence between E120 and adult anagen HFs, reflecting a conserved molecular framework for follicular growth. Using hdWGCNA, we identified a high-consensus gene module defining a core “Hair Follicle” population (Figure 1A). Trajectory and RNA velocity analyses inferred a developmental continuum from quiescent HFSCs to an active matrix state. By constructing TF-target networks, we identified key lineage-specific regulators and their downstream gene cascades, providing a systematic view of the transcriptional control driving progenitor activation and differentiation (Figure 1B). These computational inferences were supported by the spatial localization of candidate factors, such as *GATA3* and *LEF1*, within the HF structure.

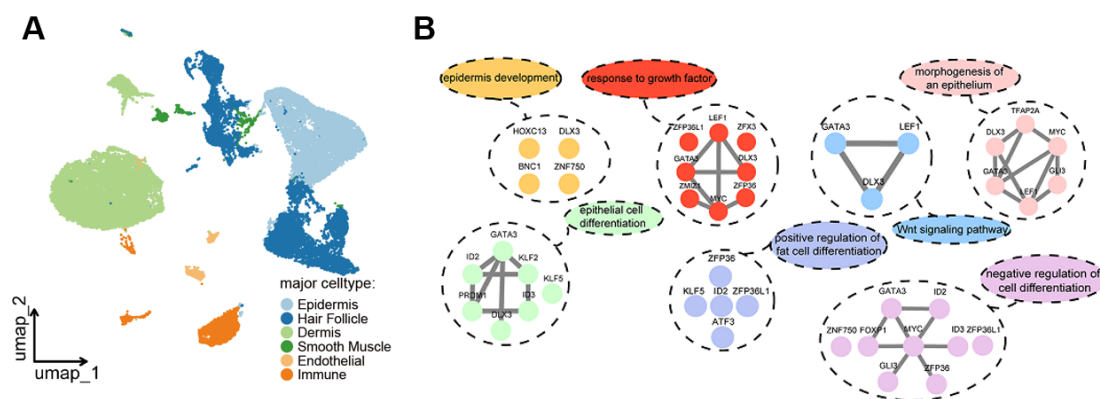


Figure 1. Integrated single-cell map of hair follicle cycles and core regulatory network for development in cashmere goats

Keywords: Cashmere goat, Single-cell transcriptomics, Hair follicle cycling, Morphogenesis, Gene regulatory network

FAPs-Derived LAMA2 Regulates Myogenic Differentiation and Slow Fiber Specification via DAG1-FAK Signaling in Goats

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Abstract: Skeletal muscle growth and fiber-type composition are major biological determinants of meat production and meat quality in livestock. Skeletal muscle satellite cells (SMSCs) are essential for postnatal muscle growth because they provide new myonuclei through proliferation and myogenic differentiation. However, the regulation of SMSCs by non-myogenic cells within the muscle microenvironment remains incompletely understood in goats. This study aimed to clarify whether fibro/adipogenic progenitors (FAPs) regulate goat SMSC fate through the secretion of laminin subunit alpha-2 (LAMA2), and to further identify the underlying signaling mechanism. Based on single-nucleus RNA sequencing and cell communication analysis of goat longissimus dorsi muscle, FAPs were identified as an abundant non-myogenic cell population with strong interactions with myogenic cells, and LAMA2 was screened as a key FAP-derived extracellular matrix ligand. Primary goat FAPs and SMSCs were isolated and cultured, and a Transwell co-culture system, small interfering RNA-mediated knockdown, recombinant LAMA2 supplementation, EdU staining, CCK-8 assay, immunofluorescence staining, RT-qPCR, Western blotting, protein interaction prediction, co-localization analysis, and co-immunoprecipitation were used to evaluate cellular function and molecular mechanisms. FAPs showed a high capacity to communicate with SMSCs, and LAMA2 expression increased during postnatal muscle growth and SMSC differentiation. Knockdown of LAMA2 in FAPs reduced LAMA2 secretion and significantly inhibited SMSC proliferation, whereas exogenous LAMA2 promoted DNA synthesis, cell viability, and the expression of proliferation-related genes. Although LAMA2 interacted with dystroglycan 1 (DAG1), DAG1 knockdown enhanced SMSC proliferation, indicating that LAMA2-driven proliferation is not mainly dependent on DAG1. During myogenic differentiation, LAMA2 knockdown reduced myosin heavy chain-positive myotube formation, fusion index, and myogenic marker expression, whereas LAMA2 supplementation enhanced SMSC differentiation. LAMA2 also promoted slow-twitch muscle fiber formation by increasing MYHCI-positive myotubes and slow-fiber marker expression without markedly promoting fast-fiber formation. Mechanistically, LAMA2 interacted with DAG1 and activated focal adhesion kinase (FAK) phosphorylation. DAG1 knockdown or FAK inhibition weakened the pro-differentiation and slow-fiber-promoting effects of LAMA2, and combined blockade of DAG1 and FAK largely abolished these effects. These findings demonstrate that FAP-derived LAMA2 is an important extracellular matrix signal in the goat skeletal muscle microenvironment. LAMA2 promotes SMSC proliferation through a DAG1-independent mechanism, while it regulates myogenic differentiation and slow-twitch fiber formation mainly through the LAMA2–DAG1–FAK signaling axis. This study provides new evidence for cell–matrix communication in livestock muscle development and offers a potential theoretical basis for improving meat-producing traits.

Keywords: FAPs, LAMA2, SMSCs, Myogenic differentiation, Slow muscle fiber formation

Revealing the RNA landscape of muscle tissue during critical developmental stages in goats using nanopore direct RNA sequencing

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Abstract: Understanding the RNA landscape of muscle tissue is crucial for elucidating the complex mechanisms of muscle growth, development, and metabolism in goats. However, current knowledge remains limited, as traditional short-read RNA sequencing relies heavily on incomplete gene annotations and struggles to accurately resolve the diverse full-length transcripts generated during critical developmental stages. To overcome these limitations, this study employed a comprehensive multi-omics approach combining Nanopore direct RNA sequencing (DRS) and short-read RNA-seq. This method comprehensively profiled the RNA metabolic landscape of the longissimus dorsi muscle in goats across key developmental stages, particularly during the rapid growth phase. This research discovered a substantial number of novel transcripts and alternative splicing isoforms that traditional short-read RNA-seq cannot effectively resolve. Furthermore, it identified hundreds of genes with significant stage-specific expression, thereby unveiling novel regulatory pathways in muscle development. Through a comparative analysis of transcriptomic features across different stages, this study revealed significant dynamic shifts over time in gene expression, transcript isoforms, and their regulatory networks. Additionally, Nanopore DRS exposed multifaceted dynamic changes in transcript poly(A) tail lengths and post-transcriptional modifications, such as m6A, many of which are finely tuned in a stage-specific manner. These dynamic changes likely play a central role in driving the expression of key muscle genes, muscle fiber type transitions, and the metabolic specialization of the muscle. Altogether, these findings illuminate previously underappreciated layers of genomic and post-transcriptional regulation, offering a fresh perspective for a deeper understanding of the complex regulatory mechanisms underlying muscle metabolism.

Galectin Network Dynamics Identify LGALS-11 and LGALS-14 as Genetically Relevant Markers of Seasonal Parasite Resistance in Grazing Goats

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Abstract: Gastrointestinal nematodes are a major constraint to goat productivity and a priority trait for genetic improvement in pasture-based systems. In the North Carolina Piedmont, the late winter-to-spring transition is characterized by increasing ambient temperature, enhanced larval survival on pasture, and periparturient immune modulation, resulting in the spring rise in parasite burden. Resistance to helminths is partially heritable, yet genetically informative immune markers that capture seasonal host-parasite interactions under natural grazing conditions remain limited. This study evaluated seasonal regulation of the galectin network with emphasis on LGALS-11 and LGALS-14 as genetically relevant markers of parasite resistance. Ten adult Boer × Spanish does were continuously grazed on pasture at the North Carolina A&T State University farm across a six-week late winter-to-spring period (February–April). Whole blood was collected at weeks 1, 4, and 6. Total RNA was isolated, quality-assessed, ribosomal RNA-depleted, and sequenced using Illumina-based RNA sequencing. Reads were aligned to the *Capra hircus* reference genome and analyzed using count-based differential expression with false-discovery rate control. Targeted quantitative polymerase chain reaction was used to assess temporal expression of multiple galectins and associated ligands. Plasma secretion of Galectin-1, Galectin-3, and Galectin-9 was quantified by enzyme-linked immunosorbent assays. RNA sequencing detected 21,162 transcripts, of which 66 were upregulated, 5,056 downregulated, and 16,040 unchanged between early and late sampling points. Differentially expressed genes reflected seasonal reprogramming of metabolic, mitochondrial, oxidative stress, and immune signaling pathways. Galectin genes were expressed but did not meet differential expression thresholds using RNA sequencing. In contrast, targeted molecular and plasma-based analyses revealed distinct temporal regulation of multiple galectins, particularly LGALS-11 and LGALS-14, demonstrating their functional relevance during the spring rise. These findings establish the galectin network as genetically relevant and seasonally responsive, supporting its potential integration into genomic selection and breed evaluation strategies for improving parasite resilience in grazing goat populations.

Deciphering the genetic basis underlying the formation of superior flavor traits in goats based on multi-omics technologies (*Capra hircus*)

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Objective: Improving mutton quality and flavor has long been the core goal of meat goat breeding. Among them, variety differences are one of the key factors affecting the flavor. Hubei Province, as a major goat breeding province in the south, has abundant forage resources and a strong breeding foundation. Numerous studies have reported the growth, reproduction and physiological characteristics of various goat breeds in southern region, but research on their flavor traits remains scarce. Therefore, we focuses on excellent goat breeds in Hubei, employing multi-omics analysis to elucidate the genetic basis of superior flavor traits in meat goats, and fill the gap in multi-omics flavor research on mutton in Hubei region.

Methods: Select 6 castrated Chubao black-head goats, Boer goats, Macheng black goats, and Matou goats aged 9-10 months and in good health. All animals were raised under a total confinement system and uniformly fattened for two months. During the feeding period, record daily feed intake and body weight changes. After the fattening period, measure the slaughter performance of each goat. For each breed, three goats were randomly selected to determine net meat weight, and calculate the dressing percentage and carcass net meat percentage were calculated. Extract the longissimus dorsi muscle located from the left half-carcass between the 12th and 13th ribs. Measuring the meat quality indicators, nutritional indicators, amino acids and fatty acids determination, as well as sequencing analyses of the transcriptome, untargeted metabolome, and volatile metabolome.

Results: Based on phenotypic indicators, the omics analysis identified core pathways associated with meat quality and flavor, including the biosynthesis of unsaturated fatty acids, arachidonic acid metabolism, adipocyte cytokine signaling pathways, AMPK signaling pathways, glycine, serine, and threonine metabolism, taurine and hypotaurine metabolism. Differentially expressed genes (DEGs) related to lipid deposition, including *PLA2G2C*, *PROCA1*, *ALOX5*, *PTGS2*, *ACACB*, *PCK2*, *GGT5*, *FBP1*, *SCD*, *GAMT*, and *AOC2*, were enriched in these pathways.

Conclusion: This study systematically elucidated the phenotypic characteristics and molecular basis of superior flavor traits in Hubei excellent goat breeds. The results demonstrate that different goat breeds exhibit significant differences in meat quality, nutritional composition, and flavor profile. The identified core pathways. key DEGs and differentially accumulated metabolites (DAMs) provide important theoretical basis for analyzing the molecular mechanisms of superior flavor traits in mutton, optimizing southern goat breeds, and precise flavor regulation.

Keywords: Goat, Transcriptomics, Metabonomics, Flavor characteristics

Genome-Wide Association Analysis of Dorsal Black Stripe Trait in Youzhou Dark Goat

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Objective: The dorsal black stripe trait is widespread among mammals and holds significant importance for breed identification, genetic breeding, and evolutionary studies. This research aims to reveal the genetic basis of this trait by screening molecular markers and candidate genes associated with the dorsal black stripe trait in Youzhou dark goats, thereby providing scientific support for the conservation and utilization of local genetic resources.

Methods: 137 healthy adult Youzhou dark goats were phenotyped by the dorsal black stripe trait. Genomic DNA from venous blood was subjected to WGS; after quality control, the data were aligned to the goat reference genome ARS1 to identify genome-wide SNP loci. High-quality SNPs were screened via Plink software. Principal component analysis (PCA) and Admixture analysis were used to clarify the population genetic background, and the pairwise algorithm was applied to assess the linkage disequilibrium (LD) level. Genome-wide association study (GWAS) was performed with GEMMA (threshold = 7.57×10^{-7}) to screen SNPs associated with the trait; Bedtools was used to annotate the loci and mine candidate genes. VCFtools (50 kb sliding window, 10 kb step) was used to conduct genome-wide selective sweeps to calculate the population genetic differentiation index (F_{st}) and nucleotide diversity ratio (π -ratio); the overlapping top 5% regions of the two indices were selected for gene annotation and KEGG enrichment analysis. Additionally, SNPs in chromosome 18 (12403900–17000000 bp) were extracted and annotated via ANNOVAR to analyze the variation distribution in this region.

Results: Phenotypic results showed that among the 137 Youzhou Dark Goats, 60 individuals exhibited the dorsal black stripe phenotype while 77 did not. Whole-genome sequencing generated 4.04 Tb of valid data, and after quality control, 13,211,396 high-quality SNPs were retained for subsequent analysis. Population structure analysis revealed incomplete differentiation between the dorsal black stripe and non-stripe groups. GWAS revealed three SNPs significantly associated with the dorsal black stripe trait in goats (threshold = 7.57×10^{-7}), with SNP1 and SNP2 located within introns of the peroxisomal biogenesis factor 5-like (PEX5L) gene, and SNP3 within an intron of genetic suppressor element 1 (GSE1). Selection signature analysis detected 4,373 regions, annotating 1,544 candidate genes (including PEX5L and GSE1), which were significantly enriched in 18 pathways ($P < 0.05$), such as the cAMP signaling pathway, gap junctions, and adherens junctions. In-depth analysis of chromosome 18 showed that GSE1 exhibited the highest variation richness, significantly exceeding that of other genes in the region.

Conclusion: Integrating WGS-based GWAS and selection signature analyses, this study identifies PEX5L and GSE1 as key candidate genes for the dorsal black stripe trait in Youzhou dark goats. The findings provide a theoretical foundation for elucidating the molecular genetic mechanisms underlying this trait in goats and will facilitate marker-assisted selection in breeding programs as well as sustainable utilization of local genetic resources.

Keywords: GWAS; Youzhou dark goat; Dorsal black stripe trait; Selection signature analysis; Whole-genome sequencing (WGS)

Genomics-Assisted Marker-Assisted Breeding for Improving Fiber Quality and Yield in Pashmina Goats

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Abstract: Changthangi Pashmina goats are a valuable genetic resource of the cold-arid Himalayan region and are globally recognized for producing ultra-fine Pashmina fiber. However, improvement in fiber yield and quality through conventional selection remains slow due to the complex genetic nature of fiber traits, long generation intervals, and limited availability of validated molecular markers. We are working to develop a genomics-enabled marker-assisted breeding program for enhancing Pashmina fiber quality and yield in Changthangi goats. The study will involve systematic phenotypic evaluation of economically important fiber traits such as fiber diameter, staple length, fiber yield, and overall fleece quality, followed by genome-wide marker discovery using high-throughput sequencing approaches. Candidate genomic regions, SNPs, and trait-associated markers linked with superior fiber production and quality will be identified and validated in representative Pashmina goat populations. The generated genomic information will support the development of reliable molecular markers for early selection of elite animals, thereby improving breeding accuracy and accelerating genetic gain. This work is expected to strengthen conservation-oriented genetic improvement of Changthangi Pashmina goats and provide a scientific foundation for sustainable Pashmina production in Ladakh and the Himalayan region. This study is funded by the Anusandhan National Research Foundation (ANRF) under the Prime Minister Early Career Research Grant (PM-ECRG) scheme.

Keywords: Pashmina fiber, Marker-assisted Breeding, Improve Yield, Fiber quality, Pashmina genetic markers.

Effects of Genetic Polymorphism of Melanocortin 4 Receptor Gene on Growth and Metabolic Traits, Rumen Microbial Community, and Signal Transduction Mechanism in Goats (*Capra hircus*)

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Abstract: Feed intake is a critical determinant of goat production performance. As an essential central molecule governing feeding behavior in animals, melanocortin 4 receptor (MC4R) has been proven to profoundly regulate feed intake and growth performance in goats; however, its underlying regulatory mechanism remains poorly understood. In this study, seven SNP loci were identified by screening and genotyping the PCR-amplified CDS sequences of the MC4R gene in 561 goats. Phenotypic data recorded at 3, 6, and 12 months of age were collected for association analysis. Mutant MC4R plasmids were constructed and transfected into cells to evaluate the effects of individual SNPs on cellular signal transduction. Subsequently, the C906A locus of the MC4R gene was selected as the target site for genotyping. Three Boma crossbred goats with consistent physical conditions were screened for each genotype (CC, CA, and AA) and subjected to a 60-day grouped feeding trial. Multiple indicators, including growth traits, slaughter parameters, serum energy metabolism profiles, and rumen microbiota, were comprehensively analyzed. The results demonstrated that among the seven identified SNPs, A359G, T360C, T363C, A612G, and C906A significantly affected goat growth traits. Notably, only the C906A mutation induced substantial alterations in the tertiary structure of the MC4R protein, accompanied by decreased cell surface expression of MC4R and suppressed activities of the PKA and MAPK signaling pathways, indicating that C906A is a loss-of-function mutation. Goats with the AA genotype exhibited superior feed intake, growth performance, and slaughter traits compared with CC and CA individuals. In addition, the AA genotype was markedly enriched with fiber and polysaccharide-degrading microorganisms, such as Firmicutes and Ciliophora. Multiple signaling pathways associated with autophagy, endocytosis, protein processing, and cell cycle were significantly enriched in the KEGG functional annotation. In conclusion, the loss-of-function C906A mutation inhibits the activity of downstream signaling pathways by altering the spatial conformation of the MC4R protein, while modulating the composition and function of rumen microbiota. These changes ultimately regulate feeding behavior, growth, and slaughter performance in goats. The present study clarifies the multidimensional regulatory mechanism of MC4R involved in goat growth and metabolism and provides a theoretical basis for utilizing the MC4R gene and its interaction with rumen microbiota as molecular markers to implement marker-assisted selection in goat breeding.

Keywords: Goat, MC4R, SNP, Growth traits, Signal transduction mechanism, Rumen microbiota

Investigating the Regulatory Role of *METTL25* in Goat Brown Adipocyte Thermogenesis

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Introduction: Brown adipose tissue (BAT) plays a critical role in maintaining body temperature and resisting cold environments due to its exceptional capacity of non-shivering thermogenesis (NST). Our preliminary analyses identified methyltransferase-like 25 (*METTL25*) as a potential key regulator of BAT thermogenesis in goats. In this study, we characterized the expression patterns of *METTL25* and investigated its effects on the thermogenesis of goat brown adipocytes. This work was funded by the National Natural Science Foundation of China (No. 32372834).

Materials and methods: We manipulated *METTL25* expression by interfering or overexpressing it in goat brown adipocytes. Then, we examined the effects of *METTL25* on the adipogenic differentiation, thermogenesis, and mitochondrial functions in goat brown adipocytes, and identify potential target genes regulated by *METTL25*.

Results: *METTL25* expression was significantly downregulated during adipogenic differentiation of goat brown preadipocytes, suggesting it may negatively regulate this process. Further results confirmed that *METTL25* inhibited lipid droplet formation and differentiation in goat brown adipocytes. Furthermore, *METTL25* significantly inhibited the expression of key thermogenesis-related genes, including *UCP1* and *PGC1 α* . Moreover, *METTL25* knockdown significantly increased mitochondrial DNA content, activated mitochondria enrichment, and the expression of mitochondrial electron transport chain (ETC) complexes in goat brown adipocytes, whereas *METTL25* overexpression had the opposite effect. RNA-Seq analysis revealed that differentially expressed genes (DEGs) following *METTL25* overexpression were significantly enriched in TNF, PPAR, and metabolic signaling pathway. Finally, we hypothesize that *HMGCS2* is a potential target gene of *METTL25*, as *METTL25* significantly affects its expression.

Conclusin: *METTL25* inhibits the adipogenic differentiation, mitochondrial enrichment, and thermogenesis in goat brown adipocytes. *METTL25* affects *HMGCS2* expression, but further studies are needed to verify the direct targeting relationship between them.

Keywords: Goat, Brown adipocyte, *METTL25*, Adipogenic Differentiation, Thermogenesis

Investigation of the Secondary Follicular Cycle Patterns in Inner Mongolia Cashmere Goats Based on Skin Transcriptome Data

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Objective: Based on skin transcriptome data, we depicted the molecular dynamics of the growth, catagen and telogen phases of secondary hair follicles in Inner Mongolia cashmere goats, and identified the key genes and core pathways in each period, which laid a foundation for analyzing the growth law of secondary hair follicles in cashmere goats in Inner Mongolia.

Methods: Four skin transcriptome items (PRJNA470971, PRJNA382893, PRJNA592400, PRJNA832904) of Inner Mongolia cashmere goats in the NCBI database were downloaded, and the transcriptome data were renumbered according to the hair follicle growth period IMCG_a01 (Anagen), IMCG_c01 (Catagen), and IMCG_t01 (Telogen). Quality control of sequencing data was performed using Trimmomatic software (0.39). The quality inspection and filtering sequencing data were compared with the goat genome (version number: GCF_001704415.2_ARS1) using HISAT2 (2.2.1) software, the skin tissue samples of cashmere goats in Inner Mongolia were quantitatively analyzed by StringTie software (2.2.1), and finally the mRNA expression matrix data were analyzed by R (4.5.3) and Rstudio (2026.01.2+418). Included: principal component analysis using the prcomp function of the stats (4.5.3) package, differential expression analysis using DESeq2 (1.46.0), parameter set to $|\log_2FC| > 1$, the correction *P-value* (*P-adj*) < 0.01 , the PCA plot and the differential gene volcano map were plotted using the ggplot2 (4.0.3) package, the DEGs clustering heatmap was plotted using the pheatmap(v 1.0.12) R package, and the Wayne plot was plotted with the help of <https://www.bioinformatics.com.cn/static/other/s/jvenn/example.html>. DAVID 2021 was used to perform GO functional enrichment analysis and KEGG pathway enrichment analysis for DEGs.

Results: A total of 1440 genes were removed from the genes of the three growth periods, and a total of 13 genes were removed from the three periods, including *LOC102190903*, *LOC102188576*, *LOC108634363*, *LOC108633210*, *LOC102188300*, *LOC108634884*, *LOC102168852*, *LOC102191166*, *LOC102180194*, *LOC106503120*, *BPIFB2*, *KRT4*, *LTF*. There were 30 GO entries for differential genes, covering 10 biological processes, 10 cell components, and 10 molecular functions. KEGG results showed that the differential genes were mainly concentrated in the *cAMP* signaling pathway, the *Relaxin* signaling pathway, and the *Estrogen* signaling pathway.

Conclusion: In this study, 1440 genes were identified from the skin transcriptome sequencing results of Inner Mongolia cashmere goats in through differential expression, of which 13 genes were continuously expressed from the anagen phase, catagen phase, and telogen phase, KEGG enrichment analysis showed that *cAMP*, *Relaxin*, and *Estrogen* signals were involved in the regulation of hair follicles, and GO annotation showed that the differential genes were mainly involved in biological processes such as extracellular space and calcium ion binding, and a total of 8 key genes were obtained. Functional verification analysis can be performed in the later stage to further clarify the regulatory effect of key genes.

Keywords: Inner Mongolia cashmere goats, skin transcriptome, differentially expressed genes, hair follicle cycle

Effects of goat *PINK1* gene polymorphisms on ovarian granulosa cell function

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Objective: *PINK1* is a mitochondrial serine/threonine protein kinase that plays an important role in maintaining mitochondrial homeostasis and cell survival. However, the association between the *PINK1* gene and litter size in goats, as well as its functional mechanism in granulosa cells (GCs), remains unclear. Therefore, the objective of this study was to identify single nucleotide polymorphisms (SNPs) of the *PINK1* in Dazu black goats, analyze their association with litter size, and explore the regulatory effects of *PINK1* on granulosa cell proliferation, apoptosis, and mitophagy.

Methods: In this study, 128 Dazu black goat does with similar body condition were selected. Genomic DNA was extracted from blood samples to identify single nucleotide SNPs loci in the *PINK1* gene. Population genetic analysis was performed using software such as DnaSP and POPGENE 32. Then, Ovarian granulosa cells were isolated and cultured in vitro. Gene function was further assessed by immunohistochemistry, siRNA knockdown/overexpression transfection, CCK-8, EdU, flow cytometry, qPCR, and Western blot.

Results: Six SNP loci were identified in the *PINK1* gene, and all loci were in Hardy-Weinberg equilibrium. Among them, the g.3974684G>A and g.3979274T>C loci were significantly associated with litter size in Dazu black goats at the fifth and first parity. This gene exhibited the highest expression level in ovarian tissues of Dazu black goats. Knockdown of *PINK1* increased the expression of apoptotic factors and decreased proliferation factors and key mitophagy proteins. In contrast, overexpression of *PINK1* had the opposite effect. Moreover, the g.3979274T>C mutation could further enhance the regulatory function of *PINK1*.

Conclusion: In Dazu black goats, the identified SNPs were significantly associated with litter size. Meanwhile, *PINK1* could promote granulosa cell proliferation, inhibit cell apoptosis and regulate mitochondrial mitophagy. Moreover, the g.3979274T>C mutation could further enhance such biological effects of *PINK1*.

Keywords: Number of lambs born by goats; Granular cells; *PINK1*; SNPs; Mitochondrial autophagy

Design and Verification of 15K Liquid Chip for Dairy Sheep Selection

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Abstract: In response to the difficulties in tracing the bloodline of hybrid offspring in current dairy sheep breeding and the lack of integration of disease-resistant molecular markers, this study designed and verified a 15K liquid chip. This chip is based on the genome-wide data of the three parental populations (Awassi, East Friesian, and Hu sheep) and their hybrid offspring. Firstly, Fst analysis was conducted to screen out high-differentiation loci with $F_{st} > 0.35$. The allele frequency differences (ΔRAF) between each population were calculated for the selected loci, and they were sorted from largest to smallest. The 13,408 loci with the highest ΔRAF were selected as breed-specific markers (AIMs). The QTL database was used to download 1,952 functional loci related to milk production, disease resistance, growth and development, and these were combined with the AIMs, after which duplicates were removed to obtain 15,998 loci as candidate loci for the 15K liquid chip. The high-quality SNP loci selected include ancestral information markers (AIMs) for population genetic structure analysis and bloodline identification, as well as functional SNP loci related to immunity, disease resistance, milk components, and growth and development. The site distribution is uniform, and the sequencing data efficiency, base quality, alignment rate, and other indicators are good. The verification results showed that the chip could clearly distinguish the three purebred parents (Awassi, East Friesian, and Hu sheep) and their hybrid offspring, and could quantitatively estimate the proportion of each bloodline. The chip successfully captured the reported disease-resistant SNP loci, covering key immune pathways such as TLR, IL, TNF etc. as well as milk component and growth and development-related genes such as *CSN* and *S100*. The 15K multiplex SNP liquid chip designed in this study has excellent performance and provides a low-cost, high-throughput molecular tool for multi-variety breeding of dairy sheep.

Keywords: Dairy sheep, 15K Liquid chip, Breed identification, Disease resistance loci, Pedigree tracing

Identification of Coding Circular RNAs Potentially Involved in the Regulation of Follicular Atresia Based on RNA-Seq of Goat Follicles

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Objective: Follicular atresia impairs reproductive performance, reducing livestock production efficiency and economic benefits. Follicular development relies on coordinated interactions among granulosa cells, theca cells, and oocytes, under strict transcriptional control. However, the role of non-coding RNAs, especially circRNAs, in this network remains poorly understood. Thus, systematically identifying circRNAs that regulate follicular growth provides key theoretical support for molecular breeding to improve goat reproduction.

Methods: CircRNA-seq was performed on healthy (HF) and late atretic (LAF) follicles of Chengdu Ma goats. Differentially expressed circRNAs (DECs) were identified using a threshold of $P < 0.05$ and $|\text{fold change}| > 2$. The potential for translation was predicted by integrating open reading frame (ORF) analysis, Coding Potential Calculator 2 (CPC2) predictions, junction reads detection, and internal ribosome entry site (IRES) predictions. CircRNAs that exhibited Pfam domains, an IRES score greater than 0.5, junction reads support, and CPC2 coding classification were intersected using a Venn diagram to identify translation-competent circRNAs. DECs that overlapped with these were selected, and their host genes were subjected to GO and KEGG enrichment analyses.

Results: A total of 557 DECs (261 up-regulated, 296 down-regulated) and 185 translation-competent circRNAs were identified, as shown in Figure 1A and 1B, respectively. The intersection of these two sets yielded 23 candidate circRNAs (Figure 1C). GO and KEGG enrichment analyses of the host genes associated these 23 candidates revealed that five of them were significantly enriched in specific KEGG pathways, including TGF- β signaling pathway, Lysosome, and Autophagy–animal (Figure 1D). This suggests that these five circRNAs may be involved in the regulation of follicular atresia through the aforementioned pathways.

Conclusion: This study identified five circRNAs, including circATG4C and circZFYVE16, that may regulate goat follicle atresia through their encoded peptides.

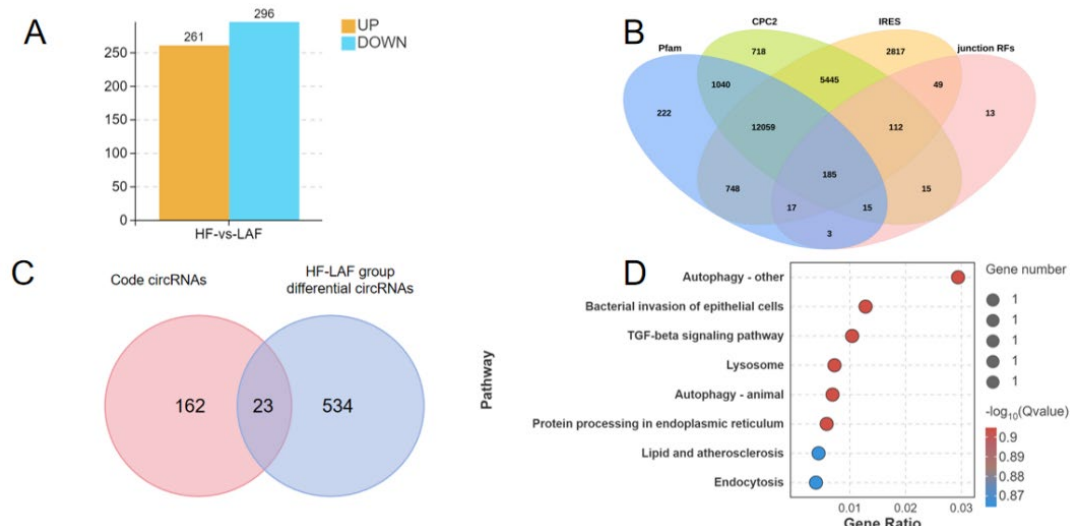


Figure 1. Identification and Functional Enrichment Analysis of Coding-Potential Differentially Expressed CircRNAs in HF and LAF Groups

Keywords: RNA-seq, Follicle development, Coding CircRNAs, Goat

Methylation of ELF5 gene promoter regulates β -casein synthesis in goats (*Capra hircus*)

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Abstract: β -casein is a key indicator of milk quality. Elucidating the regulatory mechanisms underlying β -casein synthesis in goats is of great scientific significance for improving goat milk quality. The transcription factor E74-Like Factor 5 (ELF5) regulates the expression of β -casein, while DNA methylation affects the activity of the ELF5 gene promoter. In this study, dCas9 technology was used to investigate the effects of ELF5 promoter methylation on ELF5 and β -casein expression, providing a theoretical basis for improving goat milk protein quality through molecular breeding. The location of CpG islands in the promoter region of the goat ELF5 gene was predicted using the online tool MethPrimer. Six small guide RNAs (sgRNAs) were designed for ELF5 gene promoter region, and six corresponding PX459-sgRNA vectors were constructed. Primary goat mammary epithelial cells were isolated and cultured. The group transfected with the empty dCas9-DNMT3A vector was set as the negative control, while the six experimental groups were co-transfected with each of the six sgRNA vectors and the dCas9-DNMT3A vector, respectively. At 48 h post-transfection, bisulfite sequencing, RT-qPCR and Western blot assays were performed. Bisulfite sequencing results showed that four of the six sgRNA treatment groups exhibited satisfactory methylation efficiency. RT-qPCR and Western blot results revealed that the mRNA and protein expression levels of ELF5 and β -casein in two sgRNA treatment groups were significantly lower than those in the negative control group. Collectively, DNA methylation at specific sites of the ELF5 gene inhibits the expression of ELF5 and β -casein in goat mammary epithelial cells. This study provides a theoretical basis for exploring the molecular mechanism by which ELF5 promoter methylation regulates β -casein synthesis, and offers a reference for improving the protein quality of goat milk.

Keywords: Goat mammary epithelial cells, DNA methylation, dCas9, ELF5, β -casein

Integrated Electronic Nose, Metabolomics and Mammary Proteomics Reveal the Metabolic Basis of Flavor Differences among Goat, Sheep and Cow Milk

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Objective: Goat, sheep, and cow milk differ markedly in flavor, yet the mammary metabolic mechanisms underlying these interspecies differences remain insufficiently understood. This study aimed to characterize the flavor-related chemical profiles of the three ruminant milks and to identify mammary metabolic and proteomic features associated with flavor precursor formation.

Methods: Electronic nose analysis, headspace solid-phase microextraction gas chromatography–mass spectrometry (HS-SPME-GC-MS), gas chromatography–flame ionization detection (GC-FID), widely targeted metabolomics, and Astral data-independent acquisition mammary proteomics (Astral-DIA) were integrated to compare odor fingerprints, volatile compounds, flavor-related fatty acids, milk metabolites, and mammary protein expression among goat, sheep, and cow milk.

Results: Electronic nose analysis clearly distinguished the three milk types, indicating species-specific odor fingerprints. HS-SPME-GC-MS putatively identified 76 volatile compounds, among which 2-heptanone and 3-methyl-4-heptanone were more abundant in goat and sheep milk than in cow milk. Goat milk showed the highest proportion of short- and medium-chain fatty acids, including C4:0–C12:0, accounting for 28.22%, followed by sheep milk at 24.38% and cow milk at 18.80%. In particular, C6:0, C8:0, and C10:0 were markedly enriched in goat milk. Widely targeted metabolomics annotated 594 milk metabolites and revealed species-dependent differences in fatty acid degradation, linoleic acid metabolism, propanoate metabolism, and branched-chain amino acid metabolism. Mammary proteomics identified 4,974 proteins and highlighted coordinated differences in lipid metabolism, amino acid catabolism, energy metabolism, and peroxisome-related pathways. Multi-omics integration further showed that PCCB and HADHA were positively associated with flavor precursor accumulation, whereas ECHDC1 showed an opposite association pattern.

Conclusion: This study provides an association-based food chemistry and mammary-omics framework for understanding interspecies differences in ruminant milk flavor. The findings identify candidate metabolic and proteomic nodes that may support future functional validation of flavor formation mechanisms in goat, sheep, and cow milk.

Keywords: Goat, Sheep and Cow milk; Volatile compounds; Short- and medium-chain fatty acids; Mammary proteomics

Differences in Amino Acid Composition Among Skeletal Muscles from Different Anatomical Sites in Goats and the Role of Ornithine in Muscle Fiber Differentiation

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Abstract: Muscle fiber types in mammalian skeletal muscle determine meat quality, and muscles from different body regions exhibit heterogeneity in fiber composition. Amino acids not only serve as the building blocks of proteins but also play a signaling and regulatory role in the formation of muscle fiber types. This study used six muscle samples and serum from 10-month-old Tianfu goats (n=9), combining metabolomics, cellular, and mouse models to screen for and validate the regulatory role of ornithine in muscle fiber type determination. Immunofluorescence results showed that the proportion of slow-twitch fibers in the supraspinatus (45.04%) and infraspinatus (37.35%) muscles was significantly higher than in the longissimus dorsi (25.95%), psoas major (23.46%), semitendinosus (32.9%), and semimembranosus (25.13%) muscles, whereas the latter four were predominantly fast-twitch. Amino acid-targeted metabolomics identified a total of 37 amino acid metabolites; muscles with a predominance of slow-twitch fibers were enriched in glutamine and ornithine, while those with a predominance of fast-twitch fibers were enriched in carnosine and anserine, with metabolic profiles consistent with fiber type. Correlation analysis revealed a consistent positive correlation between hydroxyproline levels in muscle and serum, suggesting its potential as a serum biomarker. Ornithine promoted the differentiation of goat muscle satellite cells in a dose-dependent manner, with 20 mM being optimal; this concentration increased myotube length, the differentiation index, and MYH1 expression. It promoted MYH7 expression in the early stages of differentiation and MYH1 expression in the middle and late stages. Results from a mouse cardiotoxin (CTX) injury model indicated that 75 mM ornithine was more effective in promoting skeletal muscle regeneration and structural repair, reducing the proportion of central-nucleated fibers, and increasing the MYH1/MYH7-positive area. This study systematically revealed differences in muscle fiber type composition and amino acid metabolic characteristics among various muscle regions of Tianfu goats. It screened and validated the regulatory role of ornithine in myogenic differentiation and muscle fiber type conversion, providing new insights into nutritional regulation for improving goat meat quality.

Keywords: Goat; Skeletal muscle; Amino acid profile; Ornithine; Muscle fiber type

Association between a novel CSN1S1-CSN2 haplotype and milk composition in the Carpathian goat breed

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Abstract: The *CSN1S1* gene in goats influences milk composition through 19 alleles classified by expression level: strong (A, B), medium (E), weak (F), and null (01), with protein yields ranging from 3.5 to 0 g/L per allele. Casein-rich milk, essential for cheese production, is associated with strong *CSN1S1* alleles, whereas weak alleles correspond to reduced α S1-casein levels across several goat breeds. Romania ranks third in the EU for goat breeding, with over 1.6 million Carpathian goats. In our previous work, we identified the absence of α S1-casein in several Carpathian goat milk samples using isoelectric focusing, and attributed this phenotype to a deletion on chromosome 6 involving the *CSN1S1* gene, which we designated as the 03 allele. In homozygous goats, the absence of α S1-casein co-occurred with a β -casein variant showing a cathodic shift in its theoretical isoelectric point (5.25) relative to the A variant (5.13).

This study aimed to characterize this potential novel *CSN2* allele, to determine the frequency of the *CSN1S1*-*CSN2* haplotype, and to assess its influence on milk composition in Carpathian goats. Comparative cDNA sequencing of five *CSN2* AA goats and five goats carrying the putative new *CSN2* allele demonstrated that the cathodic shift observed for this protein variant is attributable to a p.Asp47Tyr substitution, arising from a G>T mutation at nucleotide position 13 of exon 7. The new *CSN2* allele was designated H, and genotyping confirmed complete linkage on chromosome 6 with the *CSN1S1* 03 allele. Genotyping of 830 Carpathian goats revealed haplotype frequencies ranging from 0.05 to 0.17 across the analysed populations. Association analyses comparing the *CSN1S1* AA - *CSN2* AA haplotype with the *CSN1S1* 03/03 - *CSN2* H/H haplotype in a total of 156 goats revealed significant differences in milk composition, particularly in total protein (4.07 ± 0.13 vs. 3.60 ± 0.20) and whole casein (3.00 ± 0.10 vs. 2.61 ± 0.15) percentages. These findings indicate that selecting goats carrying strong *CSN1S1* alleles can enhance producers' economic sustainability by increasing cheese yield.

Keywords: Carpathian goat, *CSN1S1*, *CSN2*, polymorphism, milk composition

Effects of AAV-Mediated *METTL25* Overexpression on Thermogenesis in Goat Brown Adipose Tissue

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Objective: In China, the peak lambing season for goats mostly occurs during the cold winter and spring seasons, and low-temperature stress is the primary environmental factor limiting the survival of newborn lambs. Brown adipose tissue (BAT), as a key driver of non-shivering thermogenesis (NST), plays an irreplaceable role in protecting newborn lambs from cold stress and maintaining body temperature. The survival rate of individual lambs is highly dependent on the thermogenic capacity of BAT. Our research group previously screened and identified methyltransferase-like protein 25 (*METTL25*) as a key regulator of proliferation, apoptosis, differentiation, and mitochondrial metabolism in goat brown adipocytes. However, the specific molecular mechanism by which *METTL25* mediates BAT thermogenesis in live lambs remains unclear. Therefore, this study used Dazu black goats as the experimental model and established an in situ *METTL25* overexpression model in goat perirenal adipose tissue (PAT) to investigate the effects of *METTL25* overexpression on PAT remodeling and thermogenic function, thereby providing a theoretical basis for BAT research in goats.

Methods: This study constructed an adeno-associated virus (AAV) overexpressing the goat *METTL25* gene, explored the feasibility of injecting the AAV into goat PAT using ultrasound-guided puncture techniques, and investigated the regulatory effects of *METTL25* overexpression on PAT remodeling and thermogenic function via HE staining, Oil Red O staining, immunofluorescence, qPCR, and Western blotting. Furthermore, RNA-seq and proteome sequencing were employed to screen for potential target genes through which *METTL25* regulates PAT remodeling and thermogenesis, and to elucidate the molecular mechanisms by which *METTL25* overexpression drives the whitening process of goat PAT and inhibits its thermogenic function.

Results: In this study, an AAV overexpression vector targeting the goat *METTL25* gene was constructed. By means of multi-point injection under direct surgical visualization, a live animal model of in situ *METTL25* overexpression in goat PAT was successfully established. Overexpression of *METTL25* specifically inhibited the inner mitochondrial membrane functional proteins UCP1 and CPT2, thereby blocking the non-shivering thermogenesis pathway while also hindering the oxidative degradation of long-chain fatty acids. Consequently, this impaired the thermogenic capacity of the tissue and forced the uncatabolized fat to undergo compensatory whitening.

Conclusion: Ultrasound-guided AAV delivery requires further optimization; direct injection via surgical laparotomy with visual guidance can successfully deliver AAV to goat PAT. Overexpression of *METTL25* can promote the whitening process of goat PAT and suppress its thermogenic function; *METTL25* may target and inhibit the expression of UCP1 and CPT2, thereby inhibiting thermogenesis in goat PAT.

Keywords: Goat; *METTL25*; AAV; Thermogenesis; Whitening.

Multi-omics profiling of chromatin accessibility and H3K27ac reveals super-enhancer-mediated regulatory networks governing endometrial receptivity in goats

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Abstract: Endometrial receptivity (ERE) is a transient uterine state that determines the success of blastocyst implantation; however, the epigenomic regulation underlying ERE establishment in goats remains unclear. Here, we profiled transcriptional and epigenomic features of endometrial tissues from pregnant goats during the peri-implantation window and nonpregnant control goats in the regressed luteal phase to uncover the transcriptional regulatory networks responsible for ERE establishment in goats, utilizing RNA-seq, ATAC-seq, and H3K27ac CUT&Tag. A total of 3,143 differentially expressed genes (DEGs) were identified, accompanied by significant alterations in chromatin accessibility and H3K27ac modifications between receptive and non-receptive endometria. The targeted genes associated with these epigenetic changes were significantly enriched in pathways related to cell adhesion, immune tolerance, and embryo attachment. Motif enrichment and transcription factor (TF) footprinting analyses identified members of the FOS/JUN, SOX, HNF1, CEBP, and BATF families as candidate regulators, implicating downstream genes involved in ERE establishment, including SPP1, FOXO1, KLF4/6, STAT1, IFI6, ITGB8, PLAC8, DUSP4, NR1D1, ISG15, RUFY4, and PIK3R3. In addition, numerous super-enhancers were identified, indicating regions of high regulatory activity and potential long-range gene-enhancers interactions in the endometrium. Integration of multi-omics datasets revealed a strong correlation ($r > 0.7$) among chromatin accessibility, H3K27ac activation, and the expression of 172 DEGs. Furthermore, a set of hub genes (KLF6, IFI6, MCL1, SDC4, SUSD6, MAFF, and IL6R) that appear to coordinate TF binding and distal super-enhancers activity associated with ERE establishment. Our data provided an integrated epigenomic atlas of endometrial receptivity establishment in goats and identify candidate regulatory elements and transcription factors that may orchestrate uterine preparation for implantation. These findings offer valuable insights and testable targets for improving fertility in ruminant livestock.

Keywords: Chromatin accessibility, Endometrial receptivity, Goat, H3K27ac, Transcriptional regulation

A multi-tissue atlas of allele-specific expression reveals tissue-dependent cis-regulatory variation in goats

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Abstract: Allele-specific expression (ASE), characterized by unequal expression of the two alleles of a gene, provides a powerful approach for dissecting cis-regulatory effects and prioritizing regulatory variants. However, the landscape of allele-specific regulation in goats remains poorly understood. Here, we conducted a multi-tissue ASE analysis using 189 RNA-seq samples derived from 11 tissue types across 20 goats. Following alignment to the reference genome using STAR+WASP, genome-wide heterozygous SNPs were detected and aggregated at the haplotype level for ASE quantification. RNA-seq identified 664,855 autosomal heterozygous SNPs spanning 19,696 genes that were tested for ASE. We found that 50.03% of genes exhibited significant ($FDR < 0.05$) ASE in at least one tissue. The proportion of ASE genes varied significantly across tissues ($p = 4.48 \times 10^{-26}$), ranging from 3.15% in hypothalamus to 8.43% in liver. Furthermore, 434 tissue-level highly imbalanced ASE genes (bias coefficient (ϕ) ≥ 0.4 and tissue detection rate $\geq 30\%$) were detected, most of which displayed strong tissue specificity and limited functional enrichment. We further performed expression quantitative trait loci (eQTL) analysis using omiGA. A total of 1,475 cis-eQTL-associated genes (cis-genes) were identified in the spleen. Integration of highly imbalanced ASE genes and cis-eQTL analyses revealed 26 common genes, with a significantly greater overlap than expected by chance ($p \leq 1.0 \times 10^{-6}$). Among these, 13 genes were annotated as immune-related candidates, including BSG and CD48, representing high-priority targets for future functional validation. The multi-tissue ASE resource and candidate genes identified in this study provide a foundation for future investigations of gene regulation and the genetic basis of complex traits in goats.

Keywords: Allele-specific expression; Goat; Multi-tissue; Cis-regulatory variation; RNA-Seq

Mechanism of H3K18 Lactylation Regulates Myoblast Differentiation via the ATP5H/AMPK Axis in Goat

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Abstract: Metabolic reprogramming is closely associated with myogenesis. Histone lactylation is a metabolism-related histone modification that plays a crucial role in transcriptional regulation of genes, but the mechanism in goat primary myoblasts (GPMs) development remains unclear. This study investigated the mechanism by which histone lactylation modifies transcription of downstream genes to regulate differentiation in GPMs. Here, we observed that lactate, lactylation and histone H3 lysine 18 lactylation (H3K18la) levels were positively correlated with myogenic differentiation levels. Mechanistically, H3K18la promoted myogenic differentiation by mediating ATP synthase peripheral stalk subunit d (ATP5H) transcription, ATP5H modulated adenosine triphosphate (ATP) production, thereby regulating the adenosine 5'-monophosphate-activated protein kinase (AMPK) pathway. Collectively, our findings indicated that H3K18la regulates ATP5H transcription, drives myotube formation through suppression of AMPK pathway. These findings not only unveil a novel mechanism of targeted metabolic-epigenetic interaction in skeletal muscle development but also provide a fundamental in vitro molecular perspective for understanding goat skeletal muscle development.

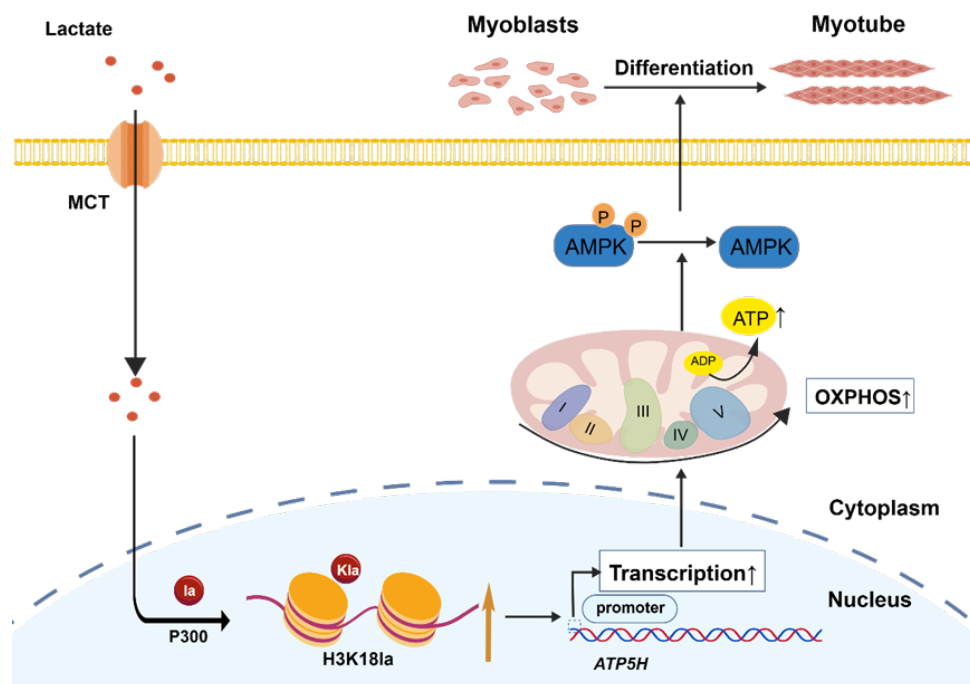


Figure 1 H3K18 Lactylation Regulates Goat Myoblast Differentiation via the ATP5H/AMPK

Keywords: H3K18la, Myoblast Differentiation, Goat

Genome-wide association study and selection signature analysis identify genetic loci and candidate genes associated with the beard trait in goats

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Objective: Beards are specialized hair follicles on the mandibular region of goats, serving as a distinctive morphological trait for breed identification and potentially playing roles in thermoregulation, social signaling, and environmental adaptation. However, the genetic basis of this trait remains incompletely characterized. This study aimed to identify genomic regions and candidate genes associated with beard presence and length in Chinese indigenous goats.

Methods: We integrated a genome-wide association study (GWAS) and selection signature analysis using whole-genome resequencing data from 366 individuals across 12 Chinese indigenous goat breeds. GWAS for beard length was performed on 336 bearded individuals using a linear mixed model. Selection signature analysis (F_{ST} and π -ratio) compared 30 bearded versus 30 non-bearded Leizhou goats to detect genomic regions under positive selection. Candidate genes were annotated and subjected to KEGG pathway enrichment and cross-species PheWAS analyses. Candidate gene expression profiles were further examined using publicly available goat tissue transcriptomic data (HTIRDB, 104 tissues).

Results: GWAS identified 198 significant SNPs ($P < 1 \times 10^{-5}$) associated with beard length, resolving into 69 quantitative trait loci and 79 candidate genes. A prominent signal on chromosome 11 (80.93–80.94 Mb) near *VSNI1* showed a heterozygote advantage (GA > AA) for beard length. Selection signature analysis revealed 125 genomic regions harboring 131 candidate genes under selection, with the strongest signals near *TAOK3* (chromosome 17) and *BNC2* (chromosome 8). Kyoto Encyclopedia of Genes and Genomes (KEGG) enrichment highlighted pathways regulating hair follicle cycling, including cAMP, cGMP-PKG, oxytocin, and relaxin signaling. Cross-species PheWAS confirmed evolutionary conservation of these genes in hair-related traits across goats, humans, and pigs. Tissue expression profiling across 104 goat tissues revealed that *TAOK3* was ubiquitously expressed, *VSNI1* showed neural-specific high expression (>1,300 RPKM in hypothalamus and cerebellum), and *BNC2* exhibited moderate expression in skin and adipose, supporting their distinct roles in beard development.

Conclusion: This study identifies *VSNI1*, *TAOK3*, and *BNC2* as key candidate genes influencing goat beard traits, providing molecular markers for marker-assisted selection and establishing a foundation for functional validation in hair follicle biology and environmental adaptation.

Keywords: Goat; Beard; Selection signature; GWAS; Candidate gene

PART 5: Meat Production

Integrated metabolomic and volatilomic profiling characterizes breed-related flavor variation in indigenous goat (*Capra hircus*) meat under controlled rearing conditions

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Objective: To characterize breed-related variation in flavor-associated traits of indigenous goat meat under standardized rearing conditions and to identify metabolic pathways associated with such variation.

Methods: Longissimus thoracis et lumborum muscle samples from three indigenous goat breeds in Guizhou, namely Guizhou Black (GB), Guizhou White (GW), and Qianbei Brown (QB), were evaluated after controlled and identical rearing. Meat quality traits, amino acid composition, fatty acid composition, untargeted metabolomics, and GC×GC-TOF-MS-based volatile profiling were integrated to compare breed-dependent differences in flavor-associated characteristics.

Results: GW showed higher glycine and proline, whereas QB showed higher methionine (Figure 1A). GW also showed higher n-3 polyunsaturated fatty acids, whereas GB and QB showed higher total polyunsaturated fatty acids and Σ n-6, resulting in a lower n-6/n-3 ratio in GW (Figure 1B-D). In parallel, GW showed higher moisture content, lower shear force, and lower overall volatile intensity, whereas QB showed stronger volatile abundance patterns and GB remained intermediate. Metabolomic and volatile profiling clearly separated the three breeds. Pathway and correlation analyses further indicated that amino acid- and lipid-related metabolism, especially glycine, serine and threonine metabolism and glycerophospholipid metabolism, was associated with breed-dependent variation in flavor precursors and volatile compounds.

Conclusion: Indigenous goat breeds differed substantially in flavor-associated biochemical traits even under identical rearing conditions. GW tended to exhibit a comparatively milder flavor-related profile, QB a stronger volatile-related profile, and GB intermediate characteristics. These findings provide a clearer biochemical basis for breed-specific meat quality evaluation and support the value-added utilization of local goat genetic resources.

Keywords: Indigenous goat; Goat meat; Flavor variation; Volatile profiling; Metabolomics

Characterization of Mutton Volatile Compounds in Youzhou Dark Goats and Local White Goats Using Flavoromics, Metabolomics, and Transcriptomics

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Abstract: Native goat breeds in China are highly valued for their distinctive flavor. This study integrated flavoromics, metabolomics, and transcriptomics to analyze the flavor compounds in the meat of Youzhou Dark (WY) and Local White (BY) goats. Ten 12-month-old castrated male WY and BY goats, five each, were selected for slaughter after undergoing the same feeding and management conditions. Longissimus dorsi muscle were collected from each group and subjected to flavoromics, metabolomics, and transcriptomics analyses. Flavoromics identified 228 volatile compounds, of which alcohols, ketones, and esters were the most prominent. Using multivariate statistical analysis and variable importance on projection (VIP) methods, 85 differential flavor compounds between WY and BY goats were identified. The key characteristic compounds, heptanal, 1-octen-3-one, 2,3-butanedione, 2-methyl-butanal, and 2-pentyl-furan, effectively distinguished between the volatile profiles of the two goat breeds. Untargeted metabolomics identified a total of 47 differential metabolites with significant differences between WY and BY goats. Differences in flavour compounds between the two goat breeds were linked to the expression of genes in metabolic pathways. The genes involved in tyrosine and phenylalanine metabolism were different in the two groups of goat meat. This variation may contribute to the differences in the sensory flavor profiles of WY and BY goats. Overall, these findings provide insight into the molecular mechanisms of flavor formation in native Chinese goats and offer a foundation for improving meat quality.

Keywords: Goat meat; Volatile compounds; Flavoromics; Untargeted metabolomics; Transcriptomics

Effects of grazing intensity and grazing method on goats (*Capra hircus*) and forage biomass

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Abstract: In Southern China, while grassland resources are abundant, the vast majority of forage resources remain underdeveloped and underutilized, and even those already in use suffer from issues such as low grazing capacity and irrational utilization practices. This study investigated the effects of grazing intensity and grazing method on body weight, serum biochemical indicators, and forage biomass in Guizhou black goat ewes, using a combination of weighing and mowing techniques. The results indicated that both grazing intensity and method significantly influenced forage biomass and its recovery rate post-grazing. Compared to continuous grazing, rotational grazing by blocks was more conducive to the sustainable utilization of grassland. Increased grazing intensity negatively affected pasture recovery. Under the same grazing intensity, goats in the continuous grazing group showed better weight gain in the early stage (18 days earlier) than those in the rotational grazing group, but lower weight gain in the later stage (18 days later). Under the same grazing method, higher grazing intensity adversely affected goat weight gain. Both grazing intensity and method also influenced blood biochemical indexes, with goats in the rotational grazing group demonstrating better disease resistance than those in the continuous grazing group. Based on comprehensive analysis, under a concentrate supplementation of 0.15 kg per head per day, the optimal grazing strategy for Guizhou black goats was determined as a stocking rate of 15 heads per hectare, with a rotational grazing cycle of 24 days and a grazing duration of 6 days per paddock.

Keywords: Southern China, Artificial mixed grassland, Grazing technology, Goat

Chemometric and machine-learning discrimination of goat and beef meat using quality characteristics and electronic-nose responses

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Objective: This study aimed to discriminate goat (*Capra hircus*) and beef (*Bos taurus*) meat based on routine quality descriptors and an eight-channel metal-oxide-semiconductor (MOS) electronic-nose array, to identify a set of discriminant biomarkers, and to assess nine machine-learning (ML) classifiers against classical chemometric models for rapid and non-destructive species authentication in the red-meat supply chain.

Methods: Sixty *longissimus thoracis et lumborum* samples (30 goat, 30 beef) were characterized for 27 variables including ultimate pH, CIELab colour, drip and cooking loss, texture profile (hardness, adhesiveness, springiness, cohesiveness, gumminess, chewiness, shear force), proximate composition, and eight Figaro TGS MOS e-nose channels (MOS-1 to MOS-8). The data underwent log₂-transformation and Pareto scaling prior to conducting analysis of PCA, PLS-DA and orthogonal PLS-DA (OPLS-DA) where 1000× permutation and 7-fold cross-validation (CV) were performed. Classification biomarkers were retained when VIP > 1, $P < 0.05$, false-discovery rate (FDR) < 0.05 and fold change (FC) > 1.5 or < 0.67. The AUC, accuracy, recall, precision, F₁ and Matthews correlation coefficient (MCC) of nine ML classifiers (DT, RF, SVM-RBF, GB, NN, CN2, kNN, NB, AdaBoost) were evaluated by 10 × 5-fold stratified CV which was tested by Friedman and Nemenyi post-hoc analysis.

Results: PCA explained 66.2% of variance on PC1–PC2 with complete species separation. OPLS-DA achieved $R^2Y = 0.945$ and $Q^2 = 0.894$ with 98.3% CV accuracy (AUC = 1.000), $P = 0.001$ under 1000× permutation and a Q^2 permutation-line intercept of −0.320, confirming the absence of over-fitting. Seven variables passed all four biomarker criteria, all elevated in beef: chewiness (FC = 19.6), springiness (FC = 4.3), gumminess (FC = 4.4), hardness (FC = 3.9), and three MOS channels — MOS-4/TGS 2603 (FC = 3.8; methyl mercaptan / trimethylamine), MOS-7/TGS 2620 (FC = 2.9; C₁–C₈ alcohols) and MOS-2/TGS 2600 (FC = 2.4; smoke / low-molecular-weight alcohols). MOS-8/TGS 2444 (ammonia) was the only channel higher in goat (FC = 0.65), consistent with faster deaminative proteolysis. All nine ML classifiers achieved MCC ≥ 0.958; Nemenyi post-hoc testing (critical difference = 1.70) detected no significant difference among them ($P > 0.05$).

Conclusion: The combination of log₂ + Pareto-processed quality characteristics and E-nose responses enables near-perfect goat-versus-beef discrimination (AUC = 1.000) across classical chemometric and ML models. A seven-variable quality biomarker panel (four TPA parameters plus MOS-2, MOS-4 and MOS-7) offers a rapid, non-destructive and cost-effective species-authentication tool.

Keywords: Goat meat; Beef authentication; OPLS-DA; Electronic nose; Machine learning

Tissue-specific volatile profiles and goaty flavor characterization in Chengdu grey goat

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Objective: Adipose and muscle tissue are the key flavor reservoirs, yet volatile differences between specific adipose depots and muscle tissues remain understudied. This study systematically characterized the volatile profiles of subcutaneous fat (PXZF), perirenal fat (SZZF), and the longissimus dorsi (BZ) in Chengdu grey goats using an electronic nose (E-nose) and volatile metabolomics. By identifying metabolites highly correlated with goaty flavor, we provide a scientific basis for quality improvement and molecular breeding.

Methods: Tissue samples (PXZF, SZZF, and BZ) were collected from 14 Chengdu grey goats ($n = 14$), categorized into High-odor and Low-odor groups ($n = 7$, per group) based on sensory evaluation. To stabilize volatile compounds, samples were heated (60 °C, 30 min) and subsequently cooled (20 °C, 30 min). E-nose parameters were set to a 30 s cleaning time, 50 s sampling time, and 1 L/min flow rate. Differential metabolites (DMs) were screened using criteria of $\log_2FC \geq |1|$ and $P < 0.05$.

Results: E-nose analysis demonstrated that PXZF possessed a significantly more intense volatile profile compared to SZZF and BZ. Sensors 1, 5, 11, 12, 15, and 17 carried the highest weights in distinguishing these tissues. PLS-DA and correlation clustering confirmed distinct tissue-specific groupings. PXZF exhibited higher responses for alkanes, ammonia, ketones, alcohols, and volatile organic compounds (VOCs) compared to the other tissues. Metabolomics identified 563 volatile compounds across 13 classes, with PCA and PLS-DA revealing clear separation between tissues. Heatmap results indicated that each tissue possessed a unique expression pattern, with hydrocarbons and organic acids being the most prevalent. A total of 194 DMs were identified: PXZF vs SZZF (154 DMs), PXZF vs BZ (30 DMs), and SZZF vs BZ (10 DMs). These DMs were primarily classified as aldehydes, ketones, and esters. ROAV analysis showed that PXZF exhibited uniquely high odor contributions from fecal, carbolic acid, and tarry notes. Specifically, concentrations of 2-methylisoborneol, 1-hexanol, and 2-methoxyphenol in PXZF were significantly higher than in SZZF, and the odor contribution of 2,3-diethyl-5-methylpyrazine was higher than in BZ. Within PXZF, 7 DMs were identified, with 3,4-dimethylphenol and 3,5-dimethylphenol showing higher contributions in the High-odor group, exacerbating phenolic and earthy notes.

Conclusion: PXZF is the primary source of goaty flavor in Chengdu grey goats. Compounds such as 2-methoxyphenol and dimethylphenols drive goaty intensity, providing critical targets for meat quality optimization and breeding selection.

Keywords: Chengdu Grey Goat; Adipose tissue; Muscle; Goaty flavor; E-nose; Volatile metabolomics

Role and Molecular Mechanism of BTF3 in Regulating Lipid Deposition in Intramuscular and Subcutaneous Preadipocytes of Meat Goats

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Objective: BTF3 is a key transcription factor for RNA polymerase II. It is involved in the progression of multiple cancers and regulates cell proliferation, cell cycle and apoptosis. BTF3 has been reported to promote glycolysis in hepatocellular carcinoma via FOXM1-GLUT1 axis, but its role in goat lipid deposition remains unknown. This study aimed to explore the function and mechanism of BTF3 in regulating lipid deposition in intramuscular and subcutaneous preadipocytes of meat goats. Overexpression and RNA interference were used to detect the effects of BTF3 on adipocyte proliferation, differentiation and marker gene expression. Key molecules of the cAMP/PKA pathway were measured, and rescue experiments with pathway activators were performed to verify the regulatory mechanism.

Methods: Intramuscular and subcutaneous preadipocytes were isolated and cultured from 7-day-old male Jianzhou Big-ear goats under sterile conditions. Goat BTF3 overexpression and RNA interference were used to upregulate and downregulate gene expression, respectively. Total cellular RNA was extracted and reversely transcribed into cDNA, and the expression levels of related genes were detected by quantitative real-time PCR (qPCR). Lipid droplet deposition and cell differentiation were evaluated by Oil Red O staining, Bodipy staining, and triglyceride content assay. Cell proliferation was analyzed by MTT assay, colony formation assay, and EdU staining. Statistical analysis was performed using SPSS software. The t-test was used to determine significant differences between groups, and multiple comparisons were used to analyze p-values for more than two groups. All experiments were performed with three biological replicates.

Results: BTF3 inhibited differentiation and promoted proliferation in goat intramuscular preadipocytes, while it inhibited both differentiation and proliferation in goat subcutaneous preadipocytes. BTF3 exerted its regulatory effects by suppressing the cAMP/PKA signaling pathway. Functional rescue experiments confirmed that the cAMP/PKA pathway is the key downstream signaling axis of BTF3.

Discussion: Collectively, the findings on differentiation and proliferation in goat intramuscular and subcutaneous preadipocytes revealed that BTF3 suppresses lipid deposition in both cell types, and its downstream signaling pathway was verified in this study. BTF3 inhibited the activation of the cAMP/PKA signaling pathway in both intramuscular and subcutaneous adipocytes. BTF3 regulates lipid deposition in goat intramuscular and subcutaneous preadipocytes via the cAMP/PKA signaling pathway.

Keywords: Goat; BTF3; cAMP/PKA

From surplus to table_ exploiting the growth potential of male Tenerife Sur goat kids through targeted feeding strategies

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Abstract: The use of male goat kids not selected for breeding represents an opportunity to exploit their growth potential and generate a distinctive gastronomic product. Twenty-four Tenerife Sur breed kids from two flocks of the breed selection nucleus in the south of Tenerife were assigned to one of two dietary treatments (Diet 1, n=12; Diet 2, n=12). Diet 1 kids received natural suckling until two months, a rearing concentrate until four months, and a conventional maintenance feed during fattening (DM 88.92%, CP 14.01%, NDF 25.41%, ADF 13.91%, EE 2.52%, ash 6.40%, NE 83.9 UFL cal/kg). Diet 2 kids were raised on Bacilactol milk replacer (CP 23.0%, crude fat 23.0%, crude fibre 0.0%, ash 7.0%) until two months, the same rearing concentrate until four months, and a specific fattening concentrate formulated by Graneros de Tenerife (DM 87.86%, CP 14.50%, NDF 19.21%, ADF 8.97%, EE 3.80%, ash 6.16%, NE 95.9 UFL cal/kg). In both groups, ryegrass, white straw, concentrate and water were available ad libitum. After weaning, all animals were housed at the Instituto Canario de Investigaciones Agrarias until slaughter under standardised veterinary care and individual fortnightly weighing. Linear regression of live weight on age showed that Diet 1 kids achieved a mean daily gain of 165.4 ± 28.1 g/day ($R^2=0.90$) versus 146.5 ± 19.5 g/day for Diet 2 ($R^2=0.93$), a 12.8% advantage for Diet 1 ($p=0.081$). Projected days to reach 25 kg were 131 vs. 160 (29-day difference), widening to 284 vs. 330 days at 50 kg (46-day difference). Despite Diet 2 providing higher energy density and lower fibre content, naturally reared kids grew faster, possibly reflecting a positive effect of natural suckling on early rumen development.

Keywords: Goat kids, Tenerife Sur, Daily gain, Dietary treatment, Meat production

PART 6: Milk Production

Prevalence, patterns, association with biofilm formation, effects on milk quality, and risk factors for antibiotic resistance of staphylococci from bulk-tank milk of goat herds

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Objective: The objectives were to study the prevalence and the patterns of antibiotic resistance of staphylococcal isolates from bulk-tank milk of goat herds across Greece, to assess possible associations of the presence of antibiotic resistance with the quality of milk in these herds and to evaluate herd-related factors associated with presence of antibiotic resistance among these staphylococcal isolates.

Methods: A cross-sectional study was performed on 119 goat herds in Greece. Bulk-tank milk samples were collected for bacteriological examination; in total, 80 staphylococcal isolates were evaluated for resistance to 20 antibiotics.

Results: Oxacillin-resistant, resistant to at least one antibiotic, and multi-resistant staphylococcal isolates were recovered from 5.0%, 30.3%, and 16.0% of herds, respectively. Of the isolates, 7.5% were resistant to oxacillin, 50.0% were resistant to at least one antibiotic and 27.5% were multi-resistant. Resistance was more frequent among coagulase-negative staphylococci (59.3%) than among *Staphylococcus aureus* (23.8%). Resistance was more frequent against penicillin and ampicillin (41.3% of isolates). No association was found with biofilm formation by staphylococci. For recovery of oxacillin-resistant isolates, the presence of working staff in the herds emerged as a significant factor; respective factors for the isolation of staphylococci resistant to at least one antibiotic were part-time farming and high (>10) number of systemic disinfections in the farm annually. The same three factors were also significant for the recovery of multi-resistant isolates.

Conclusion: The findings focused on identifying variables in goat herds that can be related to the presence of resistant isolates in raw milk. These findings should act as a guide to allow the application of good practices, thus contributing to preventing the development of resistance and supporting the ‘one health’ concept. The recovery of resistant staphylococci in bulk-tank milk in goat farms, which is intended for human consumption, raises concerns within the ‘one health’ concept.

The Impact of Polymerized Whey Protein on the Physicochemical Properties, Microstructure, Probiotic Survivability, and Sensory Properties of Hemp Extract-Infused Goat Milk Yogurt

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Abstract: Goat milk yogurt infused with hemp extract (HE) is a novel dairy product. However, unpleasant flavors from hemp terpenes and goat milk may impact its acceptance. This study investigated the effect of polymerized whey protein (PWP) on mitigating the hempy flavor of HE-infused goat milk yogurt, as well as its impact on the physicochemical properties, microstructure, and probiotic survivability. Goat milk yogurt samples were infused with either nothing (plain flavor), HE, HE-whey protein isolate (WPI), and HE -PWP. Compared with the control group, the addition of PWP significantly increased the viscosity of goat milk yogurt from 25.76 ± 14.07 mPa·S to 88.11 ± 29.57 mPa·S ($p < 0.05$). Microstructure analysis revealed that adding PWP formed a compact gel network compared to the irregular open protein matrixes in other groups. Regarding probiotic survivability, *Bifidobacterium* BB-12 maintained a viability above 10^6 cfu/g over nine weeks of storage. Sensory evaluation results ($N = 19$) indicated that PWP significantly improved the consistency of HE goat milk yogurt ($p < 0.05$). In terms of flavor profile, the Goaty flavor score was highest in the control goat milk yogurt (2.50 ± 1.64), those in HE/HE-WPI/HE-PWP-added group were all around 1.00. For the hempy flavor, HE goat milk yogurt reached a high score of 4.00 ± 1.40 , while the addition of PWP reduced the score to 2.50 ± 1.22 . Notably, panelists reported the least hempy flavor in the PWP-fortified group compared to other treatments. In conclusion, PWP effectively improved the texture and mitigated the unpleasant flavors of HE-infused goat milk yogurt.

Keywords: goat milk yogurt; polymerized whey protein; hemp extract; flavor; probiotics

Assessment of Non-Genetic Factors Affecting Milk Yield and Composition in the Beni Aarous Goat Breed

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Abstract: This study investigates the effect of non-genetic factors on the milk and chemical composition of Beni Aarous goat. A total of 386 lactations from 377 goats were analyzed. Milk yield was measured once per month and milk samples were collected during the lactation period. Milk production was 71.75 ± 31.72 kg / lactation. The mean milk composition values for fat, protein, lactose, and solids-not-fat were 3.18%, 3.79%, 4.82%, and 9.45%, respectively. Milk yield was significantly influenced by litter size, season, and year of kidding ($p < 0.001$). Does with multiple births produced significantly more milk than those with single births, and higher yields were observed in does kidding during winter–spring compared to summer–autumn. The management system had a significant effect on milk composition ($p < 0.01$), with higher levels of fat, protein, lactose, and solids-not-fat contents recorded under extensive conditions. Litter size significantly affected milk fat and protein contents ($p < 0.01$), with higher values in single births. Kidding season also influenced protein, lactose, and solids-not-fat contents ($p < 0.05$), with higher values in summer–autumn. These findings highlight the importance of environmental and management factors in milk production and quality in Beni Aarous goats; selection programs can also play a major role in improving the production potential of this breed.

Differential milk cytology in goats: impact of dietary stress and comparison of analytical methods in an experimental setting

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Objectives: Milk somatic cell counts (SCC) are widely used as indicators of udder health in dairy ruminants and support management decisions such as treatment or culling. In goats, however, SCC interpretation is limited by the influence of numerous non-infectious factors, which complicates the detection of intramammary infections. Differential somatic cell counting, enabled by the routine use of Fossomatic 7DC technology (providing the proportions of lymphocytes and polymorphonuclear neutrophils – LPN - expressed as a ratio), may improve the assessment of udder infection status. An exploratory study was conducted under experimental conditions to evaluate measurements obtained with this technology by comparison with Fluorescence-Activated Cell Sorting (FACS), considered as a reference method for detailed milk cell population analysis.

Materials and methods: The study was conducted at the INRAE experimental unit in Bourges using 52 primiparous goats from a divergent selection experiment for longevity: High Longevity (LGV+) and Low Longevity (LGV-) lines. Animals were subjected to a controlled dietary restriction challenge. Milk samples were collected before and during the challenge period and analyzed using both Fossomatic 7DC and FACS. The FACS method employed the DRAQ5 fluorescent probe for nuclear DNA labelling to differentiate neutrophils, lymphocytes/monocytes, and epithelial cells.

Results: Dietary stress induced a significant but transient increase in both SCC and LPN values. The geometric mean SCC increased approximately tenfold at the peak. This increase was not attributable to a simple concentration–dilution effect, as total milk cell counts also increased significantly. Goats from the LGV- line exhibited a more pronounced response, with higher SCC and a marked increase in “other DRAQ5+” cells, suggesting enhanced cellular apoptosis compared with the LGV+ line. A strong correlation ($r = 0.92$) was observed between SCC measured by Fossomatic 7DC and total DRAQ5+ cells quantified by FACS. The quality of the fit between the two variables varies according to: i) the test day: lower at Day 3 of the challenge period; ii) the goat line considered: lower for goats from the LGV- line. Absolute counts of LPN (Fossomatic 7DC) and neutrophils (FACS) were highly correlated ($r = 0.84\text{--}0.85$). In contrast, the correlation between LPN values (Fossomatic 7DC) and neutrophil percentage (FACS) was weak, indicating that the two methods target distinct cell populations and rely on different reference denominators.

Conclusions: A physiological stress markedly alters the milk cellular profile independently of infection in goats. The observed increase in SCC does not appear to be associated with enhanced epithelial cell shedding but rather with changes in inflammatory cell dynamics and survival. Further work is needed to establish relevant interpretation thresholds for LPN proportions to better discriminate between infectious and physiological variations.

Keywords: goat, somatic cell counts, milk differential cytology, Fossomatic 7DC, Fluorescence-Activated Cell Sorting (FACS), dietary stress

Financial support: ANICAP, Nouvelle-Aquitaine Region, Project carried out with the support of the REXCAP Cluster

Differential Cytology of Goat Milk using Fossomatic 7DC: Infectious and Non-Infectious Factors of Variation

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Objectives: Somatic cell count (SCC) is an indicator of udder health in goats but lacks specificity due to non-infectious factors. Differential cell counting using Fossomatic 7DC enables routine quantification of the cellular fraction comprising lymphocytes and polymorphonuclear neutrophils (LPN percentage) and may provide additional biological insight. This study aimed to establish first reference values with Fossomatic 7DC under field conditions and assess its added value for predicting mammary infection status.

Methods: Data were collected from eight commercial goat herds and one experimental unit between October 2019 and April 2022, representing 3,426 goats and 58,653 milk samples from Alpine and Saanen breeds. Milk sampling was performed at each performance recording, in both morning and evening sessions. Recorded variables included parity, stage of lactation, breed, pasture access (two farms), and artificial insemination (six farms). SCC values were log₂-transformed prior to statistical analysis. In the absence of bacteriological data, presumed udder infectious status was inferred from SCC, following French performance recording rules: number of exceedances of thresholds at 750,000 and 2 million cells. Descriptive statistics, longitudinal analyses, and predictive modelling using Random Forest and logistic regression were applied to evaluate factors influencing SCC and LPN% and to estimate infection status.

Results: Mean LPN% was 79.4%, with low variability (2.1% of samples with LPN% below 45%). SCC differed significantly between morning and evening milkings (geometric means: 922 vs. 1,205 × 10³ cells/mL), whereas LPN% remained stable (79.6% vs. 79.3%). Both SCC and LPN% increased with parity and, in mixed herds, were higher in Saanen than Alpine goats. Extended lactation was associated with lower SCC during early stages but slightly higher LPN% throughout lactation. Non-infectious events significantly affected both indicators: moderate increases in SCC and LPN% induced by pasture access; marked but transient increases following artificial insemination. LPN% increased with presumed infection severity based on SCC levels; however, relatively high baseline values in presumed healthy animals reduced its discriminative power. Given the approach used to define udder infectious status, predictive models reached an overall accuracy of 83%, combining SCC, LPN%, and animal-related variables, with SCC, lactation stage, and LPN% as main predictors. Inclusion of LPN% in addition to SCC alone provided limited improvement.

Conclusion: These results provide the first large-scale reference dataset for caprine differential cytology using Fossomatic 7DC. Although differential cytology complements SCC by reflecting shifts in cellular populations, limits of interpretation of Fossomatic 7DC measurements were highlighted: LPN% was unreliable at SCC below 100 × 10³ cells/mL and potentially biased at SCC above 10 × 10⁶ cells/mL; interpretation remained constrained by the narrow physiological range of LPN% (~60–84%)

and its sensitivity to non-infectious factors and management practices. Further work should define robust interpretation thresholds for LPN%, integrate bacteriological data to better characterise udder infection status, and investigate immune responses in the caprine udder to improve biological interpretation.

Keywords: goats, milk somatic cell count, differential cell count, udder health, Fossomatic 7DC

Financial support: ANICAP, Nouvelle-Aquitaine Region, Project carried out with the support of the REXCAP Cluster

Differential expression analysis of milk fat globule membrane proteins in colostrum and mature milk of Wanlin White goats based on DIA proteomics

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Objective: Newborn livestock have underdeveloped immune systems and intestinal barrier functions, making them highly susceptible to environmental stressors. Milk serves as a critical source of nutrition and immune support for lambs in their early life. Colostrum provides passive immunity and helps ensure the health of young animals, whereas the composition of mature milk meets the energy requirements for lamb development. In modern intensive farming practices, lactation periods are often shortened, and milk replacers are used as substitutes for natural milk, which may compromise lambs' immunity and intestinal health, thereby affecting their growth performance. Therefore, research on the differences between goat colostrum and mature milk can provide theoretical support for precise early-life nutrition management in lambs and the development of functional milk replacers.

Methods: This experiment was conducted at a goat farm in Fuyang City, Anhui Province. Twelve Wanlin White goats were randomly selected based on similar body weight, parity, body condition score, and overall health status. Colostrum and mature milk were collected on the first and fifteenth day postpartum, respectively. Milk samples from the 12 healthy goats were pooled into 3 colostrum pools and 3 mature milk pools. After collection, the samples were centrifuged at high speed at 4°C for 15 minutes to collect the lipid layer. The lipid layer was washed three times with 5 volumes of pre-chilled PBS and once with distilled water, and then stored at -80°C for subsequent DIA-MS analysis. Prior to MFGM isolation, the basic nutritional composition of the pooled colostrum and mature milk was determined using an automatic milk composition analyzer. Immunoglobulin G (IgG) was quantified with a commercial ELISA kit, strictly following the manufacturer's standard protocol.

Results: The results showed that the contents of fat, protein, and immunoglobulin in colostrum were significantly higher than those in mature milk, while the lactose content was lower. A total of 3,129 proteins were identified in this experiment, among which 95 MFGM proteins were significantly upregulated and 54 were significantly downregulated in colostrum. The top three proteins with the highest fold change were three homologous Ig-like domain-containing proteins, whose levels in colostrum were significantly higher than those in mature milk. Furthermore, KEGG enrichment analysis of the differentially expressed proteins revealed that the significantly upregulated MFGM proteins in colostrum were mainly enriched in pathways such as intestinal IgA production, riboflavin metabolism, tryptophan metabolism, and complement and coagulation cascades. The downregulated MFGM proteins were primarily enriched in focal adhesion, ferroptosis, and leukocyte transendothelial migration pathways.

Conclusion: This study found that, compared with mature milk, colostrum contains higher levels of fat, protein, and immunoglobulins. Furthermore, functional enrichment analysis of the differentially expressed MFGM proteins revealed that the proteins significantly upregulated in colostrum are primarily enriched in pathways related to innate immunity. These findings indicate that colostrum can provide newborn lambs with more energy and immune-active components, which is beneficial for the establishment of the primary immune system in neonates.

Keywords: Goat milk, Colostrum, Mature milk, Milk fat globule membrane proteins, DIA proteomics

Drivers of Preference for Goat Milk: Perception and Observed Milk Quality in a Traditional Management Setting

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Abstract: The aim of this study was to assess the drivers of goat milk consumption in traditional farming settings of Botswana, focusing on consumer perception and observed milk quality. Descriptive frequencies and logistic regression were applied on data from 40 valid questionnaires collected from the southeastern district. In addition, milk samples were randomly collected from 30 lactating goats at 80 and 90 days postpartum to evaluate milk yield and composition. The mean $\pm$ se of milk quality parameters were observed at 1–2 years and ≥ 3 years of age. The survey revealed that 50% of respondents consumed goat milk, persuaded by the high cost of cow milk (65%), with nearly one-third of consumers aged 46 or older. Compared to cow milk, 63% of respondents rated goat milk higher for its nutritional value (30%), health advantages (27.5%), and accessibility (27.5%). Furthermore, 45% preferred goat milk for its taste, while 82.5% believed there is an existing market demand for goat milk. Consumption pattern was not significantly swayed by gender or household size and income. However, education had a significant positive effect, with respondents holding secondary education being 4.67 times more likely to consume goat milk. Milk yield ranged from 100 to 250 ml at both 80 & 90 days postpartum across all age groups. At 80 days postpartum, younger goats (1–2 years) produced milk containing $4.27 \pm 0.52\%$ fat, $5.50 \pm 0.42\%$ protein, and $4.39 \pm 0.32\%$ lactose, while older goats (≥ 3 years) had $4.83 \pm 0.39\%$ fat, $5.86 \pm 0.08\%$ protein, and $4.54 \pm 0.13\%$ lactose. At 90 days postpartum, milk from the younger age group contained $4.11 \pm 0.18\%$ fat, $3.69 \pm 0.16\%$ protein, and $4.60 \pm 0.05\%$ lactose, compared to $3.86 \pm 0.32\%$ fat, $4.03 \pm 0.39\%$ protein, and $4.39 \pm 0.16\%$ lactose in goats aged ≥ 3 years. Generally, older goats produced milk with slightly higher fat and protein content in 80 days, but the values declined by 90 days postpartum. The findings suggest that consumer preference for goat milk in Botswana is primarily driven by affordability, perceived nutritional and health benefits, and accessibility. Strengthening public awareness, improving goat management systems, and expanding market access may enhance the contribution of goat milk to sustainable dairy production and food security.

Keywords: Botswana, goat milk, milk yield, perception, lactose, sustainable dairy production.

Astral-DIA proteomics: Identification of differential proteins in sheep, goat, and cow milk

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Abstract: Dairy products are of great benefit to human health, and the nutritional differences between different dairy products have attracted attention. In this study, DIA proteomics technique, combined with parallel reaction monitoring (PRM) as a validation method, was used for the qualitative and quantitative analysis of proteins in sheep, goat, and cow milk. In total, 4316 proteins were identified. Beta-2-glycoprotein 1 and aminopeptidase can be used as potential biomarkers for sheep milk, fibrinogen alpha chain and Alpha-1-B glycoprotein can be used as potential biomarkers for goat milk, and angiogenin-1 and Serpin family G member 1 can be used as potential biomarkers for cow milk. Functional analysis showed that these different proteins were enriched through different pathways, such as complement and coagulation cascades. These data reveal the differences in protein content and physiological functionality and provide an important basis for the study of dairy nutrition and adulteration identification.

Keywords: DIA proteomics, Dairy, Functional analysis

Udder Conformation and Thermal Imaging as Indicators of Udder Health in Saanen Dairy Goats

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Objective: Improving udder health is an important goal in dairy goat production, as it affects milk quality, milking efficiency, and animal welfare. This study evaluated whether udder and teat conformation traits, milk somatic cell count (SCC), bacteriological findings, and udder surface temperature could jointly provide useful information on udder health status in Saanen goats.

Methods: The study involved 70 multiparous Saanen dairy goats kept under commercial farm conditions in Hungary. Udder and teat morphology were assessed during early lactation using a linear scoring system. The evaluated traits included udder depth, fore udder attachment, udder cleft, rear udder width and height, teat placement, teat orientation, teat length, and teat form. Milk samples were collected at three stages of lactation and examined for SCC and mastitis-associated bacteria. Udder surface temperature was measured using infrared thermography. The relationship between morphological traits and SCC was analysed by stepwise multiple regression.

Results: The herd showed notable variation in udder morphology, particularly in teat placement and teat form. The average somatic cell count (SCC) was $997.12 \pm 902.85 \times 10^3$ cells/mL, indicating substantial differences in udder health among animals. Among the evaluated traits, teat form, fore udder attachment, teat length, and udder cleft were significantly associated with SCC. The final regression model accounted for 39% of SCC variation, suggesting that udder structure contributed to differences in milk quality. More favourable teat shape, stronger fore udder attachment, shorter teats, and a more pronounced udder cleft were associated with lower SCC. Bacteriological examination showed that 45.0% of the milk samples contained udder pathogens, with coagulase-negative *Staphylococcus* and *Corynebacterium* spp. being the most frequent. The proportion of pathogen-positive samples increased in the higher SCC categories. Infrared thermography detected higher udder surface temperatures in pathogen-positive samples than in pathogen-negative samples, with mean values of 37.21 °C and 36.92 °C, respectively ($P < 0.01$; **Figure 1**). In contrast, udder surface temperature did not differ significantly among SCC categories.

Conclusion: Udder and teat conformation were associated with SCC in the examined Saanen goat herd. More favourable teat form, stronger fore udder attachment, shorter teat length, and a better-defined udder cleft were linked to lower SCC values. Infrared thermography also showed higher udder surface temperature in pathogen-positive samples, suggesting that it may be useful as a complementary tool in udder health monitoring. These findings support the inclusion of udder conformation traits in selection programs aimed at improving milk quality and reducing mastitis risk.

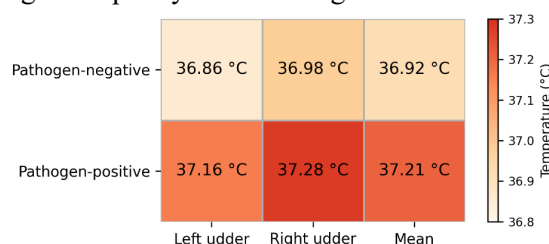


Figure 1. Mean udder surface temperature according to bacteriological status.

Keywords: Saanen goat; udder; teat morphology; somatic cell count; infrared thermography; mastitis

Identification of metabolite biomarkers for lactation stage classification in Saanen dairy goats using untargeted and targeted metabolomics

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Abstract: Lactation stage drives alterations in milk composition; however, milk metabolites underlying such physiological shifts in dairy goats are poorly characterized. This study adopted a two phase strategy to screen candidate milk metabolites associated with lactation stage and assess their feasibility for lactation phase discrimination. In the discovery phase, pooled milk samples from Saanen dairy goats collected at 21, 120, and 240 days postpartum (corresponding to early, mid, and late lactation, respectively) were subjected to untargeted metabolomic analysis. Six candidate metabolites were identified by comparing mid- and late-lactation milk samples, namely DL-arginine, creatine, citric acid, lactic acid, hypoxanthine, and biotin. In the validation phase, these metabolites were quantified via commercial assay kits using longitudinal individual milk samples obtained from the same Saanen dairy goat herd across a 10-month lactation period. Using targeted quantification data, creatine, arginine, and citric acid were selected to construct a multinomial logistic regression model for lactation stage classification, whose performance was validated by leave-one-out cross-validation. The three-metabolite panel yielded an overall classification accuracy of 79.17% (95% CI: 65.01–89.53%) and a Cohen's kappa coefficient of 0.6774. Classification sensitivity varied across lactation stages, with the highest value for mid lactation (0.9500), followed by late lactation (0.7143) and early lactation (0.6429). One-versus-rest Receiver Operating (ROC) analysis further revealed superior discriminatory power for mid lactation (Area Under Curve, AUC = 0.9179), followed by early lactation (AUC = 0.8929) and late lactation (AUC = 0.7983). Misclassification was primarily observed between early and late lactation samples. Collectively, these results demonstrate that the metabolite panel consisting of creatine, arginine, and citric acid exhibits moderate capacity to classify lactation stages with particularly high performance in identifying mid lactation samples.

Keywords: dairy goat, lactation stage, metabolomics, targeted validation, multinomial logistic regression

Metabolomics reveals environmental impacts on regional milk composition in dairy goats

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Objective: Understanding the environmental drivers and metabolic mechanisms underlying regional differences in milk composition is crucial for dairy goat breeding and nutritional management. However, a systematic understanding of how environmental factors affect milk composition across different regions at the metabolic level remains limited. This study aimed to characterize regional variations in the milk composition of dairy goats from three regions in Shaanxi Province (Fuping, Yangling, and Qianyang) and to elucidate their metabolic basis under varying environmental influences.

Methods: Ninety dairy goats in peak lactation (30 per farm) were selected from three farms across the aforementioned regions. Milk composition, temperature, and humidity were recorded over a 21-day period, and water samples and total mixed ration (TMR) from each farm were collected for analysis. Non-targeted metabolomics of milk samples was performed to investigate the metabolic basis underlying the observed regional differences.

Results: Among the three regions, Qianyang showed a markedly lower temperature-humidity index (THI) and a significantly higher dietary crude fat content, with no significant differences in drinking water quality. Regarding milk composition, goats in Qianyang exhibited significantly higher milk fat, protein, and total solids contents ($P < 0.01$), but lower lactose content ($P < 0.01$); no significant difference was observed in solids-not-fat (SNF). Additionally, significant regional differences were found in specific milk minerals (e.g., P, Ca, Mg) and amino acid levels, with Qianyang displaying a generally superior nutritional profile. Non-targeted metabolomics revealed that diet-derived furan fatty acids and microbial co-metabolites, such as muramic acid, were significantly elevated in the milk of Qianyang goats. Concurrently, lipid synthesis intermediates (e.g., 3-oxotetradecanoyl-CoA, CDP-glycerol) and cofactors (e.g., riboflavin, nicotinamide) were notably upregulated in Qianyang milk. Weighted metabolite co-expression network analysis (WMCNA) identified a metabolite module positively correlated with milk fat percentage ($r = 0.657$, $P < 0.001$). This module was significantly enriched in the aforementioned differential metabolites, further corroborating their close association with the high milk-fat phenotype.

Conclusion: Collectively, these findings indicate that the superior milk composition observed in Qianyang goats is driven by the combined effects of regional environmental factors. This process likely involves the enhanced delivery of dietary and microbial precursors through systemic circulation, alongside elevated intrinsic mammary lipogenic activity. This study provides novel metabolic insights into how regional environmental conditions affect milk composition in dairy goats.

Keywords: Dairy goat; Environment; Milk composition; Metabolomics; WMCNA

Rapeseed as a dual-purpose strategy for methane mitigation and milk quality in dairy goats: Bridging experimental evidence and farm practice

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Abstract: Dairy goats play a key role in sustainable livestock production systems, particularly in regions relying on outfield pasture. Goats emit methane and the aim of this study was to identify feed-based mitigation strategies that reduce enteric methane emissions while maintaining milk production, milk quality, animal welfare and consumer's acceptance. Goats tolerate higher levels of dietary fat than dairy cows, making unsaturated lipids from rapeseed a promising option for reducing enteric methane emissions without compromising milk yield or milk quality. This study evaluated the effects of rapeseed-based supplementation on methane emissions, feed intake, milk yield, milk composition and cheese quality in dairy goats within the MetanHUB project. MetanHUB is a Norwegian research- and implementation initiative aiming for identification of feeding strategies for safe and documented methane reduction in ruminants under Norwegian production systems. In a controlled feeding experiment conducted in 2024, 48 lactating goats were allocated to four dietary treatments (four different compound feeds) during the indoor feeding period (spring and autumn): 1) control, compound feed added either 2) calcium nitrate, 3) rapeseed or 4) rapeseed + calcium nitrate. 50 min methane emissions were measured individually in lots of 10 using portable accumulation chambers 5 days in a row repeated three times during each of the feeding periods. Individual dry matter intake, milk yield and live weight were recorded. Milk samples were analyzed for gross composition, fatty acid profile and coagulation properties. Preliminary results from the controlled experiment showed that rapeseed and calcium nitrate supplementation reduced enteric methane emissions by approximately 11% and 5%, respectively, compared with the control diet during the indoor feeding periods. No additive effect of the combination of rapeseed and calcium nitrate was observed. Goats fed rapeseed showed a tendency towards higher dry matter intake and milk yield. No adverse effects on rumen function or animal health were observed in any of the treatment groups. Based on the promising results from the controlled experiment in 2024, rapeseed supplementation was subsequently tested the following year in 5 conventional dairy goat herds volunteering to participate. In these on-farm trials, rapeseed was supplied both as ingredient in compound feed (15% rapeseed) and as whole rapeseed (70 g/goat/day) in TMR, allowing evaluation of palatability, feeding strategies, and applicability within conventional farm management systems. Bulk milk was analyzed every third day recording milk volume, and total production of fat, protein, lactose and groups of fatty acids. Samples of individual goats were analyzed monthly for milk composition. A sensor was installed in the barn of one farm for continuous CH₄ and CO₂ measurements (1 minute interval) for three consecutive months. Rapeseed supplementation reduced methane emission, increased milk yield, total fat yield and unsaturated fatty acids in milk. The milk and cheese maintained normal coagulation properties and sensory qualities. Overall, the results indicate that rapeseed supplementation can function as a dual-purpose feeding strategy in dairy goats, contributing to methane mitigation while maintaining, and even improving milk production and milk quality.

Keywords: Methane emissions, rapeseed supplementation, sustainable feeding strategies, milk quality, milk fatty acids

PART 7: Nutrition

Effect season and host on the nutritive value of *Plicosepalus kalachariensis* parasitic browse attached to different trees in semi-arid areas

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Abstract: Mistletoe plants such as *Plicosepalus kalachariensis* have the potential to be incorporated in ruminant diets due to their high nutritive value and has been utilized for medicinal purposes in humans and livestock, and as a protein source for livestock. The study was conducted was to determine the season and host species effect on the quality (nutritive value, *in vitro* and *in sacco* fermentation and nitrogen solubility) of *Plicosepalus kalachariensis* in the Limpopo province, South Africa. The harvesting of *Plicosepalus kalachariensis* leaves was done in summer and winter on five randomly selected host species (*Senegalia nigrescens*, *Dichrostachys cineria*, *Vachellia nilotica*, *Albizia harveyi*, *Vachellia tortilis*). Harvested samples were dried and ground for chemical analysis and ruminal degradability analysis. *Plicosepalus kalachariensis* harvested from *A. harveyi* in winter had a higher (192 g/kg DM) crude protein (CP) concentration than *P. kalachariensis* harvested from all other host species in the same season. Within each season, *P. kalachariensis* harvested from *V. tortilis* in summer had a higher acid detergent fibre (ADF) and acid detergent lignin (ADL) (399 g/kg DM and 246 g/kg DM, respectively) concentrations than *P. kalachariensis* harvested from all other host species during summer. After 48 hours of incubation, *P. kalachariensis* harvested from *S. nigrescens* and *D. cineria* in summer had a higher (948 g/kg DM and 900 g/kg DM) *in sacco* than *P. kalachariensis* harvested from same host species in winter. Buffer soluble nitrogen ranged from 36.59 to 81.90 % SI in summer and 42.34 to 74.11 % SI in winter. Generally, most macro minerals concentration were higher in most in winter than in summer, while micro minerals were low in winter. Therefore, it was concluded that *Plicosepalus kalachariensis* plant can also be utilized as a supplement for ruminant livestock during dry seasons when the nutritious forages are in short supply.

Keywords: Feed scarcity, CP, Semi-arid, Small ruminants, Mistletoe, ruminal fermentation

The effects of the proportion of forage in the diet on daily weight gain, nutrient digestibility, rumen parameters and greenhouse gases emission of growing goats

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Abstract: The study was conducted to evaluate the effect of the proportion of forage in the diet on feed and nutrient intake, daily weight gain, nutrient digestibility, rumen parameters, and greenhouse gas emissions in growing crossbred Boer goats. The experiment was arranged in a 4×4 double Latin square design with four treatments, each representing different levels of Elephant grass (*Pennisetum purpureum*) in the diet: 20%, 40%, 60%, and 80% (DM basis), corresponding to the treatments EG20, EG40, EG60, and EG80. Eight goats, including 4 males and 4 females, were used in the experiment. Experimental goats were fed a dry matter content of 3.5% of body weight and 5.5 g CP/kg body weight. The CH₄ and CO₂ emissions of experimental goats were measured during the last 2 continuous days of each experimental period using a respiratory chamber with an Infrared Gas Analyzer from Yokogawa Electric Corporation (Model IR200). The experimental results showed that nutrient and metabolizable energy intakes were significantly decreased ($P<0.05$) by increasing elephant grass in the diets, except for fiber items. The nutrient digestibility, nitrogen retention, and daily weight gain were higher ($P<0.05$) in the EG20 diet than in other diets. The pH value, N-NH₃, and VFAs of rumen fluid were not significantly different ($P>0.05$) among treatments. Methane emissions from rumen fermentation decreased, and CH₄ per daily weight gain (L/kg) increased with increasing levels of elephant grass in the diet ($P>0.05$). The results concluded that diets with high forage levels could negatively affect nutrient intake and digestibility, nitrogen retention, and greenhouse gas emissions in growing crossbred Boer goats.

Keywords: Forage, Goat, Nutrient digestibility, Methane emission

Effect of forage feeding frequency on intake, milk production and behaviour in dairy goats

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Objective: In France, dairy goats are predominantly housed indoors for part of the year and are commonly fed forages several times a day, based on the assumption that increasing feeding frequency stimulates intake and improves production, despite increased labour. However, the actual effect of feeding frequency on intake, milk production, and behaviour remains poorly documented. This study aimed to evaluate the impact of forage feeding frequency on performance and ingestive behaviour in lactating dairy goats.

Methods: Five experimental trials were conducted in France (INRAE : PEGASE, FERLus, MoSAR ; et ferme du Pradel - EPLEFPA Olivier de Serres) using Alpine dairy goats in mid-lactation under indoor feeding conditions. Feeding frequency ranged from 1 to 3 distributions per day depending on the trial. Diets included cut-and-carry fresh grass, lucerne hay, barn-dried multispecies hay, and total mixed rations based on maize silage or beet pulp. Forages were offered *ad libitum*, with targeted refusals of 10–15% to ensure sufficient availability. The amount of concentrate supplied ranged from 400 to 800 g per day, depending on the trial. No feed push-up, concentrate delivery, or any other intervention occurred between forage distributions, ensuring that feeding events were the only external stimuli. Between 24 and 96 goats were used per trial, following crossover or Latin square designs over successive periods of 2 weeks. Intake, milk yield and composition, body weight, and feeding behaviour were measured either individually or at group level.

Results: Across all five trials, feeding frequency had no significant effect on dry matter intake, despite *ad libitum* feeding conditions with 10–15% refusals, nor on total daily feeding time or time spent lying. Although each distribution stimulated a short-term increase in feeding activity, this did not affect total daily intake. Milk yield remained unchanged in most trials and increased slightly (+60 g/day) in one trial when increasing feeding frequency from two to three times per day. Milk fat and protein contents were not, or only marginally, affected by feeding frequency. Feeding frequency also modified the daily pattern of feeding behaviour without altering overall feeding duration or efficiency.

Conclusion: Increasing forage feeding frequency does not improve intake or milk production in indoor-housed dairy goats when forages are offered *ad libitum*. While each distribution triggers feeding activity, goats regulate their intake over the day independently of feeding frequency. These results suggest that reducing feeding frequency is possible in French dairy systems without compromising performance, provided that forage availability remains sufficient, offering opportunities to simplify feeding management and reduce labour.

Keywords : Dairy goat, feeding frequency, forage intake, milk production, feeding behaviour

Effect of feeding order of two forages on intake, milk production and behaviour in dairy goats

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Objective: In France, dairy goats are predominantly housed indoors for at least part of the year, and offering two different forages daily is a common practice to optimise forage use and diet balance. However, when these forages are distributed separately (e.g. morning and evening), goats cannot choose simultaneously between them, and the impact of feeding order on intake, milk production, and behaviour remains poorly documented. This study aimed to evaluate the effects of the feeding order of two forages on intake, performance, and feeding behaviour in lactating dairy goats.

Methods: Five experimental trials were conducted in France (INRAE PEGASE) using Alpine dairy goats in mid-lactation under indoor feeding conditions. Each trial compared two feeding sequences, in which the same two forages were distributed either in the morning or in the evening. Forage combinations included cut-and-carry fresh grass and partial mixed ration, lucerne hay and maize silage, grass haylage and lucerne hay, lucerne hays of contrasting quality, and cut-and-carry fresh grass with low-quality grass hay.

In each trial, 24 goats were used in crossover designs with 3 or 4 successive periods of 2 weeks. Forages were offered *ad libitum*, with refusals generally ranging from 10 to 20%. The amount of concentrate supplied ranged from 300 to 600 g per day, depending on the trial. No feed push-up, concentrate delivery, or other intervention occurred between forage distributions, ensuring that feeding events were the only external stimuli. Intake, milk yield and composition, body weight, and feeding behaviour were measured.

Results: Goats expressed variable but sometimes strong preferences between the two forages, leading to large differences in their relative intake (from 50:50 to 90:10 in the diet). A given forage was consistently more consumed when offered in the evening than in the morning (+53% on average), mainly due to longer access time. Feeding order strongly affected the proportion of each forage in the diet, modifying diet composition by up to 10–20 percentage points. In contrast, total dry matter intake was only slightly affected, with a tendency to increase when the preferred forage was offered in the evening. Effects on milk yield and composition were inconsistent across trials and depended on differences in forage preference, nutritive value, and resulting changes in total intake and diet composition. Feeding behaviour was markedly altered, with goats adapting their daily intake pattern and sometimes delaying consumption of a less preferred forage for several hours.

Conclusion: Dairy goats are able to anticipate feeding events and adapt their feeding behaviour according to forage preference when two forages are offered separately during the day. Feeding order mainly affects the proportion of each forage in the diet rather than total intake or milk production.

In practice, feeding order can be used as a management tool when the difference in preference between forages is moderate, allowing farmers to influence diet composition and potentially animal performance when nutritive values differ. In contrast, when one forage is strongly preferred, goats adjust their behaviour to prioritise its consumption, and feeding order has little effect on the final diet.

Keywords : Dairy goat, feeding order, forage intake, feeding behaviour, diet selection

Prediction of the chemical composition of the forage selected by dairy goats

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Objective: In France, dairy goats are predominantly housed indoors for at least part of the year and are fed a wide variety of forages, differing both in botanical composition and conservation methods. Dairy goats are known for their strong ability to sort forages, which can substantially modify the chemical composition of the ingested diet compared to the offered forage. This behaviour, combined with the diversity of forage types and feeding practices, makes it difficult to predict intake quality and to manage refusals. This study aimed to quantify the effects of forage type and refusal level on the chemical composition of ingested forage and to develop predictive equations.

Methods: A database was built from 21 experimental trials conducted at four experimental sites in France (INRAE: PEGASE, FERLus, MoSAR, and the Pradel experimental farm – EPLEFPA Olivier de Serres). The final dataset included 260 paired samples of distributed and refused forages, covering eight forage types. Chemical composition (crude protein, fibre) and dry matter quantities offered and refused were recorded. Regression and covariance models were developed to predict the composition of ingested forage from the composition of offered forage, refusal rate, and forage type.

Results: Forages were classified into three groups according to their sorting potential: low, intermediate, and high (lucerne hay). Refusals were generally poorer in crude protein and richer in fibre than offered forages, confirming selective feeding behaviour. As a result, ingested forage was on average richer in crude protein (+7 g/kg DM) and lower in fibre than offered forage. The magnitude of this effect strongly depended on forage type and refusal level. For lucerne hay, crude protein content of ingested forage increased by +0.8 percentage points for each additional 10% of refusals, compared with +0.5 for intermediate forages and +0.1 for low-sorted forages. Similar patterns were observed for fibre contents, which decreased as refusal level increased. Prediction models based only on offered forage composition were accurate, but including refusal rate and forage type significantly improved prediction accuracy.

Conclusion: The chemical composition of forage ingested by dairy goats differs from that of the offered forage due to selective feeding behaviour. This effect depends strongly on forage type and refusal level. Accounting for these factors improves prediction of intake quality and can support better feeding management in dairy goat systems.

Keywords : Dairy goat, forage sorting, refusal rate, intake quality, prediction.

Effects of diets with different concentrate-to-roughage ratios on the growth rate, serum biochemical indexes, and rumen fermentation of Guangfeng goats

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Abstract: We evaluated the effects of different concentrate-to-roughage ratios on the growth rate, serum biochemical indexes, and rumen fermentation of Guangfeng goats. Thirty-nine healthy Guangfeng goats with similar body weight were randomly divided into three treatment groups (n=13). The concentrate-to-roughage ratios in the three groups were 40 : 60 (I), 45 : 55 (II), and 50 : 50 (III), and the experimental period was 90 days. The results indicate that: 1) Different concentrate-to-roughage ratios in the diets had no significant effects on the body height, chest circumference, cannon circumference, average daily gain, average daily feed intake, and feed conversion ratio of Guangfeng goats ($P>0.05$); however the body length of group III was significantly greater than that of group I ($P<0.05$). 2) The serum total protein, albumin, globulin, and total cholesterol levels in group III were significantly higher than those of the other groups; the tetraiodothyronine content was significantly lower than that in group II, and the triiodothyronine content was significantly lower than that in the other groups ($P<0.05$). The serum urea nitrogen content in group I was significantly lower than that in the other groups ($P<0.05$). 3) The rumen papilla length in group III was significantly higher than that in group I, and the ileal villus length was significantly higher than that in group II ($P<0.05$); the rumen organ index in group I was significantly lower than that in the other groups, and the muscle fiber diameter was significantly higher than that in the other groups ($P<0.05$). In conclusion, different concentrate-to-roughage ratios of diets affect the metabolism of Guangfeng goats and their muscle quality.

Early Supplementary Feeding Improves Hair Follicle Development in Northwest Xizang White Cashmere Goats: An Analysis Based on Skin Multi-Omics

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Abstract: Northwest Xizang White Cashmere goat has a high global reputation for good goat cashmere germplasm characteristics, and its cashmere industry is the economic pillar of the herdsmen in the northwest plateau of Xizang. The purpose of this study was to reveal the effects of early supplementary feeding on the growth performance and secondary hair follicle development of lambs. Thirty single lambs (14 days old; 4.46 ± 0.80 kg BW) were randomly assigned to two groups ($n=15$; 8 rams and 7 ewes): a control group (grazing with ewes) and a supplementary feeding group (grazing + ad libitum concentrate pellets supplemented with rumen-protected methionine and Lactobacillus). The experiment lasted 67 days, including a 7-day pre-test and a 60-day formal test. Results showed that early supplementary feeding significantly increased ($P<0.05$) the secondary hair follicle density, total hair follicle density, and S/P value of lambs. However, there was no ($P>0.05$) significant difference in the average cashmere fineness between the two groups. Integrated skin multi-omics analysis revealed that nutritional intervention modulated the expression of key structural genes (*KRT10*, *KRT18*, *KRT26*, *ITGB2*, *CSF1R*, *AKT1*, *COL6A6*, *COL6A2*, and *COL6A1*) and signaling molecules (RBP4, KAP13-3, KRTAP3-1, KRTAP27-1, DKK3, *ITGB2*, and *DUSP23*) crucial for HF morphogenesis. Furthermore, the identification of differentially expressed metabolites, such as 15-Deoxy-delta12,14-Prostaglandin J2 and TXB2, suggests that early feeding may indirectly drive HF development by modulating prostaglandin signaling pathways. In conclusion, supplementary feeding starting from 2 weeks of age effectively promotes secondary HF development in Northwest Xizang White Cashmere goats. These findings provide a scientific basis for optimizing nutritional management and unlocking the genetic potential of cashmere production in high-altitude pastoral systems.

Keywords: Northwest Xizang White Cashmere goat; secondary hair follicles; early supplementary feeding; multi-omics

Effects of level and type of fiber sources on feed intake, milk production and composition and nutrient utilization in Alpine dairy goats

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Abstract: Thirty Alpine does and 32 doelings, averaging 45 ± 1.5 days-in-milk, were used to assess the effects of level and type of neutral detergent fiber (NDF) sources on dry matter (DM) intake, average daily gain (ADG), digestion, and milk production. The 60C, 50C, 50W20S, and 40W30S diets were 60, 50, 30, and 30% concentrate and 40, 50, 50, and 40% forage, with 20 and 30% soybean hulls in 50W20S and 40W30S, respectively. The diet NDF concentration was 35.7, 39.3, 51.6, and 51.7% and crude protein was 15.8, 15.3, 11.4, and 11.8% for 60C, 50C, 50W20S, and 40W30S, respectively. Average daily gain (ADG) was lower ($P < 0.05$) in high-roughage diets (50W20S, 40W30S) compared with 60C, though differences were modest. Dry matter intake (DMI) was reduced ($P < 0.05$) in 50W20S and 40W30S relative to 60C and 50C. Body condition score in doelings was lowest for 50W20S ($P < 0.05$), while does showed no differences among treatments ($P > 0.05$). Fiber intake and digestibility were higher ($P < 0.05$), whereas crude protein intake and digestibility were lower ($P < 0.05$) in 50W20S and 40W30S compared with 60C and 50C. Milk fat concentration was highest in 40W30S ($P < 0.05$), and total solids were greater in 40W30S than 60C and 50W20S ($P < 0.05$), while 50C was higher than 50W20S but not different from 60C ($P < 0.05$). Milk urea nitrogen was highest in 50C, intermediate in 60C, and lowest in 50W20S and 40W30S ($P < 0.05$). Ruminal ammonia-N was lowest in 40W30S ($P < 0.05$). Although acetate:propionate ratio was unchanged ($P > 0.05$), acetate increased and ranked $60C < 50C < 50W20S = 40W30S$ ($P < 0.05$). Propionate was highest in 60C, lower in 50C and 40W30S, and intermediate in 50W20S ($P < 0.05$), while butyrate was higher in 60C and 50C than in soybean hull diets ($P < 0.05$). Blood metabolites showed diet effects: total protein was highest in 50W20S ($P < 0.05$), albumin was higher in 50C than in 50W20S and 40W30S ($P < 0.05$), and blood urea nitrogen followed a similar pattern. Cholesterol was higher in 60C and 50C than in 50W20S ($P < 0.05$), and triglycerides were higher in 50C than in soybean hull diets ($P < 0.05$). Thyroxine was lowest in 60C ($P < 0.05$) compared with other diets. Overall, despite variations in intake, digestion, rumen fermentation, and blood metabolites, Alpine goats appear to be well adapted to these diets differing in fiber level and source, maintaining acceptable productivity during mid- to late lactation.

Keywords: Dairy goats, diet composition, fiber adaptation

Influence of *Asparagopsis taxiformis* on Methane Emissions and Rumen Antimicrobial Resistance Gene Profiles in Goats

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Abstract: Dietary supplementation with red algae (*Asparagopsis taxiformis*) has emerged as a promising strategy for mitigating enteric methane emissions and modulating rumen microbial ecology in ruminants. Nonetheless, its impact on antimicrobial resistance (AMR) within the rumen microbiome remains poorly characterized. Accordingly, this study investigated the effects of red algae supplementation on methane production and antimicrobial resistance gene (ARG) abundances in the rumen of mature Spanish goats. Four treatments were evaluated: two forage types (alfalfa hay or Bermuda grass hay) with or without red algae supplementation at 4 g/kg dry matter intake (DMI), with eight goats per treatment. Ruminal fluid was collected after 21 days of feeding, and metagenomic DNA was extracted for Illumina shotgun sequencing (150 bp; ~60 million reads per sample). Sequence reads were analyzed using the Resistance Gene Identifier in BWT mode against the Comprehensive Antibiotic Resistance Database. Red algae supplementation decreased methane production by 58% (33.3 versus 14.1 ppm/kg DMI, respectively) measured using laser methane detector and 75% measured using respiration calorimeter (41.9 versus 10.4 g/kg DMI). Average ARG abundance was $0.31 \pm 0.02\%$ of total reads (range: 0.27–0.36%), with 138 ± 15.3 (mean $\pm$ standard deviation) ARGs identified per sample and 58 core ARGs shared across samples. The most abundant ARGs included *tet(Q)* and *tet(W)*, along with 16S rRNA mutations associated with resistance in *Mycobacteroides abscessus* (gentamicin), *Mycolicibacterium smegmatis* (neomycin), and *Salmonella enterica* (spectinomycin), and 23S rRNA mutations in *Clostridioides difficile* (erythromycin and clindamycin), *Escherichia coli* (clindamycin), *Streptococcus pneumoniae* (macrolides), and *Chlamydia trachomatis* (macrolides). Overall, ARGs were most frequently associated with resistance to tetracycline, macrolide, lincosamide, and aminoglycoside antibiotics. Pairwise PERMANOVA indicated that ARG profiles differed among treatment groups ($P < 0.05$). Bermuda grass hay feeding increased ($P < 0.10$) resistance to aminoglycoside, rifamycin, streptogramin–streptogramin A–pleuromutilin, peptide, and phenicol classes compared with alfalfa hay. In alfalfa hay diet, red algae supplementation decreased ($P < 0.10$) the abundance of seven ARGs, including *tet(44)*, *Mycobacterium tuberculosis* 16S rRNA mutation (amikacin resistance), and *Staphylococcus aureus rpoC* (kirromycin resistance). However, it increased ($P < 0.10$) ARGs such as *Escherichia coli* 16S rRNA (spectinomycin) and 23S rRNA (clindamycin) mutations and *lsaB* and by drug class, increased ($P < 0.10$) AMR associated with peptide, streptogramin–streptogramin A–pleuromutilin, and cephalosporin–penicillin β -lactam classes. For Bermuda grass hay, red algae affected ($P < 0.10$) 46 ARGs, including reductions in 23 ARGs, and by drug class decreased ($P < 0.10$) resistance to phenicol, tetracycline, pactamycin-like antibiotics, and macrolides–streptogramins, while increasing AMR to peptide, aminocoumarin, and cycloserine-like antibiotics. In conclusion, red algae effectively mitigates methane production. Bermudagrass hay may increase resistance to several antibiotic classes compared with alfalfa hay, whereas red algae supplementation may reduce resistance to some antibiotic classes in the goat rumen microbiome.

Keywords: antimicrobial resistance gene, forage type, goat, red algae, methane, ruminal fluid

MicroRNA profiles in colostrum and transition milk of non-dairy goats fed with or without resveratrol

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Objective: MicroRNAs are non-coding RNAs that regulate gene expression at the post-transcriptional level. To aid research on support the study of microRNAs in goat milk, we provide a dataset describing the microRNA profiles of small extracellular vesicles from colostrum and transition milk of dairy goats fed either a standard diet or a diet supplemented with resveratrol (RSV).

Methods: Eighty multiparous Beichuan goats (first parity, 10 mo of age, and average 35 kg of body weight) were divided into two groups: The control group was fed a standard total mixture (TMR, n = 40), and the treatment group was fed a standard TMR supplemented with 2 g RSV per goat per day (n = 40). Colostrum and transition milk samples were only collected from goats with twin kids, at least one of which was male. Under these criteria, a total of 30 samples were collected, including 7 colostrum (C0) and 6 transition milk samples (C7) from the control group and 9 colostrum (T0) and 8 transition milk samples (T7) from the treatment group. Colostrum and transition milk were collected within 30 min and 7 d after birth, respectively. The sEVs of milk samples were isolated and subjected to microRNA sequencing.

Results: A total of 406 known microRNAs were identified, mainly let-7c-5p (10.48% ± 0.54%), followed by let-7a-5p (9.18% ± 0.47%) and let-7f-5p (8.19% ± 0.43%) (Figure 1). The milk samples were clustered into two groups (0 d and 7 d) regardless of RSV supplementation (Figure 2).

Conclusion: Our study enables comparative studies of microRNA composition in goat colostrum and transition milk, facilitates research into the effects of diet on milk microRNAs, and supports studies on the transmission and function of microRNAs in neonatal development.

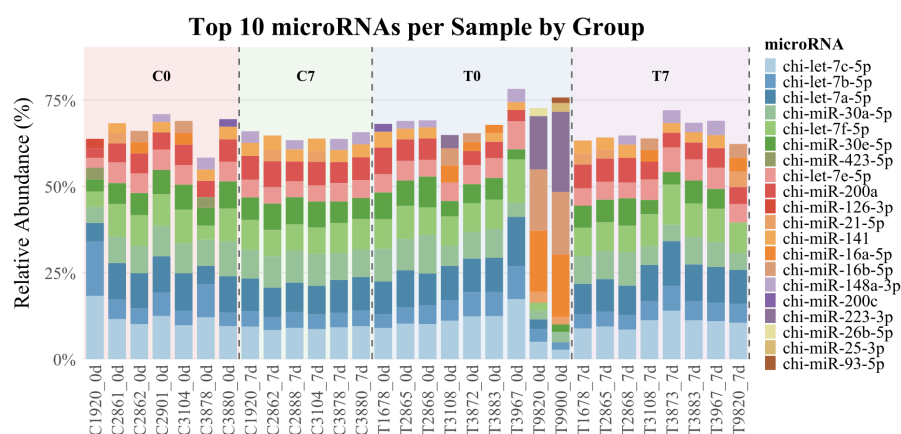


Figure 1. The relative abundance of top 10 microRNAs in the small extracellular vesicle of each milk sample collected from non-dairy goats supplemented with or without resveratrol. C0, colostrum sample collected from non-dairy goats supplemented without resveratrol

Keywords: Colostrum, Transition milk, Resveratrol, MicroRNA, Goat

Integrated multi-omics reveals *Enterococcus faecalis* JM263 alleviates high-concentrate diet-induced hepatic injury via the gut-liver axis in goats

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Objective: High-concentrate diets (HCD) are widely used in intensive goat production to improve short-term growth, but they can impair intestinal barrier integrity and induce systemic inflammation, oxidative stress, and hepatic injury. This study evaluated whether dietary supplementation with *E. faecalis* JM263 could alleviate HCD-induced gut-liver dysfunction in goats and explored the underlying mechanisms using integrated microbiome, metabolome, and proteome analyses.

Methods: Twenty-four healthy 4-month-old male Yudong black goats were randomly assigned to four groups (n = 6 per group): a control HCD group without *E. faecalis* JM263 supplementation (CON) and three HCD groups supplemented with 0.1, 0.5, or 1.0 g/kg *E. faecalis* JM263 (HCD1, HCD2, and HCD3, respectively) for 60 d. Growth performance, serum antioxidant and immune indices, jejunal morphology and barrier function, hepatic inflammation, apoptosis, and oxidative stress were assessed. Jejunal 16S rRNA sequencing and liver metabolomic/proteomic analyses were conducted in the CON and HCD2 groups. A schematic summary of the proposed mechanism is shown in **Figure 1**.

Results: *E. faecalis* JM263 improved average daily gain, antioxidant capacity, and immune status in HCD-fed goats, with the 0.5 g/kg dose showing the most favorable overall effects. Supplementation enhanced jejunal villus morphology, increased goblet cell abundance and glycoprotein distribution, reduced epithelial apoptosis, and upregulated tight junction markers, indicating improved intestinal barrier integrity. Serum and hepatic lipopolysaccharide levels were reduced, accompanied by lower hepatic inflammatory and apoptotic responses. *E. faecalis* JM263 also enhanced hepatic antioxidant defense through coordinated changes in *Nrf2/Keap1* signaling and downstream antioxidant targets. Multi-omics analyses showed enrichment of *Muribaculaceae* and *Acetatifactor* and significant remodeling of hepatic proteomic and metabolomic profiles, particularly in the arachidonic acid metabolism pathway.

Conclusion: *E. faecalis* JM263 is a promising probiotic candidate for alleviating HCD-induced intestinal and hepatic injury in goats through coordinated modulation of the gut-liver axis.

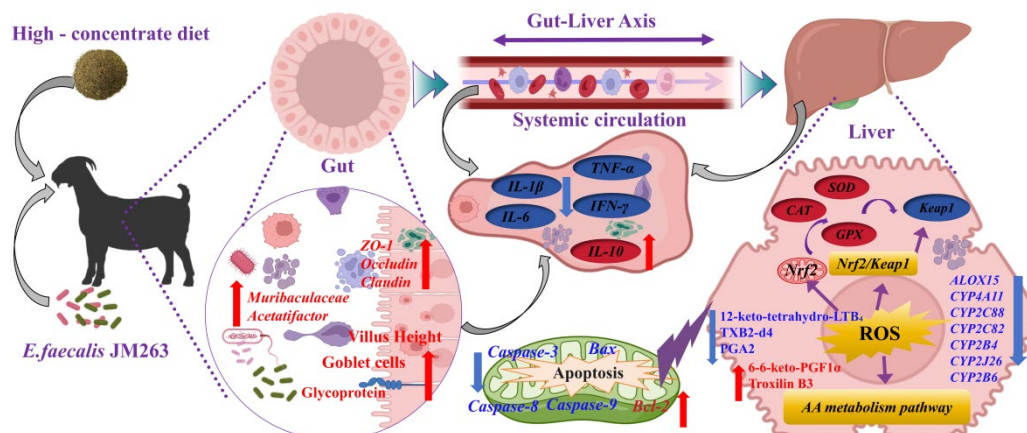


Figure 1. Proposed mechanism by which *E. faecalis* JM263 alleviates HCD-induced systemic inflammation and hepatic oxidative stress via the gut-liver axis.

Keywords: *Enterococcus faecalis* JM263; goat; gut-liver axis; high-concentrate diet; *Nrf2/Keap1*; arachidonic acid metabolism

Effect of Feeding Level on Growth and Slaughter Performance, and Allometric Growth of Tissues and Organs in Female Growing Saanen Dairy Goats

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Abstract: This study aimed to investigate the effect of feeding level on the growth and slaughter performance, and allometric growth of tissues and organs in female growing dairy goats. The trial included 10–20 and 20–30 kg weight stages with 48 female goat kids. The 24 goat kids in each stage were divided into 8 blocks based on weight, with 3 kids per block. Then, three kids from each block were randomly assigned to one of the three treatments, namely ad libitum (AL100), 70% of ad libitum (AL70), or 40% of ad libitum (AL40). The slaughter trial was conducted when the AL100 kids reached the target weight of 20 or 30 kg. The results showed that the ADG and feed conversion rate showed a linear decline as the feed level decreased ($p < 0.05$). Compared with the AL70 and AL100 groups, the AL40 group exhibited lower shrunk body weight, empty body weight, hot carcass weight, net meat rate, carcass meat rate, and visceral fat weight ($p < 0.05$) in both stages. Moreover, the AL40 group showed lower weights for skin and mohair, blood, rumen, small intestine, large intestine, mammary gland, and uterus than the AL70 and AL100 groups ($p < 0.05$) in both stages. However, feeding level did not affect organ indices in the two stages ($p > 0.05$). The bone, skin and mohair were isometric ($b \approx 1$), but the muscle, visceral fat, and most internal organs were positive ($b > 1$) in both stages. In conclusion, feeding level affects the growth and development of dairy goats, which vary depending on the body weight stage and specific tissues and organs.

Keywords: Saanen dairy goats; growth performance; slaughter performance; organ index; allometric growth

Analysis of Energy and Protein Requirements of Growing Saanen Dairy Goats

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Abstract: The aim of this study was to estimate the energy and protein requirements for maintenance and growth of Saanen dairy goats from 10 to 40 kg by means of data models. To determine the model parameters, the literature was collected by means of database retrieval. According to the exclusion criteria of literature, nine literatures including the data of 419 Saanen dairy goats were included for Meta-analysis. The following quantitative data extracted from the literature were included: body weight (BW), empty body weight (EBW), average daily gain (ADG), empty body gain (EBG), heat production (HP), Metabolizable energy intake (MEI), retained energy (RE), Metabolic protein (Metabolizable protein intake, MPI) and body protein content (BPC). The regression equations established were as follows: for Net Energy for maintenance (NE_m): $\text{LogHP}(\text{MJ/kg EBW}^{0.75} \text{ d}^{-1}) = -0.53408(\pm 0.02501) + 0.42445(\pm 0.02040) \times \text{MEI}(\text{MJ/kg EBW}^{0.75})$; for Net Energy for gain (NE_g): $NE_g(\text{MJ/kg EBW}^{0.75} \text{ d}^{-1}) = 1.29471 \times 10^{0.64454} \times \text{EBW}^{0.29471}(\text{kg})$; for Metabolizable Protein for maintenance (NP_m): $RN(\text{g/kg EBW}^{0.75}) = -0.45621(\pm 0.51435) + 3.03590(\pm 0.63835) \times NI(\text{g/kg EBW}^{0.75})$; for Net Protein for gain (NP_g): $NP_g(\text{g/d}) = 0.94717 \times 10^{2.3188} \times \text{EBW}^{-0.0583}(\text{kg})$. The NE_m requirement was 0.29 MJ/kg $\text{EBW}^{0.75}$, and the Metabolizable energy for maintenance requirement was 0.4830 MJ/kg $\text{EBW}^{0.75}$. The NP_m requirement was 2.85 g/kg $\text{EBW}^{0.75}$, and the Metabolizable protein for maintenance requirement was 3.3147 g/kg $\text{EBW}^{0.75}$. The NE_g requirement ranged from 0.74 to 3.41 MJ/d, the Metabolizable energy for gain requirement ranged from 4.94 to 19.17 MJ/d, the NP_g requirement ranged from 12.00 to 34.33 g/d, and the Metabolizable protein for gain requirement ranged from 17.14 to 49.04 g/d for goats with BW ranging from 10 to 40 kg and ADG ranging from 100 to 250 g/d respectively. In conclusion, the results obtained by Meta-analysis in this paper support the hypothesis that energy and protein requirements of Saanen dairy goats are within a reasonable range and different from those of local breeds, and recommended parameters such as NRC. Therefore, the energy and protein requirements of Saanen dairy goats derived in this paper differed slightly from the NRC recommended values, and the requirement formula and parameters derived from this study can be used as a reference.

Key words: Meta-analysis; Saanen dairy goats; Energy; Protein; Nutrient requirements

Bacillus pumilus 315 improves intestinal microbiota and barrier function to alleviate diarrhea of neonatal goats

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Abstract: Diarrhea is the leading cause of mortality in postnatal goat kids, seriously impacting breeding efficiency. This study aimed to explore the effects of *Bacillus pumilus* 315 (*B. pumilus*) on goat kids' diarrhea and its regulatory mechanism. Thirty-six 1-day-old goat kids were assigned into four treatments, the control (CON) group and low-, medium- and high-dose groups supplemented with *B. pumilus* at 1×10^8 (BP1), 5×10^8 (BP5), and 1×10^9 CFU/d (BP10). Each group consisted of 9 replicates with 1 goat kid per replicate. The results showed that the incidence of diarrhea and fecal scores decreased significantly ($P < 0.05$). A dose of 5×10^8 CFU/d *B. pumilus* reduced pro-inflammatory factors (including tumor necrosis factor- α [TNF- α], interleukin-1 β [IL-1 β], interleukin-6 [IL-6], $P < 0.05$), increased the expression levels of anti-inflammatory factors (including transforming growth factor- β [TGF- β], peroxisome proliferate-activated receptor- γ [PPAR- γ], interleukin-10 [IL-10], $P < 0.05$), immune indicators (including immunoglobulin G [IgG], immunoglobulin A [IgA], immunoglobulin M [IgM], secretory immunoglobulin A [sIgA], $P < 0.05$) and antioxidant indicators (including total antioxidative capacity [T-AOC], superoxide dismutase [SOD], glutathione peroxidase [GSH-Px], catalase [CAT], $P < 0.05$) in both jejunum and colon, and ultimately improved the barrier function of the jejunum and colon mucosa. The enhanced gut immunity and barrier function were associated with increased abundance of *Enterococcus* and *Lactobacillus* ($P < 0.05$) and decreased abundance of *Campylobacter* and *Escherichia-Shigella* ($P < 0.05$). In conclusion, dietary addition of *B. pumilus* may improve gut health by modulating the composition and function of the flora, ultimately alleviating diarrhea in goat kids.

Key words: *Bacillus pumilus*; Goat kid; Diarrhea; Immunity; Microbiota

Effects of Rumen-Protected Methionine on cashmere fibre fineness and Hair Follicle Development in Yanshan Cashmere Goats

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Objective: Dietary supplementation with methionine has been shown to promote hair follicle development and improve cashmere fibre fineness. Hair follicle development occurs mainly before birth but continues after birth, with weaned lambs at a critical stage of this continuous process. However, the molecular mechanisms by which methionine regulates hair follicle development and affects cashmere fibre fineness and density remain unclear. This study aims to identify key genes involved in methionine-regulated hair follicle development and to elucidate the molecular mechanisms underlying its effects on cashmere fibre fineness and density.

Methods: Sixty healthy, 2-month-old weaned lambs were randomly assigned to two groups. The control group was fed a basal diet, while the treatment group received the same diet supplemented with 0.5% rumen-protected methionine. Each group had 30 replicates of one lamb each, and the experiment lasted 60 days. Cashmere, skin tissue, and blood samples were collected from each lamb before and after the experiment. cashmere fibre fineness was measured using a fiber analyzer, and hair follicle morphology was observed via hematoxylin and eosin staining. Blood amino acid levels and related metabolic indicators were quantified. Transcriptome sequencing combined with bioinformatics analysis was performed to identify differentially expressed genes, and the results were validated by real-time quantitative PCR.

Results: After 60 days, the treatment group showed significantly greater increases in hair follicle density, diameter, and S/P ratio than the control group ($P < 0.05$). The treatment group significantly attenuated the increase in cashmere fibre fineness ($P < 0.05$) and reduced epidermal thickness compared with the control group ($P < 0.05$). Blood methionine levels were elevated in the treatment group, while glutamic acid, isoleucine, and asparagine were reduced ($P < 0.05$). Transcriptome analysis identified 2,242 differentially expressed genes, among which ARHGAP5 and AFDN were highlighted as key potential regulators of hair follicle development and cashmere traits.

Conclusion: Rumen-protected methionine improves cashmere fibre fineness and promotes hair follicle development in Yanshan cashmere goats, suggesting that ARHGAP5 and AFDN may be involved in the regulatory mechanism.

Keywords: Rumen-protected methionine, Cashmere goat, Hair follicle development, ARHGAP5, AFDN

Goat gut microbiome as a reservoir for microorganism-encoded short peptides: regulation by host development age and nematode challenge

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Abstract: Short peptides are a promising class of antimicrobial agents with efficacy against multidrug-resistant pathogens. While host-derived defence peptides from animals and plants have been widely characterized, the landscape of microbial-encoded short peptides, particularly those with antimicrobial activity that can mitigate antibiotic resistance, remains underexplored. In this study, we identified 1147 novel microorganism-encoded short peptides (MSPs) from the goat gut microbiome, most of which lack homology to existing database entries. The microbial communities producing these MSPs were altered by the developmental stage of the goat, whereas the overall composition and diversity of these populations remained unchanged during nematode infection, despite significant correlations between certain MSPs and type 2 immunity. Notably, two MSPs demonstrated potent antimicrobial activity with lower cytotoxicity, exhibiting remarkable efficacy against methicillin-resistant *Staphylococcus aureus* and *Streptococcus agalactiae*. Collectively, our findings establish the goat gastrointestinal tract microbiome as a distinctive and promising reservoir for the discovery of antimicrobial and immunoregulatory peptides.

Keywords: Microorganism-encoded short peptide, Abomasum microbiota, Nematode infection, Dietary transition, Antimicrobial activity

Effects of dietary lignin polyphenol on growth performance, serum biochemical indices and intestinal microbiota in weaned Huanghuai goats

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Objective: Weaning stress compromises intestinal integrity and elevates diarrhea incidence in goats. This study evaluated the effects of dietary lignin polyphenol (LP) supplementation on growth performance, serum biochemistry, and rectal microbiota composition in weaned Huanghuai goats.

Methods: Twelve 0-day-old Huanghuai goats were randomly assigned to control group (CON) and LP group (6 per group). The LP group received daily oral administration of LP at 5 g/kg body weight for a 30-day trial period. All goats were weaned simultaneously on day 29, and sampling was conducted 24 h post-weaning. Serum antioxidant and immune parameters were measured using biochemical analyzer and ELISA kits. Rectal microbiota was analyzed by 16S rRNA gene sequencing. Data were analyzed by one-way ANOVA using SPSS 26.0.

Results: LP supplementation significantly reduced diarrhea incidence compared with CON group ($P < 0.01$). Serum glutathione peroxidase (GPx) activity was significantly elevated in LP group ($P < 0.05$), while malondialdehyde (MDA) levels tended to decrease and immunoglobulin A (IgA) concentrations tended to increase ($0.05 \leq P < 0.10$, **Figure 1A**). Alpha-diversity analysis revealed that ACE and Chao1 indices were significantly higher in LP group ($P < 0.05$), with Shannon index showing an increasing trend. LP significantly enriched the relative abundances of short-chain fatty acid (SCFA)-producing genera, including *Oscillibacter*, *Lachnospiraceae_UCG-010*, and *Anaerobutyricum* ($P < 0.05$, **Figure 1B**).

Conclusion: Supplementation with lignin polyphenols effectively mitigates weaning stress in Huanghuai goats by enhancing antioxidant status, suppressing inflammatory responses, and modulating cecal microbiota structure. These findings suggest LP as a potential functional feed additive for improving goat health and production performance during the critical weaning transition.

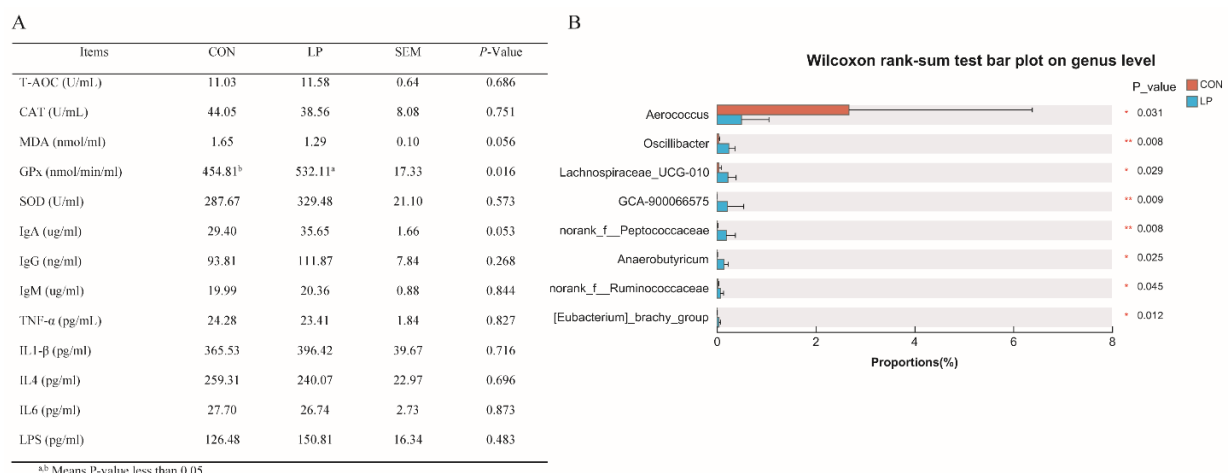


Figure 1. Effects of lignin polyphenols on goats. (A) Effects on serum immune and antioxidant status. (B) Differentially abundant bacterial genera at the genus level in the rectal contents

Keywords: Lignin polyphenol, Weaning stress, Huanghuai goats, Rectal microbiota, Antioxidant capacity

Dynamic miRNA Profiles in Hulunbuir Sheep Muscle and Their Associations with Growth and Metabolic Traits

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Objective: This study aimed to investigate the dynamic expression profiles of miRNAs in the longissimus dorsi muscle of Hulunbuir sheep at different growth stages and to analyze their associations with body weight and metabolic indicators.

Method: Twenty-Four healthy 90-day-old male Hulunbuir sheep with similar body weight (18.70 ± 1.30 kg) were randomly divided into four stages ($n = 6$ per stage). Samples of longissimus dorsi muscle were collected at 90 days (3 months, M3), 150 days (5 months, M5), 180 days (6 months, M6), and 240 days (8 months, M8). RNA extraction and sequencing were performed, followed by differential miRNA expression analysis, target gene prediction, KEGG pathway enrichment analysis, and weighted gene co-expression network analysis (WGCNA).

Results: The result showed as follows: 1) a total of 1,589 miRNAs were identified, among which 792 were differentially expressed across stages, including 39 commonly differentially expressed miRNAs across all growth stages. Compared with the M3 stage, the numbers of differentially expressed miRNAs in M5, M6, and M8 stages were 121, 169, and 179, respectively. Among them, 82, 95, and 100 miRNAs were significantly upregulated, while 39, 74, and 79 were significantly downregulated, respectively. 2) Compared with the M3 stage, the target genes of differentially expressed miRNAs in the M5, M6, and M8 stages were mainly enriched in pathways such as regulation of actin cytoskeleton. Compared with the M5 stage, the differentially expressed miRNAs in the M6 and M8 stages were mainly enriched in pathways such as the MAPK signaling pathway. Compared with the M6 stage, the differentially expressed miRNAs in the M8 stage were mainly enriched in pathways such as beta-alanine metabolism. 3) WGCNA identified five miRNA co-expression modules. The Blue module was significantly negatively correlated with body weight (BW) ($R = -0.43$, $P = 0.04$). The Turquoise module was significantly positively correlated with glycine (Gly) levels in peripheral blood ($R = 0.69$, $P = 0.0002$) and significantly negatively correlated with BW ($R = -0.75$, $P = 0.0003$). The Yellow module showed significant negative correlations with BW ($R = -0.58$, $P = 0.003$) and growth hormone (GH) levels in peripheral blood ($R = -0.57$, $P = 0.003$).

Conclusion: miRNA expression in muscle tissue of Hulunbuir sheep varies across different growth stages. These miRNAs may jointly regulate body weight gain and metabolic indicators by modulating pathways related to muscle development, nutrient utilization, and hormonal effects, thereby participating in the molecular regulation of growth and development in Hulunbuir sheep.

Key words: Hulunbuir sheep; longissimus dorsi; miRNA; regulation of actin cytoskeleton; weighted gene co-expression network analysis (WGCNA)

Effects of Different Melatonin Supplementation Regimens on Cashmere Production Performance in Cashmere Goat Kids (*Capra hircus*)

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Objective: Melatonin is an important photoperiodic signal involved in hair follicle activity and cashmere growth. Previous studies have shown that melatonin feeding or subcutaneous implantation can promote hair follicle development and improve cashmere quality in cashmere goat kids. However, the effects of combined melatonin feeding and implantation on cashmere production performance remain unclear. This study aimed to evaluate the effects of melatonin feeding, subcutaneous implantation, and their combination on cashmere production performance, secondary hair follicle development, and antioxidant capacity in Albas White cashmere goat kids.

Methods: Sixty healthy newborn female Albas White cashmere goat kids with similar body weight were randomly assigned to four groups: control group, melatonin feeding group, melatonin implantation group, and combined implantation plus feeding group, with 15 animals per group. The melatonin feeding group received melatonin at 3 mg/kg body weight daily from birth to 4 months of age. The implantation group received subcutaneous melatonin implants at 2 mg/kg body weight at birth and again at 2 months of age. The combined group received both melatonin feeding and implantation. At 4 months of age, skin samples were collected to assess hair follicle development, and blood samples were collected to measure antioxidant indices. Body weight was recorded at 9 and 12 months of age, and cashmere samples were collected at 9 and 12 months of age to determine cashmere fiber traits.

Results: No significant differences in body weight were observed among groups at 9 or 12 months of age. All melatonin treatments significantly improved later-stage cashmere production traits. At 9 months, compared with the control group, fiber diameter decreased by 1.24, 1.87, and 1.95 μm , fiber length increased by 1.09, 1.98, and 2.47 cm, and fiber density increased by 377, 1175, and 1499 fibers/cm² in the feeding, implantation, and combined groups, respectively ($P < 0.001$). At 12 months, implantation and combined treatments decreased fiber diameter by 1.75 and 1.88 μm and increased fiber length by 1.67 and 1.70 cm, respectively. Melatonin treatments promoted secondary hair follicle development, with implantation and combined treatments showing stronger effects. Melatonin supplementation enhanced antioxidant capacity, and the improvement was greater in the implantation and combined groups.

Conclusion: Different melatonin supplementation regimens improved cashmere production performance and antioxidant status of cashmere goat kids to varying degrees. Melatonin may improve cashmere quality by enhancing antioxidant capacity and promoting secondary hair follicle development. Among the three regimens, implantation and combined treatments were more effective than feeding alone, and the combined treatment showed the greatest overall effect.

Keywords: Melatonin; Cashmere goat; Secondary hair follicle; Cashmere quality; Antioxidant capacity

The Effects of Yucca Extract on Serum Immunological Parameters, Rumen Microbial Flora and Metabolism in Fattening Sheep

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Abstract: Yucca extract is derived from *Yucca schidigera*, a plant belonging to the *Yucca* genus of the Agavaceae family. It primarily contains active components such as yucca saponins, polyphenols and polysaccharides, and possesses various physiological functions including immune modulation, antibacterial and anti-inflammatory effects, and improvement of the ruminal microenvironment. Therefore, we investigated the effects of adding different doses of yucca extract to the diet on serum immunity, ruminal microbiota and metabolism in fattening sheep. A total of 32 healthy male Boer goats of similar body condition were selected and randomly divided into four groups of eight goats each. The control group (Group A) was fed a basal diet, whilst the experimental groups (Groups B, C and D) were fed basal diets supplemented with 200, 400 and 600 mg/kg of yucca extract, respectively. The pre-trial period lasted 7 days and the main trial period 35 days. The results showed that serum IgM levels in Group C were significantly higher than those in Groups A and B, with no significant difference compared to Group D; serum TNF- α levels in Group C were significantly lower than those in Group A, with no significant difference compared to Groups B and D. Notably, the ACE and Chao1 indices in Group C were significantly higher than those in Group D. Furthermore, a comparison of significant differences in bacterial abundance across different taxonomic levels revealed that the class *Negativospira* within the phylum *Firmicutes* played a significant role in Group C; Furthermore, analysis of differential metabolic pathways between the experimental groups and the control group revealed that the differential metabolites in Groups A and C were primarily enriched in metabolic pathways such as lysine degradation, the TGF- β signalling pathway, and gap junctions. These results indicate that the addition of 400 mg/kg of yucca extract was most effective in enhancing the diversity of the gut microbiota in fattening sheep, boosting humoral immunity and alleviating systemic inflammation.

Keywords: Yucca extract, fattening sheep, rumen microbiota, serum immune parameters

Mechanisms of melatonin in promoting intramuscular fat deposition and optimizing fatty acid profiles in fattened cashmere goats

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Abstract: Lamb is favored by consumers for its high protein, low fat, and rich functional fatty acid composition. Improving meat quality, particularly tenderness, flavor, and nutritional value, has always been a core focus of animal science research. The role of melatonin in regulating energy metabolism and adipogenic differentiation is gaining increasing attention, but its regulatory effect on fat deposition patterns and meat quality in ruminants remains unclear. To investigate the regulatory effects of melatonin on meat quality and fatty acid composition in fattened Liaoning cashmere goats, thirty newborn male kids were randomly assigned to control and melatonin-treated groups. The treated group received melatonin implants (2 mg/kg BW) at 0–3, 60, and 120 days of age. After weaning, they were fattened until approximately 50 kg (average body weight 49.16 ± 1.36 kg) and slaughtered. Longissimus dorsi muscle samples were collected for analysis. The results showed that melatonin did not alter overall body weight throughout the trial. Secondly, melatonin significantly remodeled the fat deposition pattern, increasing backfat thickness while decreasing perirenal fat, with no significant changes in omental and mesenteric fat. Histomorphology revealed decreased subcutaneous adipocyte diameter but increased intramuscular fat deposition area. Regarding meat quality, melatonin significantly improved the tenderness and water-holding capacity of the longissimus dorsi muscle, with significantly reduced shear force and cooking loss, and significantly increased crude fat and triglyceride content. Crucially, melatonin profoundly optimized the muscle fatty acid profile, increasing oleic acid content by 69.6%, providing abundant precursors for flavor compound formation; nearly doubling conjugated linoleic acid (CLA-c9t11), conferring higher health benefits to the meat; and significantly reducing the n-6/n-3 PUFA ratio, bringing the fatty acid composition closer to an ideal ratio. Mechanistic analysis indicated that melatonin enhanced the body's antioxidant capacity, synergistically upregulated key lipogenic enzymes (ACC, FAS) and lipolytic enzymes (HSL), and simultaneously activated anabolic hormones such as growth hormone (GH) and insulin (INS), establishing a systemic physiological environment conducive to the specific enrichment of intramuscular fat. In conclusion, early melatonin intervention, by systemically remodeling the energy metabolism network and fat deposition pattern, optimizes carcass fat distribution while significantly improving meat quality and nutritional value, offering a new theoretical basis and technical strategy for improving ruminant meat quality.

Keywords: Melatonin, Liaoning cashmere goat, meat quality, fat deposition, fatty acid composition, antioxidant

Effect of *Vitex negundo* cell powder byproduct on high-concentrate diet-induced oxidative stress in lactating dairy goats

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Abstract: High-concentration feed often leads to subacute rumen acidosis (SARA) and systemic oxidative stress in lactating dairy goats, thereby impairing their health and production performance. *Vitex negundo* L. is rich in bioactive components such as flavonoids and lignans, which exhibit various biological activities including anti-inflammatory and antioxidant properties. But the commercial extracts from the plant are expensive and unstable. Therefore, to achieve low-cost *Vitex negundo* L with stable bioactive components as a feed additive, we selected the by-products from supercritical extraction of in vitro cultured cells to verify their effects on oxidative stress and rumen health in lactating dairy goats under high-concentrate feeding. Thirty-three lactating dairy goats (22±9.5 days) were selected and divided them into three groups: a low-concentration diet group (concentrate:forage = 4:6), a high-concentration diet group (concentrate:forage = 6:4) and a high-concentration diet supplemented with 0.3% *Vitex* cell by-products. Evaluate the effects of *Vitex* cell by-products on the production performance, antioxidant status, rumen fermentation, rumen microbiome, and metabolome of lactating dairy goats after 42 days of feeding. The results showed that high-concentration feed significantly reduced rumen pH and dry matter intake, while increasing rumen lipopolysaccharide and butyrate content. *Quinella*, *UBA1711* and other bacterial genera that produce LPS are significantly enriched, shifting their functional pathways towards stress response. After adding *Vitex* by-products, the rumen pH partially recovered, the LPS level in the rumen returned to normal, and the oxidative damage markers also decreased. At the same time, beneficial rumen microbiota such as *Anaeroplasm* and *Fretibacterium* were enriched, restoring antioxidant related pathways. Metabolomics shows that high-concentration diet upregulates inflammation related metabolites such as 5-hydroxyindole-3-acetic acid and downregulates antioxidant metabolites such as arachidonic acid. *Vitex* increased the antioxidant metabolite ferulic acid and restored the amino acid metabolism pathway. In summary, adding 0.3% *Vitex* cell powder by-products can alleviate oxidative stress and rumen microbiota imbalance induced by high-concentration feed in lactating dairy goats by regulating the rumen microbiota and metabolic homeostasis. It is a promising low-cost plant-derived feed additive that can be used to relieve oxidative stress related to SARA in ruminants.

Keywords: *Vitex negundo* L.; Oxidative stress; High-concentrate diet; Dairy goat; Rumen microbiota; Metabolomics

Rumen microbiome differences between goat breeds impact feed efficiency

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Objective: Improving feed efficiency is essential for enhancing the productivity and economic viability of the goat industry. While the rumen microbiota is known to mediate nutrient degradation and energy harvesting, the specific mechanisms by which breed-dependent microbial populations influence the feed efficiency have yet to be fully elucidated. Therefore, this study applied an integrated approach to characterize key rumen microorganisms and their complex interactions with host metabolism in the regulation of feed efficiency.

Methods: Three-month-old Guizhou white goats and Guizhou black goats were used as experimental animals and reared under identical feeding conditions for a 90-day experimental period. Average daily feed intake, average daily gain, and feed efficiency were determined. Following the feeding trial, rumen contents and serum were sampled and processed for integrated multi-omics profiling, encompassing rumen metagenomics alongside both rumen and serum metabolomics.

Results: Guizhou white goats exhibited significantly greater feed efficiency than Guizhou black goats ($P < 0.05$) and were thus designated as the high feed efficiency (HFE) group, while Guizhou black goats were designated as the low feed efficiency (LFE) group. The HFE group showed significantly elevated concentrations of total volatile fatty acids (TVFA), acetate, and butyrate in the rumen ($P < 0.05$). *Sodaliophilus* sp900316835, *UBA1213* sp900321195, *Prevotella* sp002449845, and *Minthosoma* sp900318775 were significantly enriched in the rumen of goats in the HFE group ($\text{LDA} > 3$, $P < 0.05$). These microorganisms were positively associated with increased acetate and propionate production in the rumen, which may contribute to improved feed efficiency in goats ($P < 0.05$). These microbial taxa were positively associated with a range of metabolites involved in lipid and energy metabolism, including isobutyrylcarnitine (C4) and 1-stearoyl-sn-glycero-3-phosphate. This suggests that these microbes may contribute to enhanced energy availability by facilitating lipid turnover and the production of branched-chain volatile fatty acids in the rumen. Integrative multi-omics analysis further demonstrated that a broad set of serum metabolites ($n = 115$) were positively correlated with both the core rumen microbes and FE ($R > 0.50$, $P < 0.05$), and were consistently enriched in the HFE group. Representative metabolites, including glutaric acid, pimelic acid, Prolylhydroxyproline, LysoPS, and Octanedioylcarnitine, were mainly involved in lipid metabolism, organic acid metabolism, and mitochondrial β -oxidation pathways.

Conclusion: Overall, our findings demonstrate that breed-specific rumen microbiota contribute to differences in feed efficiency by enhancing VFA production and shaping host metabolic profiles. These microbes may serve as potential biomarkers and targets for improving feed efficiency in goats.

Keywords: Goat, Rumen microbiome, Feed efficiency, Metabolomics, Metagenomics

Effects of Precision Nutrition Supplementation Based on Nutrient Requirements of Cashmere Goats on Production Performance of Inner Mongolia Cashmere Goats

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Abstract: China is the world's largest cashmere goat breeding and cashmere exporting country, with cashmere trade accounting for more than 70% of the world's total. For a long time, there was no special feeding standard for cashmere goats at home and abroad. This is not conducive to the exertion of the production potential of cashmere goats. *Nutrient Requirements of Cashmere Goats* (NY/T 4048-2021), issued by the Ministry of Agriculture and Rural Affairs of China in 2021, is the world's first feeding standard for cashmere goats. This standard was led by Professor Wei Zhang from China Agricultural University and jointly researched by 5 units after years of systematic studies. It defines the minimum requirements of digestible energy (DE), metabolizable energy (ME), net energy (NE), crude protein (CP), digestible crude protein (DCP), minerals and vitamins for all cashmere goat growth stages, and establishes the world's largest cashmere goat feeding standard database. Based on this standard, two experiments were conducted to verify its practicability. In experiment 1, ten healthy growing female goats grazing in autumn and winter were used to determine grazing feed intake and nutrient intake by the saturated alkane method. Relying on this standard, the conventional feed of herdsmen was reconfigured to prepare supplementary diets. Two groups (270 goats each) were allocated as control (herdsmen's conventional feeding) and experimental (standard-optimized feeding) groups with average daily gain (ADG) and cashmere growth measured. In experiment 2, two flocks of female goats (230 goats aged 1 to 5 years per group) were selected as control (supplemented with common salt licks commonly used by herdsmen) and treatment (supplemented with multi-nutrient licks prepared according to the above standard), with a one-year feeding period. The results showed that in experiment 1, the intake of CP, P, Cu and other key nutrients was insufficient in the control group; the standard-optimized supplementary feeding significantly increased body weight and cashmere length ($P<0.05$), and extremely significantly increased ADG and cashmere yield ($P<0.01$) of growing cashmere goats. In experiment 2, multi-nutrient licks had no significant effect on growth performance, cashmere length or fineness ($P>0.05$), but significantly increased cashmere density and cashmere yield ($P<0.05$). Cashmere density in 3–4-year-old goats increased by 47.43% ($P<0.01$) and 37.30% ($P<0.05$), cashmere yield in 1- and 2-year-old goats increased by 22.68% and 18.77% ($P<0.01$), and cashmere yield in 3-year-old goats increased by 17.25% ($P<0.01$). In conclusion, *Nutrient Requirements of Cashmere Goats* (NY/T 4048-2021) is scientific and practical, which can effectively improve the production performance of cashmere goats.

Keywords: Nutrient Requirements, Inner Mongolia cashmere goat, Winter grazing, Supplementary feeding, Multi-nutrient lick, Production performance

Advances in Energy and Protein Requirements of Meat-type Goats

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Abstract: Goat farming in China has evolved from a focus on cashmere to meat production, with increasing standardization and scale. Compared to dairy cows, foreign sheep and goat feeding standards were published before 2010. Due to differences in breed, forage type, and feeding pattern, directly applying foreign standards cannot effectively guide meat-type goat production in China. This paper reviews recent domestic and international study of the energy and protein requirements of meat-type finishing goats, summarizing and comparing the energy and protein requirements for maintenance and growth across major meat-type goat breeds both domestically and internationally. The aim is to provide a reference for scientific research of nutrition requirements, feeding standard, and enhance China's meat-type goat breeding level. This review synthesizes studies on the energy and protein requirements of four indigenous Chinese goat breeds (Chuanzhong Black, Yunshang Black, Qianbei Ma, and Huanghuai). The compiled data included breed, sex, body weight, nutrient requirements, and methodological approaches, with most estimates derived using the factorial method. For energy, net energy for maintenance (NE_m) in local breeds such as Chuanzhong Black and Yunshang Black goats ranged from 63 to 115.2 kcal/kg $BW^{0.75}$, while net energy for growth (NE_g) ranged from 7.52 to 20 kcal/g body weight gain (BWG). In comparison, NRC (2007) recommends metabolizable energy for maintenance (ME_m) values of 108, 108, and 126 kcal/kg $BW^{0.75}$ for intact males, females, and castrates, respectively. Earlier, NRC (1981) reported an NE_g of 4.09 kcal/g BWG, whereas AFRC (1998) suggested 2.3 kcal/g BWG; values for Brazilian meat-type Saanen goats ranged from 4.83 to 10.54 kcal/g BWG. Collectively, these discrepancies indicate that maintenance energy requirements are strongly influenced by environmental temperature, sex, and breed, whereas growth requirements vary with region and change dynamically with body weight and growth stage. Compared with energy, protein requirement data for meat goats remain limited, particularly for indigenous Chinese breeds. AFRC (1998) and NRC (2007) recommend metabolizable protein requirements for maintenance (MP_m) of 2.19 and 3.07 g/kg $BW^{0.75}$, respectively, while studies in Brazil report net protein requirements for maintenance (NP_m) of 1.63–3.58 g/kg $BW^{0.75}$. In contrast, NP_m values for Chinese breeds such as Chuanzhong Black goats range from 1.60 to 1.79 g/kg $BW^{0.75}$, generally lower than those reported internationally. Net protein requirements for growth (NP_g) also vary considerably, with values of 185–192 g/kg empty weight gain (EWG) reported abroad compared with 131–134 g/kg BWG in China. These findings indicate that maintenance protein requirements are relatively stable and lower than those reported in foreign studies.

Keywords: meat-type goats, energy, protein, maintenance requirement, growth requirement

Effect of Database Choice on Taxonomic Classification of Rumen Prokaryotes in Goats

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Abstract: Accurate taxonomic classification of rumen prokaryotes is essential for understanding microbial ecology; however, results can vary depending on the reference database used. This study evaluates how different reference databases affect the taxonomic classification of goat rumen prokaryotic communities using Kraken. Two standard reference databases, the Genome Taxonomy Database (GTDB) and PlusPFP (an expanded protein family profile-based microbial reference database), were used. In addition, two custom databases were constructed: one based on Hungate (456 cultured bacteria and archaea) and rumen metagenome-assembled genomes (4,934 uncultured sequences) (RH), and another combining GTDB with RH sequences (GTRH). Eight sets of in silico 150 bp paired-end reads (60 million reads per set) were generated from RH sequences and classified using the four databases with Kraken. Furthermore, 60 million 150 bp paired-end Illumina NovaSeq reads were obtained from rumen fluid samples of eight goats for comparative analysis. The results indicated that the classification rate of in silico sequences was higher for RH and GTRH, and lowest for PlusPFP. The false-positive classification rate at each taxonomic level was highest for PlusPFP, followed by GTDB, GTRH, and RH. The abundances of numerous taxa differed significantly ($P < 0.05$) between the in silico-based expected profiles and those obtained using the four databases, with the greatest number of differing taxa observed for PlusPFP, followed by GTDB, GTRH, and RH. Using the in vivo reads, the classification rate was significantly higher for GTRH, followed by GTDB and RH, and lowest for PlusPFP. Taxonomic classification at each taxonomic level was higher for GTRH, followed by GTDB, PlusPFP, and lowest for RH. The comparison of taxonomic abundances among the four databases indicated that both the number of taxa and their relative abundances differed significantly ($P < 0.05$) among databases. Overall, the findings highlight that reference database composition strongly influences both classification efficiency and taxonomic resolution in rumen metagenomic analysis. Incorporating rumen-derived genomes into reference databases is critical for improving the accuracy and resolution of taxonomic profiling in the goat rumen.

Keywords: taxonomic classification, kraken, goat, rumen microbiome, database

Milk fatty acid profile response to quebracho condensed tannin supplementation in lactating goats

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Abstract: Milk fatty acid composition in ruminants is strongly influenced by dietary factors through their effects on ruminal lipid metabolism and the transfer of fatty acids to the mammary gland. This study investigated the relationships between dietary inclusion of a commercial purified condensed tannins (CT) extract from quebracho (*Schinopsis balansae*) and the fatty acid (FA) profile of milk in dairy goats. Eight Alpine goats were assigned to a replicated 4 × 4 Latin square design. Four diets were tested, consisting of a control ration and three levels of CT extract (2%, 4%, and 6% of dry matter). The commercial extract contained 74.1% condensed tannins on a dry matter basis. Results showed a clear diet-dependent modulation of milk lipid composition. Increasing CT inclusion led to a progressive rise in polyunsaturated fatty acids (PUFA) (4.91, 5.14, 5.65, and 6.37 g/100 g FA for 0, 2, 4, and 6% CT extract, respectively; $P = 0.004$), mainly due to increases in linoleic acid (18:2; 3.53, 3.76, 4.15, and 4.69 g/100 g FA; $P = 0.006$) and α -linolenic acid (18:3; 0.603, 0.618, 0.687, and 0.786 g/100 g FA; $P = 0.005$). This trend indicates that CT supplementation reduced the extent of ruminal biohydrogenation, allowing a greater proportion of dietary unsaturated fatty acids to escape ruminal saturation and be incorporated into milk fat. At the highest CT level, a further enhancement of rumenic acid (cis-9, trans-11 18:2) was observed, indicating that dietary treatment also influenced mammary desaturation processes. This was supported by an increase in the desaturation index, reflecting greater enzymatic conversion of vaccenic acid into rumenic acid within the mammary gland. Conversely, saturated fatty acids and de novo synthesized fatty acids (62.6, 60.1, 62.6, and 60.2 g/100 g FA; $P = 0.341$) and de novo synthesized fatty acids (<16:0; 48.0, 45.3, 48.0, and 44.8 g/100 g FA; $P = 0.222$) remained largely unaffected by dietary treatments, highlighting that the primary dietary effect was on preformed fatty acids of dietary origin. Overall, dietary supplementation with quebracho CT effectively modulated milk fatty acid composition, increasing the proportion of nutritionally desirable unsaturated fatty acids. However, higher inclusion levels of CT may impair diet digestibility, highlighting the need to optimize dietary strategies to balance improvements in milk fat quality with potential negative effects on nutrient utilization.

Keywords: Quebracho tannin; biohydrogenation; milk quality; dairy goats; polyunsaturated fatty acids; rumen lipid metabolism

Molecular mechanism of glucose regulating hepatic lipid metabolism in goats

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Abstract: Pregnancy toxemia is a prevalent metabolic disease in goats during late pregnancy, primarily induced by systemic energy supply-demand imbalance. It is clinically accompanied by ketosis, fatty liver and other symptoms, which seriously endanger ewe health and fetal survival, and cause substantial economic losses to goat industry. The liver serves as the central organ for lipid and energy metabolism; hepatic lipid metabolic disorders, such as abnormal fatty acid oxidation and excessive ketogenesis, constitute the key pathological basis underlying the occurrence and progression of goat pregnancy toxemia. As the major energy substrate, glucose is directly involved in hepatic glycolysis and lipogenesis. Abnormal glucose concentration can trigger hepatic lipid metabolic disturbance and thereby participate in the pathogenesis of pregnancy toxemia. However, the specific pattern and molecular mechanism by which glucose regulates hepatic lipid metabolism remain unclear and lack systematic research. In this study, hepatocytes were isolated and cultured using an in vitro two-step perfusion method, and treated with gradient concentrations of glucose (0, 2.5, 5, 10, 20 and 30 mM). Cell viability and the expression levels of genes related to glycolysis, lipogenesis, fatty acid oxidation and ketogenesis were determined. Transcriptome sequencing, cell model construction and dual-luciferase reporter assay were further performed to explore the molecular mechanism of glucose regulating hepatic fatty acid oxidation and ketogenesis. The results showed that hepatocyte viability in 5 mM and 10 mM glucose groups was significantly higher than that in other groups ($P < 0.05$). The expression of glycolysis-related genes GK and LDHA increased firstly and then decreased with elevated glucose concentration. The expression of lipogenic genes FAS and ACC was significantly upregulated as glucose concentration increased ($P < 0.05$). Genes involved in fatty acid β -oxidation and ketogenesis presented a trend of first decline and then elevation, with the lowest expression at 10 mM glucose ($P < 0.05$). The concentration of β -hydroxybutyric acid (BHBA) in the 0 mM glucose group was markedly higher than that in other groups ($P < 0.05$). Transcriptome sequencing was conducted in the 0 mM (CK) and 10 mM (LG) groups. A total of 340 differentially expressed mRNAs and 27 differentially expressed miRNAs were screened, which were enriched in carbohydrate metabolism, lipid metabolism, amino acid metabolism and multiple disease-related pathways. The *STEAP4* gene was differentially expressed between the two groups. Overexpression of *STEAP4* significantly increased the contents of NEFA and BHBA, and upregulated the mRNA and protein expression of *FABP1*, *CPT1A*, *HADHA* and *HMGCS2*, whereas *STEAP4* knockout exerted the opposite effects. Dual-luciferase reporter assay verified that novel-m0171-3p could directly target and inhibit the expression of *STEAP4*. This study clarified the effects of different glucose concentrations on hepatocyte metabolism in goats, and revealed the regulatory mechanism of the novel-m0171-3p/*STEAP4* axis in glucose-mediated hepatic fatty acid oxidation and ketogenesis, providing a theoretical basis and molecular targets for the prevention and control of goat pregnancy toxemia.

Keywords: Pregnancy toxemia; Glucose; Hepatic lipid metabolism; hepatocytes; *STEAP4*

Meat Quality Analysis of Different Muscle Parts of 6-Month-Old Wanlin White Goats

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Objective: Meat quality of goats is affected by multiple factors including age, muscle part, breed and feeding conditions. At present, systematic studies on the differences in meat quality among different muscle parts of Wanlin White Goats are still limited. As an excellent meat-purpose goat breed independently cultivated in Anhui Province, Wanlin White Goat exhibits fast growth rate, strong adaptability and favorable production performance. This study aimed to clarify the meat quality differences among different muscle parts of 6-month-old Wanlin White Goats, so as to provide a theoretical basis for meat quality evaluation, determination of optimal slaughter age, and development and utilization of high-quality mutton of Wanlin White Goats.

Methods: In this experiment, six 6-month-old healthy male Wanlin White Goats with an average body weight of 22.52 kg, reared under consistent feeding conditions, diet composition and management protocols, were selected for slaughter and sampling. Four muscle parts, including Longissimus dorsi, Biceps femoris, Brachiocephalicus and Latissimus dorsi, were collected to determine and analyze their physicochemical properties, nutritional composition and flavor characteristics.

Results: (1) The Longissimus dorsi had the lowest pH value and higher contents of protein and ash; the Biceps femoris presented better meat color; the Brachiocephalicus showed higher lightness, the lowest drip loss and relatively higher fat content; the Latissimus dorsi had relatively higher drip loss and cooking loss as well as higher fat content. No significant difference in shear force was observed among the four muscle parts, indicating an overall tender meat quality.

(2) A total of 25 amino acids were detected, including 9 essential amino acids and 16 non-essential amino acids. The contents of essential amino acids and partial flavor-related amino acids were higher in Longissimus dorsi and Brachiocephalicus. Among them, lysine, leucine and glutamic acid were abundant in Longissimus dorsi, while glycine and proline were higher in Brachiocephalicus. Overall, Longissimus dorsi possessed superior nutritional value, and Brachiocephalicus had prominent accumulation characteristics of flavor-related amino acids.

(3) A total of 19 fatty acids were identified, consisting of 9 saturated fatty acids, 6 monounsaturated fatty acids and 4 polyunsaturated fatty acids, with palmitic acid and oleic acid as the dominant fatty acids. The contents of most saturated, monounsaturated and polyunsaturated fatty acids in Brachiocephalicus were significantly higher than those in other muscle parts.

Conclusion: 6-month-old Wanlin White Goats have excellent meat quality with obvious quality differentiation among different muscle parts. Analysis of meat quality differences among various muscle parts can support sectional slaughter and fine processing. This study provides theoretical reference and data support for standardized slaughter, product grading, refined processing and industrial development of Wanlin White Goats.

Keywords: Wanlin White Goat; meat quality; muscle part; nutritional composition; amino acid; fatty acid

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Multi-omics research reveals the effects of dandelion extract on oxidative stress and lactation performance in dairy goats induced by high concentrate diets

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Abstract: Highly concentrated diets are widely used in modern intensive dairy goat farming to increase milk production. However, long-term use can lead to acute rumen acidosis and systemic oxidative stress, which can damage lactation performance and milk quality. Dandelion is rich in flavonoid active ingredients and possesses various pharmacological effects such as antioxidant and anti-inflammatory properties. However, its systemic regulatory mechanism in dairy goats fed high-concentrate diets remains unclear. This study aims to investigate the effects of adding dandelion extract to high-concentrate diets on the oxidative stress status and lactation performance of dairy goats, and to systematically analyze its regulatory mechanism using multi-omics technologies. Eighteen lactating Guanzhong dairy goats were randomly divided into three groups: a low-concentrate group with concentrate-to-forage ratio of 4:6, a high-concentrate group with the ratio of 6.5:3.5, and a high-concentrate group supplemented with 1% dandelion extract. The experiment lasted for 35 days. By measuring production performance, oxidative stress indicators, and lactation gene expression levels, combined with milk metabolome, serum metabolome, and milk proteome, multi-omics analysis was conducted to reveal regulatory mechanisms. The results showed that high-precision feed significantly increased feed intake and milk production, but at the same time led to oxidative stress and decreased lactation performance. Adding 1% dandelion extract to the diet exerts regulatory effects through the following pathways: (1) inhibiting excessive accumulation of propionic acid and butyric acid, reducing rumen LPS concentration; (2) Activate the Nrf2 signaling pathway, upregulate the expression of antioxidant genes, and enhance the overall antioxidant capacity of the body; (3) Promote the expression of FASN gene related to breast fat synthesis and improve breast lipid synthesis; (4) Regulate sphingolipid metabolism, glycerophospholipid metabolism, and amino acid metabolism, maintain cell membrane integrity, and reduce inflammatory reactions. Therefore, dandelion extract can be used as a plant-based feed additive to effectively alleviate oxidative stress induced by high precision feed in dairy goats and improve lactation performance.

Keywords: dandelion extract; dairy goats; high-concentrate diet; oxidative stress; lactation performance; metabolomics; proteomics

Effects of Compound Microbial Inoculants with Different Ratios on Nutrient Transformation and Maturity of Goat Manure Aerobic Composting

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Objective: With the accelerated intensification of goat farming in China, efficient resource utilization of goat manure has become a critical issue for sustainable livestock production. Aerobic composting is an effective approach for converting goat manure into organic fertilizer; however, compound microbial inoculants specifically tailored for goat manure remain limited. This study aimed to evaluate the effects of compound microbial inoculants composed of *Bacillus subtilis*, *Trichoderma viride*, and *Aspergillus niger* at different ratios on nutrient transformation, heavy metal dynamics, and maturity indices during goat manure aerobic composting in the Jianghuai Watershed region.

Methods: Goat manure and rice straw (10:1 dry weight ratio) were composted for 60 days with four treatments: a control group (CK, no inoculant), and three experimental groups supplemented with compound inoculants at 0.2% of dry weight, with *Bacillus subtilis*:*Trichoderma viride*:*Aspergillus niger* ratios of 1:1:1 (T1), 1:2:2 (T2), and 2:1:1 (T3). Temperature, pH, Total Nitrogen (TN), Total Phosphorus (TP), Total Potassium (TK), Organic Matter (OM), heavy metals (Zn, Cu, As), humic acid ratio (E4/E6), carbon-to-nitrogen ratio (C/N), and Germination Index (GI) were monitored throughout the process.

Results: T2 maintained the highest temperature during the maturation phase. At the end of composting, T2 exhibited significantly higher TN and TP ($P < 0.05$), and TK significantly higher than CK and T3 ($P < 0.01$). T2 showed the most thorough OM degradation, with significant differences compared with CK and T1 ($P < 0.001$). The highest E4/E6 ($P < 0.001$), and the lowest C/N ($P < 0.01$). GI values for T1, T2, and T3 all exceeded 80%, at 83.66%, 93.87%, and 88.70%, respectively, with T2 and T3 significantly higher than CK ($P < 0.05$). T2 exhibited the lowest arsenic accumulation (1.68 mg/kg).

Conclusion: The 1:2:2 ratio compound inoculant (*Bacillus subtilis*:*Trichoderma viride*:*Aspergillus niger*) demonstrated optimal composting performance. The higher proportion of cellulolytic fungi accelerated OM decomposition and nutrient mineralization, producing a fully mature organic fertilizer. This provides practical reference for goat manure resource utilization in goat farming systems.

Keywords: Goat manure, Aerobic composting, Compound microbial inoculants, Nutrient transformation, Maturity index

Harnessing native *Cynanchum chinense* supplementation to improve sheep performance and environmental outcomes in saline-alkali grazing systems

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Objective: Grassland animal husbandry faces the dual challenge of enhancing productivity while preserving ecosystem health. Functional native herbage, rich in bioactive compounds like flavonoids and alkaloids, offer a sustainable alternative to synthetic additives, such as antibiotics and ionophore. This study aimed to: (1) evaluate the effects of *Cynanchum chinense* supplementation on digestive metabolism, performance, and methane emissions in grazing sheep, (2) assess its impact on grazing behaviour, (3) identify the optimal supplementation level.

Methods: The study was approved by the Animal Use and Care Committee of Lanzhou University. Twenty-four 6-month-old male F1 hybrid sheep (Small Tail Han × Hu) were assigned to four treatments (n=6) in a completely randomized design. A power calculation confirmed that n=6 provided sufficient power (≥ 0.80) to detect differences in digestibility. Treatments were: control (CON, 0) and *Cynanchum chinense* inclusion at 10% (LA, 9 g/d), 15% (MA, 13.5 g/d), and 20% (HA, 18 g/d) of dry matter intake (DMI). Supplements were mixed with concentrate (50 g soybean meal/sheep/day) and offered daily. The trial had a 15-day adaptation and 60-day measurement period. Sheep grazed alfalfa/tall fescue pasture, except for a 6-day digestibility assay in metabolic cages and a 3-day CH₄ measured using open-circuit respiratory chambers. Grazing behaviour was recorded visually (07:00–19:00 h). Data was analyzed using the MIXED procedure of SAS (fixed effect: treatment; random effects: sheep and batch). Significance was $P < 0.05$.

Results: Supplementation improved performance. Liveweight gain (LWG) was greatest in MA (0.26 vs 0.14 kg/d; $P = 0.009$). MA sheep exhibited higher digestibility coefficients for crude protein (CP) and acid-detergent fibre (ADF) ($P < 0.05$). The dry matter (DM) digestibility coefficient for MA was 70.9%, significantly higher than CON ($P = 0.02$). Nitrogen (N) intake and retention were numerically highest in MA, with significantly higher N digestibility ($P = 0.039$). Supplementation tended to reduce faecal energy loss in LA vs CON ($P = 0.051$). LA showed potential for emission mitigation, with numerically lower CH₄ per unit DMI (−14.6%) compared to CON, though not statistically significant ($P > 0.05$). *Cynanchum chinense* altered behaviour; sheep spent more time grazing and less walking. MA showed the most pronounced effects, with higher rate ($P = 0.037$) and lower chewing time per bolus ($P = 0.001$).

Conclusions: Supplementation with *Cynanchum chinense* improves the performance of grazing sheep. An inclusion level of 15% of DMI is optimal for enhancing nutrient digestibility, nitrogen retention, and liveweight gain. An inclusion of 10% shows potential for mitigating methane intensity. These findings support *Cynanchum chinense* as a valuable native forage resource to promote sustainable and productive sheep farming.

Keywords: Sheep, grazing, *Cynanchum chinense*, Addition, Grazing behaviour, CH₄ emissions.

Goat milk feeding promotes growth and health of sucking goat kids by regulating hepatic NF- κ B pathway through gut-liver axis

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Abstract: Increasing the milk yield of dairy goats is a core objective of the livestock industry, as it directly affects the industry's economic efficiency and sustainable development. Under intensive farming conditions, feeding milk replacers to suckling kids has been widely adopted because it can increase the total output of marketable goat milk. However, studies have shown that milk replacers may disrupt the colonization of gut microbiota in kids, thereby leading to growth retardation or other health issues. Thus, this study aimed to elucidate the mechanisms underlying the effects of goat milk and milk replacer on growth performance and health in goat kids. A total of 90 healthy male Saanen dairy goat kids at 14 days of age, with similar body weight (4.20 ± 0.63 kg) from the same batch, were randomly divided into 3 groups, each with 3 replicates and 10 kids per replicate. The three groups were the goat milk group (GM), milk replacer group 1 (MR1), and milk replacer group 2 (MR2). The experimental period lasted from 14 days of age to 84 days of age, for a total of 70 days. Compared with the milk replacer groups, the kids in the goat milk feeding exhibited improved growth performance and higher serum cholesterol levels. Serum metabolomics revealed that the GM group was enriched in arginine and proline metabolism pathways, along with increased levels of the polyamines spermidine and spermine. Metagenomic analysis indicated that goat milk feeding enriched polyamine-synthesizing genera, including *Akkermansia* and *Sodaliophilus*, and upregulated key enzymes such as arginine decarboxylase (EC 4.1.1.19). Hepatic transcriptomics and RT-qPCR revealed reduced activation of the NF- κ B signaling pathway, reduced expression of pro-inflammatory cytokines (*TNF- α* , *IL-6*, *IL-1 β*), and increased expression of the anti-inflammatory cytokine *IL-10* in the GM group. Molecular docking further indicated that spermine and spermidine bind to NF- κ B. In summary, our findings show that goat milk improves the growth performance and health of goat kids. Goat milk feeding enriches specific gut microbes, such as *Akkermansia*, thereby enhancing microbiota-derived polyamine synthesis. These polyamines enter the liver via the gut–liver axis and bind to NF- κ B, suppressing the expression of downstream pro-inflammatory cytokines. This study provides new insights into the metabolic programming effects of goat milk and offers a potential theoretical basis to formulate functional milk replacer that target the gut–liver axis.

Keywords: Goat milk, Milk replacer, Microbiota, Polyamines, Gut-liver axis, Multi-omics

Effects of Milk Replacer Feeding on Growth Performance and Gastrointestinal Microbiota of Saanen Dairy Goat Kids

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Abstract: In kids rearing, milk replacers have been widely used. However, the effects of goat milk versus milk replacers on gastrointestinal health, nutrient metabolism, and underlying physiological changes in Saanen dairy goat kids have not been systematically elucidated, which restricts precision feeding and industrial efficiency improvement. Therefore, this experiment aimed to investigate the effects of milk replacers on the growth performance, serum biochemical parameters, and gastrointestinal microbial structure and function in Saanen dairy goat kids during the lactation period. Ninety healthy 14-day-old male Saanen dairy goat kids were selected and randomly assigned to three groups: goat milk group (GM), milk replacer 1 group (MR1), and milk replacer 2 group (MR2). Each group had three replicates with 10 kids per replicate. The experimental period lasted 70 days. The results showed that the final body weights of kids in the GM group at 28, 42, 56, 70, and 84 days of age, as well as the average daily gain from 14 to 84 days of age, were significantly higher than those in the MR1 and MR2 groups ($P < 0.05$). Serum albumin and total cholesterol levels in the GM group were significantly higher than those in the milk replacer groups at multiple time points ($P < 0.05$). Goat milk feeding promoted the enrichment of rumen fibrolytic bacteria and colonic beneficial bacteria, such as *Ruminococcus*, *Fretibacterium*, and *Lysinibacillus*. Meanwhile, the goat milk group enhanced functional pathways related to glycolipid metabolism, butyrate metabolism, and energy conversion. In contrast, the milk replacer groups showed enrichment of *Sarcina* and *Bacteroides*, which are more inclined toward complex carbohydrate degradation and genetic information processing-related functions. In summary, milk replacer feeding had certain effects on the growth performance, serum biochemical parameters, and gastrointestinal microbiota structure of Saanen dairy goat kids. Compared with milk replacers, goat milk exhibited clear advantages in promoting the growth and development and maintaining gastrointestinal microecological homeostasis of goat kids.

Keywords: Saanen dairy goat kids; milk replacer; growth performance; serum biochemical indices; gastrointestinal microbiota

Goat milk exosomes alleviate metabolic dysfunction-associated steatotic liver disease by enhancing hepatic fatty acid metabolism

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Abstract: Metabolic dysfunction-associated steatotic liver disease (MASLD) is the most prevalent chronic liver disease globally, with rising incidence linked to obesity, type 2 diabetes, and unhealthy diets. This imposes a heavy public health burden, creating an urgent need for safe and effective interventions. Goat milk exosomes are nano-sized extracellular vesicles rich in bioactive substances with excellent biocompatibility and therapeutic potential in inflammatory diseases. However, their hepatoprotective effects and molecular mechanisms in MASLD remain unclear, limiting their application in liver therapy. This study investigated the therapeutic effect and mechanisms of goat milk exosomes on high-fat diet (HFD)-induced MASLD. Exosomes were isolated from fresh goat milk by ultracentrifugation and comprehensively characterized for purity and integrity. A mouse MASLD model was established by long-term HFD feeding, followed by oral administration of goat milk exosomes. Therapeutic efficacy was evaluated via serum biochemical analyses, hepatic histopathological examination, and RT-qPCR. Transcriptomic analysis screened differentially expressed genes and predicted key signaling pathways, which were verified by in vitro cell experiments. Results showed oral goat milk exosomes were enriched in the liver and intestine, significantly alleviating hepatic lipid accumulation, inflammation, oxidative stress, and improving liver function in HFD-induced MASLD mice. Mechanistically, goat milk exosomes enhance hepatic fatty acid oxidation by upregulating hepatocyte nuclear factor 4 alpha (HNF4A) and activating the PPARA signaling pathway, promoting lipid catabolism and inhibiting synthesis to alleviate steatosis. In conclusion, oral goat milk exosomes are a promising strategy for MASLD prevention and treatment, providing a theoretical basis for the development of goat milk-derived functional foods and therapeutic agents.

Keywords: MASLD, goat milk, exosome, lipid metabolism, HNF4A

Effect of Methionine on Secondary Hair Follicle Growth and Hair Dermal Papilla Cell Proliferation in Cashmere Goats

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Objective: Studying the development of secondary hair follicles (SF) and hair dermal papilla cells (DPCs) in cashmere goats is of great significance for the production of cashmere. Methionine (Met), as an important sulfur-containing amino acid during the growth of hair follicles, is an important factor influencing the gene expression and development of hair follicles. Therefore, this study was to investigate the effects of Met on the growth of SF, and the proliferation and apoptosis of DPCs of Yan Shan cashmere goats.

Methods: The skins of one healthy male Yan Shan cashmere goat at one year old was selected, and the completely isolated secondary hair follicles were randomly divided into the Control group and the Met group, with 3 replicates for each group and 8 hair follicles for each replicate. The concentrations of the Met group were 0, 10, 15, 20, 25, and 30 µg/mL, respectively. Hair follicles were cultured for 7 days, the hair follicle growth pattern was observed and hair follicle length was measured every 24 h. DPCs were extracted and purified from the secondary hair follicles of Yan Shan cashmere goats, the cells were counted, and the growth curves of DPCs were plotted. The DPCs were randomly divided into the Control group and the Met group, with six replicates of each concentration. The concentrations of the Met group were 0, 2, 4, 6, 8, and 10 µg/mL, respectively. After 2 h of incubation, the CCK-8 kit was used to detect cell proliferation viability and the qRT-PCR was used to detect the expression of proliferation-related genes and apoptosis-related genes.

Results: Compared with the Control group, the addition of 15, 20, and 25 µg/mL Met significantly affected the growth rate and cumulative growth length of SF ($P < 0.01$), and the growth-promoting effect of 20 µg/mL Met group was the best. The addition of 6 µg/mL Met group could significantly affect the proliferation of DPCs and significantly up-regulate the expressions of *PCNA*, *CCND1*, *CDK4*, *P21*, *Bcl-2*, *K10* and *K14* mRNA expression ($P < 0.05$).

Conclusion: The addition of Met could significantly promote the growth of SF in Yan Shan cashmere goats during the long-fleece period, and the optimal additions were 20 µg/mL. The addition of 6 µg/mL Met could promote the proliferation of DPCs and inhibit apoptosis through the upregulation of for cell proliferation genes and the downregulation of apoptotic genes, which could promote the growth of SF in Yan Shan cashmere goats.

Keywords: methionine, cashmere goats, secondary hair follicles, hair dermal papilla cells, gene expression

Growth performance, ruminal fermentation and bacterial profile of indigenous goat kids supplemented with barley fodder sprouts

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Small ruminants (goats) play a vital role in the livelihoods of smallholder farmers in the developing countries, including South Africa. They contribute significantly to the socio-economic well-being or resource-poor rural communities by providing food, income, and financial security. However, livestock production is often constrained by heavy dependence on natural pasture, which are highly variable in both quantity and quality. Consequently, the use of commercial feed supplements has become necessary to sustain livestock production, but they are expensive. Therefore, this study aimed to evaluate the use of hydroponic fodder sprouts as a supplement feed for goats fed poor-quality grass hay. A total of 15 goat kids of about 4 month old with an average body weight of 13.45 ± 0.65 kg were taken from genetically preserved indigenous breeds at Agricultural Research Council (ARC). Animals were separated into three groups of 5 animal per group. First group was supplemented with commercial small stock pellets (T1), second group was supplemented with fodder sprouts, irrigated with tap water (T2), and the last group was supplemented with fodder sprouts irrigated with solution water (T3). All animals were fed *Eragrostis curvula* grass hay as a basal feed, with free access to fresh water. The results showed that supplementing fodder sprout significantly ($p < 0.05$) improved feed intake. However, animals growth performance was not affected sprout supplementation. Animals that were supplemented with sprout showed a numerically higher final body weight compared with the control group. Sprout supplementation on goat kids did not affect rumen pH, however, it's significantly ($p < 0.05$) increase ammonia nitrogen. Sprout supplementation significantly ($p < 0.05$) increased acetic acid while significantly reduced isobutyric acid. However, sprout supplementation did not affect rumen bacterial composition, at phylum level the dominant bacteria were *Proteobacteria*, *Firmicutes*, *Bacteroidetes* and *Cyanobacteria*, respectively. However, at the genus level the dominant bacteria in treatments was *Anabaena* from phylum *Cyanobacteria* which was number four of the dominating phylum. It is concluded that hydroponic fodder sprouts can be used as supplementary feed for livestock fed poor-quality grass hay.

***Asparagus Cochinchinensis* Polysaccharide Ameliorates D-Lactate-Induced Injury of Dazu Black Goat Ruminal Epithelial Cells via Autophagy-Mediated Suppression of the NLRP3 Inflammasome**

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Objective: Subacute ruminal acidosis (SARA) is a common metabolic disorder in ruminants. Excessive accumulation of D-lactate (D-LA) in the rumen can induce epithelial barrier damage and inflammatory responses, thereby severely compromising animal health and production performance. However, effective targeted nutritional interventions remain limited. *Asparagus cochinchinensis* polysaccharide (ACP) possesses anti-inflammatory and tissue-protective properties, yet its protective role and underlying mechanisms in ruminal epithelial injury remain unclear. Therefore, this study aimed to investigate the protective effects of ACP against D-LA-induced injury in ruminal epithelial cells (RECs) derived from Dazu Black goats and to elucidate the associated molecular mechanisms.

Methods: An immortalized RECs line was established through SV40 lentiviral transduction and characterized by cellular morphology, cytokeratin-19 immunofluorescence staining, and growth curve analysis to confirm epithelial characteristics and proliferative capacity. A D-LA-induced injury model was then established, with cells assigned to a control group, a D-LA group, and two ACP treatment groups receiving low-dose ACP (50 µg/mL) or high-dose ACP (100 µg/mL). The expression of epithelial barrier proteins (Claudin-1, Occludin, and ZO-1), transport-related proteins (MCT4, NHE3, AE2, PAT1, and SMCT1), and inflammatory cytokines (IL-1β and TNF-α) was evaluated. Furthermore, the autophagy inhibitor chloroquine (CQ) was employed to verify the involvement of autophagy and NLRP3 inflammasome signaling in ACP-mediated protection. The expression of LC3, P62, and NLRP3 was assessed using Western blotting, RT-qPCR, and immunofluorescence analyses.

Results: The results demonstrated that D-LA significantly reduced the expression of tight junction proteins and transport-related proteins while markedly increasing the secretion of IL-1β and TNF-α, indicating impaired ruminal epithelial barrier integrity and absorptive function. ACP treatment effectively alleviated these detrimental effects in a dose-dependent manner. In the high-dose ACP group, the expression levels of Claudin-1, Occludin, and ZO-1 increased by 1.65-, 1.52-, and 1.78-fold, respectively. Similarly, the expression levels of MCT4, NHE3, AE2, PAT1, and SMCT1 increased by 1.43-, 1.57-, 1.62-, 1.38-, and 1.71-fold, respectively. In addition, IL-1β and TNF-α levels were reduced by approximately 90% and 92%, respectively. Immunofluorescence analysis further revealed that high-dose ACP markedly enhanced LC3 fluorescence intensity while decreasing the expression of P62 and NLRP3, suggesting activation of autophagy and suppression of NLRP3 inflammasome formation. Notably, CQ treatment partially reversed the regulatory effects of ACP on LC3, P62, and NLRP3 expression and significantly attenuated its protective effects on epithelial barrier integrity, transport function, and inflammatory responses. These findings indicate that the protective actions of ACP are dependent on autophagy-mediated inhibition of the NLRP3 inflammasome.

Conclusion: ACP alleviates D-LA-induced ruminal epithelial barrier disruption, transport dysfunction, and inflammatory responses by activating autophagy and promoting P62, NLRP3 degradation. This study not only establishes an immortalized RECs model from Dazu Black goats as a novel tool for investigating mechanisms of ruminal epithelial injury but also provides experimental evidence supporting the application of ACP as a natural nutritional intervention for maintaining ruminal health in intensive goat production systems.

Keywords: *Asparagus cochinchinensis* polysaccharide (ACP); Autophagy; NLRP3 Inflammasome; Ruminal epithelial cells (RECs); Dazu black goat; Subacute ruminal acidosis (SARA)

Effects of Rumen-Derived Bio-Nano-Selenium and Graphene Oxide Nano-Selenium on the Structure, Function and Antibiotic Resistance of the Gut Microbiome in Lambs

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Objective: To investigate the effects of bio-nano-selenium (BSeNPs) and graphene oxide nano-selenium (SeNPs-GO) on plasma selenium levels, growth performance, antioxidant capacity and gut microbiota in lambs, aiming to provide a basis for the rational application of nano-selenium in ruminant husbandry and to promote high-quality industry development.

Methods: Selenium-reducing bacteria were screened from goat rumen fluid to prepare BSeNPs, while SeNPs-GO were chemically synthesized. Eighteen Dazhu Black goat kids were divided into three equal groups and fed a basal diet (control), a diet supplemented with 0.1 mg/kg BSeNPs, or a diet supplemented with 0.1 mg/kg SeNPs-GO over a 35-day trial. Faecal samples were collected for metagenomic sequencing and functional annotation.

Results: In the two nano-selenium groups, plasma selenium levels, GSH-Px activity and average daily weight gain were all significantly higher than those in the control group; SOD activity in the BSeNPs group was significantly elevated (Figure 1). The gut microbiota of the nano-selenium groups showed significantly increased α -diversity, distinct shifts in community structure, significantly reduced abundance of antibiotic resistance genes and virulence factors, and marked changes in methane metabolism pathway genes in faeces (Figure 2).

Conclusion: Both rumen-derived BSeNPs and chemically synthesized SeNPs-GO complexes significantly increased plasma selenium levels and antioxidant capacity, improved gut microbiota balance, and enhanced the growth performance of weaned lambs. Moreover, both nano-selenium forms reduced fecal antibiotic resistance genes and virulence factors and reshaped methane metabolism pathways, offering a promising strategy for environmentally friendly lamb rearing.

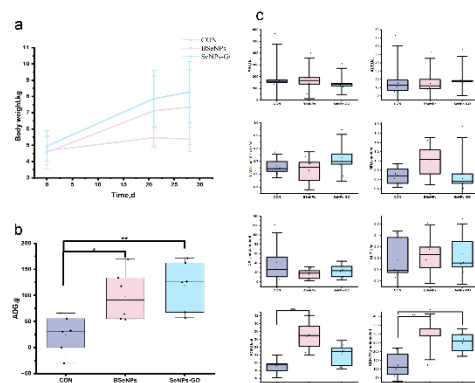


Figure 3 Growth and Physiological and Biochemical Properties

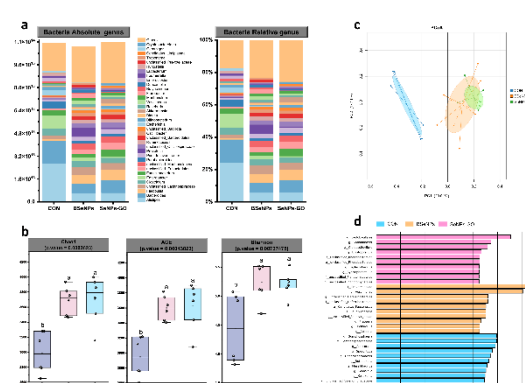


Figure 2 Composition of bacterial communities

Keywords: Gut microbiome, Lambs, Bio-nano-selenium (BSeNPs), Graphene oxide nano-selenium (SeNPs-GO), Metagenomics

Gram Positive Polysaccharide Utilization Loci of Active Cecal *Oscillibacter* Mediate Compensatory Utilization of Rumen Escaped Fiber in Goats

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Abstract: Developing non-grain feed resources is a critical national strategy to alleviate food competition between humans and livestock. In ruminants, approximately 30% to 50% of digestible fiber escapes rumen fermentation and enters the hindgut; however, the mechanism underlying the hindgut compensatory utilization of this escape fiber remains poorly understood. In this study, using goats (*Capra hircus*) as a model, we investigated the relationship between fiber digestibility, growth performance, and hindgut microbiota. Growth phenotype correlation analysis revealed that both neutral detergent fiber (NDF) and acid detergent fiber (ADF) digestibilities were significantly and positively correlated with body weight gain (NDF: $R=0.72$, $P=0.0037$; ADF: $R=0.71$, $P=0.003$) and cecal butyrate proportion ($R=0.57$, $P=0.027$). By integrating 16S rRNA gene (DNA) and transcript (RNA) sequencing, we identified *Oscillibacter* as a highly active target microbial genus in the cecum (exhibiting a high RNA/DNA ratio). Metagenomic assembly successfully reconstructed the genomes of several cecal *Oscillibacter* species (including *O. valericigenes* *Oscillibacter* sp. PEA192, and *Oscillibacter* sp. NSJ-62) that were significantly associated with fiber-degrading activity. Genomic scanning using dbCAN3 revealed that these strains possess highly organized Polysaccharide Utilization Locus (PUL) gene clusters characterized by a core glycoside hydrolase family 5 (GH5) gene co-localized with transcription factors (TF) and transporter proteins (TC). Furthermore, AlphaFold-based structure prediction and molecular docking demonstrated that the fiber-utilization pattern of these cecal *Oscillibacter* strains differs distinctly from classical rumen fiber-utilizers (such as *Ruminococcus*). Key active site residues (including GLU172, ASP305, TRP128, and ASP127) mediated high-affinity binding to highly resistant escape fiber polysaccharides. Collectively, our findings reveal a novel compensatory mechanism of escape fiber utilization driven by active cecal *Oscillibacter* via specialized PULs to promote butyrate production and host growth, providing valuable theoretical insights and microbial resources for improving whole-tract fiber digestion efficiency in ruminants.

Keywords: Goat; Microbiota; Rumen-escaped fiber; Gram-positive polysaccharide utilization loci; Cecum

Enhancing the quality of mixed ration with cassava foliage by optimization fermentation time

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Abstract: The shortage of high-quality feed and livestock feed resources has limited the production of ruminants in some developing countries. Cassava and its by-products can be used as alternatives to traditional forage in tropical regions to maintain the development of animal husbandry. silage technology enhances feed efficiency and reduces costs for farmers, implementing cassava as a dietary substitute in ruminants' diets remains challenging. To address this, the study investigated effective methods for fiber decomposition, additive fermentation, anti-nutritional reduction, and dietary incorporation. The objective was to evaluate the quality of total marketable roughage (TMR) feed produced through fermentation at varying durations and blending ratios of cassava leaves. The fresh foliage will be mixed with rice straw, soybean meal cassava pulp and premix. The distilled water will be sprayed until 55% content in total mixed ration, then, 300 g of the prepared total mixed ration diets will be packed into polyethylene bags, and the bags were sealed with a vacuum sealing machine and stored at room temperature until opening. The three replications, four treatments and four fermenting days (7, 14, 21, 28d) resulted in a total of 48 bags. The cassava leaf content in the samples was 0%, 10%, 20%, and 30% (T1, T2, T3, T4). Twelve replications of the 0 d sample will be tested without sealing. In this experiment, there were significant differences ($p < 0.05$) in the effects of time, after fermented 7 d, there have significant difference on dry matter, NDF, ADF and CP. Result of T4 was lower between other groups in dry matter, T2 was higher than higher between other groups in NDF and ADF ($p < 0.05$), there was no significant difference among groups in CP ($p > 0.05$); When it is fermented 14 d, DM of T4 was significantly lower than it in T1, T2 and T3; NDF of T2 was significantly higher than other groups ($p < 0.05$); ADF of T3 and T4 was significantly lower than T1 and T1 is lower than T2; there was no significant difference between groups of CP ($p > 0.05$); The results of this experiment showed that 28 days of fermentation had a negative impact on all indicators of the feed, and the best time of fermentation was 14d to 21d. The protein content of the feed increased with the increase of cassava leaf content, and the pH of each group was between 4.4 and 4.5, which met the pH standard of high quality fermented feed.

Keywords: Cassava foliage, Fermentation total mixed ration, fermentation parameter

Sodium Butyrate Improves Growth Performance of Dazhu Black Goat Kids and Modulates Rumen Epithelial Cell Function In Vitro: A Preliminary Investigation

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Objective: With the growing restrictions on antibiotic use in animal production, developing safe and sustainable feed additives that can both promote growth and regulate immune function has become a major focus in ruminant nutrition research. Sodium butyrate, a functional short-chain fatty acid salt, has been widely reported to improve growth performance and intestinal health in animals. However, most previous studies have mainly concentrated on its effects on growth performance and rumen microbial fermentation, while relatively few have examined whether it may also influence growth by regulating host innate immune factors. β -defensins are important endogenous antimicrobial peptides that play a key role in maintaining gastrointestinal microbial balance and protecting against pathogen invasion. However, there has been no systematic study on how sodium butyrate regulates β -defensins in ruminal epithelial cells of ruminants. Its potential role in the ruminal mucosal immune barrier, as well as the underlying mechanisms involved, therefore remains unclear and requires further investigation.

Methods: (1) Twenty 15-day-old Dazhu Black kids were randomly divided into two groups. The control group received a basal diet, and the treatment group received the same diet supplemented with 0.3% sodium butyrate. Both groups were fed for 45 days. Growth performance, including body weight changes, was recorded. Blood serum samples were collected to assess biochemical parameters and antioxidant metabolic indicators. Rumen fluid was also collected to assess pH, volatile fatty acids, and microbial diversity. (2) Ruminal epithelial cells were isolated from Dazhu Black kids. Cells were cultured in medium containing 5 mM sodium butyrate. Total RNA was extracted. cDNA was generated from total RNA via reverse transcription. Fluorescence quantitative PCR and the $2^{-\Delta\Delta C_t}$ method were used to determine the relative amount of mRNA expression.

Results: Sodium butyrate supplementation significantly increased average daily gain (ADG) in kids ($P < 0.01$), while ruminal fermentation parameters remained unchanged ($P = 0.2882$). In serum, SOD activity was significantly elevated ($P = 0.03$), and no obvious differences were observed in T-AOC, MDA, CAT or GSH-Px ($P > 0.05$). 5mM sodium butyrate significantly upregulated β -defensin-1 and β -defensin-2 expression ($P < 0.01$), increased ZO-1 ($P < 0.05$) and Claudin-1 ($P = 0.03$) expression, and elevated MCT-1 expression ($P < 0.05$). No significant changes were observed in MCT-4, TNF, or IL-6 ($P > 0.05$), while NHE-1 showed a decreasing trend ($P < 0.01$).

Conclusion: Sodium butyrate significantly promotes growth in goat kids and improves their antioxidant status. The low-dose sodium butyrate enhances the expression of both β -defensins and genes associated with epithelial function in ruminal epithelial cells. Overall, these findings suggest that sodium butyrate supports growth primarily by strengthening innate immune defenses and improving epithelial integrity and function.

Keywords: Sodium Butyrate, Growth performance, Rumen epithelial cell function, Goat

Effect of Curcumin Supplementation on Feed Intake, Nutrient Digestibility, Rumen Fermentation and Growth Performance in Meat Goats

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Abstract: Sixteen male crossbred Boer with initial body weight of 18.5 ± 1.5 kg, were used in a completely randomized design. Goats were fed total mixed ration with or without curcumin supplementation. Curcumin supplementation was added at 0.1% of total mixed ration. The experiment lasted for 150 days. TMR intake was increased in goats fed TMR containing curcumin compared with goats fed TMR. Average daily gain was 83.33 and 115.00 g/d in goats fed TMR and TMR containing curcumin. Nutrient digestibilities of goats fed TMR containing curcumin were higher ($P < 0.05$) than goats fed TMR. Rumen pH and ammonia nitrogen concentrations were lower ($P < 0.05$) in goats fed TMR containing curcumin compared with goats fed TMR. Total bacteria population was higher ($P < 0.05$) in goats fed TMR containing curcumin than goats fed TMR while total protozoa population was lower ($P < 0.05$) in goats fed TMR containing curcumin compared with goats fed TMR. So that curcumin supplementation in TMR did improve feed intake, nutrient digestibility and growth performance in meat goats.

Key words: Curcumin, Feed intake, Nutrient digestion, Rumen fermentation, Meat goats

Precision animal feed management to promote quality fattening goat production in small holder farmer

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Abstract: This activity was focused on research Technology transfer of goat farm management and transformation of goat academic outcome for stakeholders. Feed management of high quality of fattening goat has been transferred. It was reviewed that precision of feed management was successful to increasing goat performance. The suitable range for fattening goats was related to weaning weight; the recommended range was 15-18 kg/hd and fattening goat up to 40 kg/hd was affected on increasing percentage of carcass quality at 50 percent. There for goat breed management (Bloodline level) that affects good quality meat production such as Boer 50, 75 (crossbred) and precise Nutrition Management for Meat Goat Breeds (Nutrition calculation and management program based on various goat needs). Live weights of 35-40-45 kg and ADG could be 125-166-208 g/d fattening time was 120 days, and 166-222-270 g/d fattening time was 90 days, and carcass quality 42-45%, respectively. The objective of this study is to transfer research technology and knowledge regarding precise goat feed management, production of quality fattening goats and reduce production costs at the small and large farmer scales. In addition, studying information on fattening goat production and preparing a calendar price of fattening goats was setting guidelines for continuous production. Study on production costs per 1 goat in different farming management calculated during the goat weaning period (3 months), it was found that 1) pasture raising cost of goats after weaning/each was 1,130.39 baht, 2) Semi-caged, semi-free raising cost of young goats after weaning/each was 1,426.69 baht and 3) the cost of raising young goats after weaning/each was 1,277.94 baht, respectively. In 2024, farmers in the project were able to sell a total of 1,712 goats, valued at 2,713,153.00 baht, and Dan Khun Thot Agricultural Cooperative Limited, which collected from members, sold a total of 1,691 goats, valued at 2,967,387.00 baht. Trading value being according to the calendar year goat prices as follows: Purchase price of fattened goats 97.1 baht. The purchase price of a young goat is 52.5 baht, the selling price of a fattened goat is 116.7 baht, the selling price of a young goat is 67.1 baht, respectively. Currently, the price of fattening goats has increased to 170 baht per kilogram, this positively impacts farmers' income and elevates the overall quality of life for small-scale farmers.

Keywords: farm management technology transfer, goat fattening, goat price calenda

Effects of Dietary Lycopene Supplementation on Growth Performance and Antioxidant Capacity in Goats

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Abstract: Lycopene is a naturally occurring carotenoid predominantly present in tomatoes and tomato products and is recognized as one of the most potent dietary antioxidants. Lycopene is considered one of the most potent dietary antioxidants because of its remarkable capacity to quench singlet oxygen and neutralize free radicals, thereby protecting cells against oxidative damage. Dietary supplementation with lycopene has been reported to enhance antioxidant defense mechanisms by increasing the activities of antioxidant enzymes, including superoxide dismutase, glutathione peroxidase, and catalase. The objective of this study was to investigate the effects of dietary lycopene supplementation on growth performance and antioxidant capacity in goats. In this study, eighteen male Boer goats with an initial body weight of 20.00 ± 2.00 kg were randomly assigned to three dietary treatment groups, with six goats per treatment, and were housed individually in pens. The experiment was conducted using a completely randomized design (CRD). All goats underwent a 90-day feeding trial involving three dietary treatments, in which the control group received the basal diet, whereas the other groups received the basal diet supplemented with lycopene powder at levels of 50 and 100 mg/kg diet, designated as LCP50 and LCP100, respectively. The results showed that goats supplemented with 100 mg/kg lycopene (LCP100) exhibited significantly higher ($P < 0.05$) final body weight, body weight gain, average daily gain (ADG), feed intake, and nutrient intake than those in the other treatment groups. Dietary lycopene supplementation significantly increased antioxidant capacity ($P < 0.05$), as evidenced by higher total antioxidant capacity (T-AOC) and increased activities of superoxide dismutase (SOD), glutathione peroxidase (GSH-Px), and catalase (CAT), while malondialdehyde (MDA) concentrations were significantly decreased ($P < 0.05$). Therefore, dietary supplementation with lycopene improved growth performance and antioxidant capacity in goats. Based on the present findings, supplementation with 100 mg lycopene/kg feed appears to be the optimal level for mitigating environmental stress and maintaining normal physiological functions in goats.

Keywords: Lycopene, Growth Performance, Antioxidant Capacity, Goat

Fermentation Characteristics and In Vitro Gas production of LAB-Treated Sorghum Silage in Tropical Conditions

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Abstract: The objectives of this to evaluate the fermentation quality and *in vitro* gas production of 60 days whole sorghum silage supplemented with different levels of lactic acid bacteria (LAB) inoculants to address animal feed shortages during the dry season. The study utilized a completely randomized design (CRD) with four treatments: a control without LAB (T1), and sorghum supplemented with LAB at 0.1% (T2), 0.25% (T3), and 0.5% (T4). Fresh 60 days whole sorghum was chopped into 2-3 cm pieces, mixed with LAB, and ensiled in vacuum-sealed plastic bags for 0, 7, 14, 21, and 28 days. Silage samples were analyzed for chemical composition and fermentation characteristics. Furthermore, *in vitro* gas production was evaluated using goat rumen fluid over a 72-hour incubation period. During the fermentation period, the pH value and ammonia nitrogen content in all LAB-supplemented groups decreased significantly compared to the control group ($p < 0.05$), indicating minimized protein loss. Furthermore, the group supplemented with 0.25% LAB exhibited a higher gas production rate than the other groups. Cumulative net gas production increased significantly at 12, 24, 48, and 72 hours of incubation across the LAB-treated groups, indicating enhanced digestibility of the sorghum silage. The results revealed that supplementation with LAB, particularly at levels of 0.1% to 0.25%, effectively improves the fermentation quality, preserves nutritional value, and enhances the *in vitro* digestibility of sorghum silage.

Keywords: Sorghum, Silage, Lactic acid bacteria, Fermentation, *In vitro* gas production

Betaine as a mitigation supplement for stress in small ruminants: Impact on performance, blood parameters, milk and meat production and quality: A meta-analysis

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Abstract: Betaine is widely used in ruminant nutrition because of its osmoprotective and methyl-donor properties; however, its effects on small ruminant productivity remain inconsistent across studies. Therefore, this study aimed to quantitatively evaluate the effects of dietary betaine supplementation on intake, rumen fermentation, blood metabolites, antioxidant status, growth performance, carcass traits, meat quality, and milk production in sheep and goats and to identify the factors influencing animal responses. A systematic review and meta-analysis were conducted using 33 peer-reviewed studies comprising 98 independent experiments. The effect size was assessed based on raw mean differences using random-effects models, and meta-regression and subgroup analyses were used to explore the sources of heterogeneity. Betaine supplementation significantly ($P<0.05$) increased dry matter intake, and digestibility but reduced the feed conversion ratio. Betaine supplementation significantly increased haemoglobin, and total protein, while reducing indicators of stress. Animals supplemented with betaine showed improved ($P<0.05$) growth and fat and redness (a^*) of meat, but reduced shear force. Betaine increased ($P<0.001$) milk yield and fat, and fat-corrected milk but did not affect other milk parameters. Meta-regression revealed that animal breed, age, initial body weight, dietary concentrate level, supplementation duration, and betaine inclusion rate were the major factors explaining the variability among studies. Responses were generally more pronounced at supplementation levels of 3-6 g/day during longer feeding periods. In conclusion, dietary betaine supplementation is an effective nutritional strategy for improving the productivity of small ruminants. However, the magnitude of these responses depends on the animal and dietary characteristics, highlighting the importance of optimizing supplementation strategies according to production conditions.

Keywords: Betaine supplementation; Sheep and goat; Meta-analysis; Growth performance; Milk production

PART 8: Reproduction

Integrated miRNA-mRNA profiling reveals a regulatory network associated with follicular atresia in goats (*Capra hircus*)

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Objective: Follicular atresia is a major cause of ovarian reserve depletion and reduced reproductive performance in goats. Although microRNAs (miRNAs) regulate target gene expression at the post-transcriptional level and are involved in follicular atresia, the underlying miRNA-mRNA interaction network in goats remains poorly understood. This study aimed to characterize the miRNA-mediated post-transcriptional regulation of follicular atresia through integrated small RNA and transcriptome analyses and to identify potential core regulators.

Methods: Healthy follicles (HF), early atretic follicles (EAF), and late atretic follicles (LAF) were collected from 11 superovulated Chengdu Ma goats. Small RNA and transcriptome sequencing were performed to identify differentially expressed miRNAs (DEMs) and genes (DEGs). DEMs with significant dynamic changes during follicular atresia were identified by time-series analysis. Their predicted target genes were intersected with the 1,480 DEGs shared by the HF vs. EAF and HF vs. LAF comparisons to construct a miRNA-mRNA interaction network. Hub miRNAs were then identified based on network connectivity, followed by GO and KEGG enrichment analyses.

Results: A total of 467 DEMs and 4,326 DEGs were identified. Among them, 251 DEMs showed significant dynamic changes during follicular atresia, including 166 downregulated miRNAs in cluster 1 and 85 upregulated miRNAs in cluster 6 ($P < 0.001$). Functional enrichment analysis showed that the predicted targets of these DEMs were mainly enriched in the PI3K-Akt, FoxO, and Wnt pathways, as well as apoptosis, autophagy, and ferroptosis. Integrative analysis identified 37 miRNAs and 96 mRNAs, yielding 106 putative miRNA-mRNA pairs. Network analysis revealed that miR-3615-z, miR-760-y, miR-744-x, chi-miR-324-3p, miR-1247-x, and chi-miR-331-3p were hub miRNAs (Figure 1). Their differentially expressed target genes were mainly enriched in biological processes related to regulation of cell proliferation, cytoskeletal remodeling, immune response, and cell adhesion, as well as the FoxO, Ras, and MAPK signaling pathways. Related target genes included *PAPPA*, *RUNX1*, and *FOXO4*, suggesting that these hub miRNAs may participate in post-transcriptional regulation associated with follicular atresia.

Conclusion: This study systematically constructed a miRNA-mRNA regulatory network associated with follicular atresia in goats and identified six hub miRNAs and their potential target genes. These findings provide new molecular clues to the post-transcriptional regulation of follicular atresia and candidate targets for further functional validation.

Keywords: Goat, Follicular atresia, miRNA-mRNA interaction, Integrative analysis

Analysis of the characteristics of microRNA expression profiles and reproductive regulation-mediated signalling pathways in testicular sertoli derived sEVs from Leizhou goats

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Objective: In the male reproductive system, Sertoli cells (SCs) and their secreted small extracellular vesicles (sEVs) have gradually emerged as a popular area of research. The Leizhou Black Mountain Goat, a distinctive meat-goat breed in the tropical region of southern China, As a unique breed in southern China, Leizhou goats exhibit excellent growth, development, and reproductive traits, which are crucial for the development of local animal husbandry. Therefore, an in-depth investigation of the characteristics and miRNA expression profiles of SC-derived small extracellular vesicles (SC-sEVs) from Leizhou goats will provide a theoretical basis for understanding the role of SCs in Leizhou goat reproductive physiology.

Methods: A total of 8 testicles from four 2 - month - old Leizhou black mountain goats were collected. The expression of Sertoli cell marker genes was detected via RT - PCR and immunofluorescence staining. sEVs were identified through transmission electron microscopy, particle size distribution measurement, and marker protein identification. Single - end sequencing of miRNAs in three biological replicate groups was carried out using Illumina high - throughput sequencing technology. Potential additional miRNAs in the dataset were identified by means of bioinformatics analysis. Differentially expressed miRNAs were identified using the DESeq2 R package and the negative binomial distribution model. Finally, target gene predictions were performed for the significantly differentially expressed miRNAs using TargetScan (v5.0) and miRanda (v3.3a) software.

Results: The SCs and their sEVs were successfully isolated with high purity. Small RNA sequencing of sEVs (Illumina NovaSeq, n = 3) revealed 387 known miRNAs and 52 novel miRNAs. miRNAs with 19-nt lengths were predominant, and the top 20 most abundant miRNAs accounted for 61% of total reads. A total of 9176 target genes were significantly enriched in the Hippo ($P = 1.3 \times 10^{-4}$), TGF- β ($P = 3.9 \times 10^{-4}$), MAPK, JAK-STAT, Wnt, and cAMP signalling pathways.

Conclusion: In this study, the miRNA expression profile of sEVs derived from testicular Sertoli cells of Leizhou black goat rams was successfully constructed for the first time. This study systematically revealed the biological characteristics and miRNA expression features of these sEVs, as well as the reproductive regulatory signalling pathways mediated by miRNA target genes. Future research can build on this foundation to refine the study design, address current limitations, and thereby promote the continuous in-depth exploration and development of reproductive physiology research on Leizhou black goats.

Keywords: Leizhou goat, Sertoli cell sEV, MiRNA, Male reproductive signalling, Spermatogenesis regulation

Determinants of community based participatory small ruminant breeding program: evidence from smallholder goat producers in pastoral areas of Southern Ethiopia

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Abstract: Community-based smallholder goat producers' participation in breeding programs is a means of improving the production and productivity of their goats, but nowadays it does not yield significant results in pastoral and agro-pastoral areas. This is due to many determining factors, that smallholder goat producers do not participate in CBBPs. In Ethiopia, studies tried to identify the determining factors that influence smallholder goat producers' participation in CBBP but did not address the problem in the study area. As a result, this research aimed to identify the determinants of community-based goat breeding programs in the study area. A semi-structured interview schedule, focus group discussions, and key informant interviews were used to gather primary data. Primary data about the study was collected from 138 sample households. The study was conducted in the Bena-tsema district of southern Ethiopia. A probit regression model was used to analyze determinants of smallholder goat producers' participation in CBBP. In the probit regression among 13 identified independent variables, age, goat farming experience, access to credit, and distance to training center influence CBBP participation at ($P < 0.01$). Education status and veterinary service problems influence CBBP participation at ($P < 0.05$) significance level. To strengthen CBBP, government lead investment in goat breeding is important.

Keywords: CBBP participation; Determinants; Probit regression; Smallholders

Effect of different gonadotropins on estrus induction in Yanshan cashmere goats during the non-breeding season

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Abstract: This study aimed to optimize an estrus induction protocol for Yanshan cashmere goats during the non-breeding season by comparing different gonadotropin treatments. Forty-one healthy Yanshan cashmere goat does with normal estrous cycles were randomly assigned to two treatment groups: an FSH group (n=20) and a PMSG group (n=21). All does were implanted with progesterone device for 9 days. In the FSH group, 50 IU and 30 IU of FSH were administered at 18:00 on day 8 and 06:00 on day 9, respectively. Does in the PMSG group received 330 IU of pregnant mare serum gonadotropin (PMSG) at progesterone device withdrawal. Estrus detection began 12 hours after treatment. Estrus response was recorded, and follicular development was monitored at three time points: 0-1 h before suppository withdrawal, at the first appearance of estrus, and 24 h after the onset of estrus. Blood samples were collected at 0-1 h before suppository withdrawal and 0-1 h after the onset of estrus to measure the serum concentrations of estradiol (E2), progesterone (P4), follicle-stimulating hormone (FSH), luteinizing hormone (LH), and prolactin (PRL). All estrus does were artificially inseminated at 48 and 56 h after progesterone withdrawal. After artificial insemination, a breeding ram was introduced to improve conception rate. Pregnancy was confirmed by B-mode ultrasonography 45 days after mating and the pregnancy rate was calculated. The results showed no significant differences in estrus rate and pregnancy rate between the FSH and PMSG groups ($P > 0.05$). However, the estrus rate tended to be higher in the PMSG group than in the FSH group (57.1% vs 55%), whereas the conception rate among estrous does tended to be higher in the FSH group than in the PMSG group (72.8% vs 66.7%). No significant between-group differences were observed in serum E2, FSH, LH, P4, or PRL concentrations at either sampling time ($P > 0.05$). Across both treatments, serum E2, FSH, and LH concentrations were significantly higher at estrus onset than before progesterone device removal ($P < 0.01$), whereas serum P4 and PRL concentrations were significantly lower at estrus onset ($P < 0.01$). Mean follicle diameter increased from 1.59 mm before progesterone device removal to 3.24 mm at estrus onset and 4.14 mm at 24 h after estrus onset, with significant differences across time points ($P < 0.01$). No significant between-group differences in follicle diameter were detected ($P > 0.05$). In conclusion, in Yanshan cashmere goats, no significant differences were observed between the FSH- and PMSG-based estrus induction protocols in terms of estrus rate or conception rate during estrus. Nevertheless, based on overall estrus response, conception performance, and treatment cost, the progesterone device plus PMSG protocol appears to be a more practical choice.

Keywords: Cashmere goat, Estrus induction, Follicle development, Reproductive hormone, Non-breeding season

Chromatin opening and expression pattern of *LMBRD1* in Dazu Black Goat (*Capra hircus*) ovary associated with reproductive traits

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Objective: The *Dazu Black Goat* (DBG) is a high-quality local goat breed in Southwest China. During large-scale breeding, there are obvious differences in litter size and unstable lambing efficiency within the population. Although recent studies on litter size in DBG have identified a set of core genetic loci, the specific molecular basis and regulatory mechanisms underlying the high litter size phenotype of this breed remain incompletely clarified, necessitating systematic gene mining and mechanism analysis.

Methods: A total of 168 healthy goats with more than 3 parities were selected for blood sample collection, followed by whole-genome resequencing with an average depth of 10× to detect single nucleotide polymorphisms (SNPs), insertions/deletions (InDels) and copy number variations (CNVs), which were then subjected to association analysis with litter size traits. Specifically, 3 high-fecundity goats (HL group) with at least 3 parities each producing more than 3 lambs, and 3 low-fecundity goats (LL group) with at least 3 parities each producing only 1 lamb and an average litter size < 1.6 were selected. Synchronous estrus was induced using two CIDR inserts (300 mg progesterone) combined with prostaglandin (PGF2α), and ovarian tissues were collected during estrus for single-nucleus RNA sequencing (snRNA-seq) and assay for transposase-accessible chromatin with high-throughput sequencing (ATAC-seq). The function of the key candidate gene *LMBRD1* was explored by establishing an in vitro model of primary goat ovarian granulosa cells (GCs), combined with methods such as qRT-PCR, western blot, immunofluorescence, and flow cytometry.

Results: Association analysis of SNPs and InDels with litter size traits identified a set of significantly associated variant loci, which were annotated to key candidate genes including *LMBRD1*, *BMP2* and *FZD4*. The variant loci of *LMBRD1* (Chr14: 90316176 and Chr14: 90307906) were annotated to the upstream region, and the corresponding ATAC-seq accessible region was the promoter region of this gene (≤1 kb). Additionally, the expression abundance of *LMBRD1* in granulosa cells of the HL group was significantly higher than that in the LL group ($P < 0.01$). In vitro cell experiments further confirmed that *LMBRD1* could synergize with *LAMP1*, a key lysosomal protein, to positively regulate the proliferation of GCs and inhibit cell apoptosis; abnormal expression of this gene would disrupt the autophagy-lysosome homeostasis, thereby affecting the physiological state of GCs.

Conclusion: This study identified genes including *LMBRD1* associated with the high litter size trait of DBG from multiple levels, such as genome-wide association study, chromatin accessibility and cellular transcriptional heterogeneity. It clarified the functional role of *LMBRD1* in maintaining the homeostasis of GCs, providing a theoretical basis and key targets for the analysis of litter size traits and marker-assisted selection in DBG.

Keywords: *Dazu Black Goat*, Litter size traits, Ovary, Multi-omics, Granulosa cells, *LMBRD1*

Isolation, Identification and Adipogenic and Myogenic Differentiation Mechanism Analysis of Goat Bone Marrow Mesenchymal Stem Cells (*Capra hircus*)

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Objective: Bone marrow mesenchymal stem cells (BMSCs) are a type of adult stem cells with self-renewal ability and multi-directional differentiation potential. They are not only present in the bone marrow but also exist outside the bone tissue. Under the stimulation of specific signals, BMSCs can migrate from the bone marrow and move directionally to the target organs or tissues. Therefore, analyzing the directional differentiation of BMSCs into adipocytes and myocytes not only has important theoretical significance for revealing the formation of meat quality traits but also provides new ideas for the genetic improvement of meat quality in excellent breeds such as Jianzhou Daer goats.

Methods: BMSCs were isolated via the whole bone marrow adherent method, then expanded and subcultured in vitro. Comprehensive cell identification was performed via morphological assessment, surface marker determination and multilineage differentiation potential detection. In vitro directed adipogenic and myogenic differentiation of BMSCs was evaluated via morphology, immunofluorescence staining and qPCR. RNA sequencing (RNA-seq) was applied to systematically analyze the transcriptional characteristics of BMSCs at cellular and molecular levels, and elucidate the key regulatory mechanisms underlying BMSCs adipogenic and myogenic differentiation.

Results: After serial passaging to passage 31, BMSCs isolated from femurs of Jianzhou Daer Goats still retained the typical morphological characteristics of BMSCs. The expression profile of cell surface markers conformed to the minimum identification criteria for mesenchymal stem cells established by the International Society for Cell Therapy (ISCT), and they could be successfully induced to undergo directed adipogenic and myogenic differentiation in vitro. Transcriptome analysis showed that, with day 0 of adipogenic differentiation (BMSCs 0d) as the control, 3886 and 3955 significantly differentially expressed genes (DEGs) were identified in adipogenic differentiation induced 7d (7d) and 12d (12d), respectively. Compared with 7d, 12d had 765 significant DEGs. Pathway analysis indicated that adipogenic BMSCs, subcutaneous preadipocytes and intramuscular preadipocytes had significantly altered expression profiles and activated ECM–receptor interaction and Axon guidance pathways. Using day 0 of myogenic differentiation (cj0d) as the control, 2101 and 2301 significant DEGs were identified in myogenic differentiation induced 16d (cj16d) and 28d (cj28d), respectively. cj28d had 1870 significant DEGs compared with cj16d. Pathway analysis showed that myogenic BMSCs continuously activated Axon guidance, p53 signaling pathway and Motor proteins.

Conclusion: In this study, BMSCs of goats were successfully isolated and identified. By adding different inducing factors, these BMSCs were induced to undergo adipogenic or myogenic differentiation. And it has pathways and gene expression changes that are similar to the process of adipogenic differentiation of intramuscular and subcutaneous fat cells. Enrichment analysis of RNA sequencing (RNA-seq) data demonstrated that: following adipogenic, DEGs in goat BMSCs were specifically enriched in the PI3K/AKT signaling pathway and Hypertrophic cardiomyopathy pathway; following myogenic, DEGs were specifically enriched in the p53 signaling pathway and Motor proteins.

Keywords: Bone marrow mesenchymal stem cells, differentiation, RNA sequencing, Goat

Aronia berry extract supplementation improves the quality of cryopreserved dairy goat spermatozoa

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Abstract: Semen cryopreservation negatively impacts the quality and functional integrity of goat spermatozoa, mainly due to the excessive production of reactive oxygen species (ROS). Black chokeberry's (*Aronia melanocarpa*) fruits are rich in tannins, flavonoid compounds, polyphenols and other antioxidants. The aim was to evaluate the effects of supplementing semen extender with Aronia berries extract on the quality of frozen-thawed dairy goat spermatozoa. Aronia berries extract was prepared by grounding 450 g of the Aronia berries in 2 L of distilled water using Rotary evaporated-R100 (Buchi, New Castle, United States). The extract was then evaporated and subsequently freeze-dried and stored at 4 °C. The dried Aronia berries' total flavonoid and polyphenol content was determined, as well as its antioxidant capabilities. Semen was collected from four mature Saanen bucks once/week for 4 weeks using electroejaculation. Semen samples were then pooled and diluted in Andromed® extender supplemented with 0 (control), 25, 50, 100, and 200 µg/ml Aronia extract to a final concentration of 800×10^6 sperm/ml. Diluted semen was cooled at 4 °C for 3 h then frozen in 0.25 ml French straws in a programmable freezer (MiniDigitcool, IMV®, USA). Straws were then plunged into LN₂ for 1 week before being thawed in water bath at 37 °C for 30 sec. Following thawing, sperm motility and kinematics parameters (using CASA), viability (by SYBR14/PI stain), membrane integrity (by hypo-osmotic swelling; HOS test), acrosome status (by FITC-PNA stain), mitochondrial activity (by Rhodamin 123 stain), and lipid peroxidation (using BODIPY 581/591 C11 stain) were evaluated. Data were analyzed by one-way ANOVA using SPSS. Results showed that sperm motility, viability, membrane integrity (HOS+), acrosome integrity, and mitochondria activity were higher ($P < 0.05$) in 100, and 200 µg/ml than 0, and 25 µg/ml Aronia extract supplemented groups. However, the percentages of sperm with lipid peroxidation were lower ($P < 0.05$) 200 µg/ml Aronia extract supplemented group than other ones. In conclusion, supplementing semen extender with Aronia berry extract improved dairy goat sperm motility and viability following cryopreservation. These findings suggest that Aronia extract could be a potential natural antioxidant used to mitigate the damaging effects of freezing and thawing on livestock sperm quality.

Keywords: Goat, Semen, Cryopreservation, ROS, Aronia, Antioxidant, Mitochondria

Analysis of the differences of dermal papilla cells of hair follicles in Liaoning cashmere goats at different developmental stages

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Abstract: Hair follicles are micro-organs located in the skin of animals and are the ' birthplace ' of hair growth and development. The hair follicles of hair animals have periodic conversion characteristics within a biological year. This characteristic is a complex biological process involving multiple cell types and molecular regulatory networks under the regulation of nerves and body fluids. The skin hair follicles of Liaoning cashmere goats have obvious periodic growth and development characteristics in a biological year. Therefore, it is of great theoretical significance to elucidate the mechanism of cashmere growth and development by analyzing the cell composition and fate transformation of hair follicles in different cycle stages. In this study, Liaoning Cashmere Goats were used as the research object, and the skin tissues of the body and side of the Liaoning Cashmere Goats were collected in the flourishing period (November), the degenerative period (March) and the telogen period (May). Through the analysis of the differences between DP cells in the prosperous period, the degenerative period and the resting period, 1,937 differentially expressed genes were obtained in the degenerative period vs the prosperous period comparison group, 985 genes were up-regulated and 952 genes were down-regulated. In the telogen vs telogen comparison group, 2,410 differentially expressed genes were obtained, 1,674 genes were up-regulated and 736 genes were down-regulated ; a total of 1,911 differentially expressed genes were obtained, 1,394 genes were up-regulated and 517 genes were down-regulated. Further, 346 differential genes including *LEF1* and *PCNA* were screened by Wayne analysis. Using the weighted gene co-expression network analysis (WGCNA) method, a total of 16 cell modules were identified and their gene co-expression networks were constructed. The key genes closely related to hair follicle cycle transition were screened by module feature analysis, including *LEF1*, *KRT15*, *KRT14*, *FXRD3*, *SUMO2*, *GJA1*, *CXCL14* and *SFPQ*. The four main cell modules Turquoise module, Blue module, Brown module and Green module were selected for key analysis, and the key candidate genes closely related to hair follicle cycle transition were screened out : *ACTN4*, *SMARCC1*, *GPC6*, *TCF12*, *BNC2*, *HNRNPU*, *LUZP1*, *SFPQ*, *FBNPIL* and *FRMD6* in Turquoise module. *SLC38A2*, *SSBP2*, *TMEM123*, *EXOC6B*, *NFIC*, *NFIX*, *STAG1* in the Blue module

Keywords: Liaoning cashmere goat, Hair follicle, Dermal papilla cells, WGCNA

CDK1 Promotes Proliferation and Mitochondrial Respiratory Function in Goat Placental Trophoblast Cells

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Objective: The placenta is a transient mammalian pregnancy organ mediating maternal-fetal exchange, endocrine regulation and immunomodulation, essential for fetal growth and development. Goats have a cotyledonary placenta, where ruminant-specific cotyledons formed by dense chorionic villi serve as the primary site for maternal-fetal nutrient and gas exchange. Cyclin-dependent kinase 1 (CDK1), encoded by the *CDC2* gene, is a master mitotic regulator that forms a complex with cyclin B1 to drive G2/M phase transition and coordinate mitochondrial respiration. Using Dazu Black Goats as the model, this study aims to elucidate the molecular mechanism of *CDK1* regulating placental cotyledon development via *HSPA8*, providing theoretical support for improving their reproductive performance and lamb quality.

Methods: In this study, we collected postpartum placentas from 95 multiparous ewes, measured placental traits, and performed correlation analysis. Postpartum placentas were also collected from 6 multiparous Dazu Black Goats, from which large cotyledons (diameter > 3 cm) and small cotyledons (diameter < 1 cm) were isolated. Histomorphological examinations (hematoxylin and eosin (H&E) staining, n=6; scanning electron microscopy (SEM) observation, n=2) and energy metabolism indicator detections (cotyledon tissue ATP content and mitochondria-related enzyme activities, all n=3) were performed separately. Meanwhile, transcriptome sequencing was conducted on the two groups of cotyledons (large cotyledons n=3, small cotyledons n=4) to screen for key differentially expressed genes regulating placental development. Using goat placental trophoblast cells as an in vitro model, we performed knockdown and overexpression treatments on the key differentially expressed gene *CDK1* identified through screening, and detected the regulatory effects of altered *CDK1* expression levels on the proliferation and mitochondrial function of placental trophoblast cells. Proteomic sequencing was performed on the *CDK1* overexpression group to screen for the downstream target protein *HSPA8*, followed by co-immunoprecipitation (Co-IP), functional rescue assays and *HSPA8* overexpression validation.

Results: Goat placental cotyledon area is an important factor affecting litter size and birth weight. There are significant differences in capillary density and energy metabolism levels between cotyledons of different sizes, which affect the substance transport efficiency of placental cotyledons. *CDK1* can directly interact with *HSPA8* to regulate the proliferation and energy metabolism of goat placental trophoblast cells, thereby mediating the developmental process of placental cotyledons.

Conclusion: Placental cotyledon area determines goat litter size and birth weight via affecting substance transport efficiency. *CDK1* interacts directly with *HSPA8* to regulate trophoblast proliferation and energy metabolism, mediating placental cotyledon development.

Keywords: *CDK1*, Goat, Trophoblast, Placental Development, Cotyledon

Single-nucleus transcriptomics reveals cellular dynamics and signaling networks orchestrating maternal-fetal interface formation during goat embryo implantation

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Objective: Embryo implantation in ruminants involves a prolonged peri-implantation period and conceptus elongation, yet the cellular and molecular mechanisms governing uterine receptivity and maternal-fetal crosstalk remain poorly understood. Using goats as a model, this study aimed to construct a high-resolution transcriptomic atlas of the endometrium and conceptus during implantation, and to identify key signaling pathways that orchestrate maternal-fetal interface formation.

Methods: Endometrial tissues were collected from pregnant Dazu black goats at pre-implantation (Day 10, n=3) and implantation (Day 17, n=3) stages, and filamentous conceptuses were collected at Day 17. Single-nucleus RNA sequencing (snRNA-seq) was performed using the 10x Genomics platform. Cell types were identified by unsupervised clustering and marker gene annotation. Pseudotime trajectory analysis, ligand-receptor interaction analysis, and functional enrichment analyses were conducted. Immunofluorescence, siRNA-mediated knockdown, RGD peptide blockade, and trophoblast spheroid adhesion, migration and invasion assays were used for validation.

Results: We identified 16 transcriptionally distinct endometrial cell populations, including epithelial, stromal, immune, endothelial, and ciliated cells, with stage-specific remodeling during the transition to receptivity. Within the conceptus, 15 cell subtypes were resolved, including interferon-responsive and MMP7-positive lineages. Pseudotime analysis revealed parallel differentiation trajectories from cytotrophoblasts to syncytiotrophoblasts and specialized invasive subtypes. Ligand-receptor analysis uncovered the LAMC1–ITGAV/ITGB8 axis as a central adhesion pathway at the maternal-fetal interface. Functional assays showed that LAMC1 knockdown or integrin blockade significantly impaired trophoblast spheroid adhesion, migration, and invasion. Furthermore, interferon-stimulated genes (ISGs) were markedly upregulated in receptive-phase endometrial cells, suggesting their roles in immune tolerance and epithelial remodeling.

Discussion: This study provides the first single-nucleus transcriptomic atlas of goat embryo implantation, revealing coordinated cellular dynamics across epithelial, stromal, immune and trophoblast compartments. The LAMC1–ITGAV/ITGB8 axis is identified as a critical molecular bridge that spatiotemporally synchronizes fetal adhesion with maternal epithelial remodeling. Our findings fill a key knowledge gap in ruminant implantation biology and establish a valuable comparative resource for understanding early pregnancy across mammals.

Keywords: Goat, Embryo implantation, Endometrial receptivity, SnRNA-seq, LAMC1-ITGAV/ITGB8

Study on the Technology of Laparoscopic Ovum Pick-Up and InVitro Embryo Production in Chongming Goats

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Abstract: The application of laparoscopic ovum pick-up (LOPU) and in vitro production of embryos (IVEP) technologies has opened up a new path for purebred breeding and breed improvement in goats. However, due to the complexity of the procedures and multiple influencing factors, these technologies have not been widely adopted in goat production. This study explores factors affecting the efficiency of LOPU in goats by comparing the use of controlled internal drug release (CIDR) for estrus synchronization, conventional FSH versus long-acting recombinant ovine FSH (R-FSH) for superovulation, and the timing of LOPU at 48 h, 60 h, and 72 h of follicular development. The metrics evaluated included the recovery rate of cumulus-oocyte complexes (COCs), the average number of ovarian follicles, the average number of COCs, and the average number of available COCs. The results demonstrated that the efficiency of LOPU was significantly higher with two doses of R-FSH compared to the conventional FSH superovulation protocol and the control group ($p < 0.05$) with two doses of R-FSH providing a higher LOPU efficiency than one dose ($p < 0.05$). Using CIDR for estrus synchronization showed no significant difference in LOPU efficiency compared to the non-CIDR group. Similarly, the efficiency of LOPU showed no significant difference between the hormone treatments at 48 h, 60 h, and 72 h. By exploring and optimizing the factors influencing LOPU, we ultimately established a LOPU technology system for goats that meets the production needs of small ruminants.

Keywords: laparoscopic ovum pick-up; cumulus-oocyte complexes; in vitro embryo production; ovarian follicular development

Proteomic profiling reveals the synergistic effects of astaxanthin and melatonin on the inhibition of cryoinjuries in ram sperm

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Abstract: The present study aimed to investigate protective effects of astaxanthin (AST) and melatonin (MLT) on ram sperm quality-associated indicators during cryopreservation, and to explore the molecular effects of the two cryoprotectants on protein profile of the cryopreserved sperm. First, ram sperm were diluted with freezing media supplemented with different concentrations of AST and MLT, and then cryopreserved. The effects of different concentrations of AST and MLT were assessed by evaluating the motility and motile parameters, functional and structural indicators, antioxidant capacity and associated indicators of post-thawed sperm. The concentrations of 50 μ M AST (AST group), 0.5 mM MLT (MLT group), and 50 μ M AST & 0.5 mM MLT (AST.MLT group) were the most effective, as compared to the control (CON group). Furthermore, alteration of sperm proteomic profile among the three comparisons (AST vs. CON, MLT vs. CON, AST.MLT vs. CON) were determined using an Orbitrap Astral coupled with Data-independent acquisition (DIA) proteomic approach. After comprehensive bioinformatics analysis, significant differentially abundant proteins (DAPs) among the three comparisons (32 DAPs in AST vs. CON, 34 DAPs in MLT vs. CON, 116 DAPs in AST.MLT vs. CON) and their enriched molecular pathways were discovered, suggesting that AST and MLT may have synergistic effects on frozen sperm by regulating the abundance changes of proteins. In particular, certain positive proteins like ACAT2, PRDX6, G6PD, HSP90a, HSPA8, HSL, ACTN1, Ezrin, and negative proteins like Cyt c, CTSF, AFU, they were tightly associated with regulation of sperm motility, oxidative stress and other metabolic processes, may serve as novel potential biomarkers for evaluating sperm quality after freeze-thawing. In conclusion, this study provides valuable insights into the protective effects of AST and MLT on ram semen quality, and replenishes information for further clarifying the molecular mechanism based on the modification of sperm proteome during cryopreservation.

Keywords: Sheep, Sperm, Cryoinjury, Astaxanthin, Melatonin, Deep proteome

Based on metabolomics and proteomics to study the effect of *Poria Cocos* Polysaccharide on frozen semen of Dazu black goats

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Objective: The cryopreservation process inevitably inflicts freezing damage and oxidative damage on sperm, impairing the structural and functional integrity of spermatozoa and thereby reducing the conception rate. Owing to the abundance of polyunsaturated fatty acids (PUFAs) in their plasma membranes, goat spermatozoa are particularly vulnerable to oxidative stress. Accordingly, attenuating the level of reactive oxygen species (ROS) in semen and alleviating oxidative stress are pivotal to improving the quality of frozen-thawed goat semen. *Poria cocos* polysaccharide (PCP) exhibits multiple biological activities including immunoregulation, antioxidation and anti-inflammation, and can be employed as a natural antioxidant to protect goat frozen semen. To date, the effects of PCP on semen cryopreservation in ruminants have not been investigated. Here, we investigated the effects of PCP on the cryopreservation of goat semen and elucidated its underlying mechanism using metabolomics and proteomics, providing novel insights for the optimization of frozen semen technology.

Methods: Frozen semen was collected from six Dazu black goats. Different concentrations of PCP (0, 200, 400, 600, 800, and 1000 mg/L) were added to the semen extender. Sperm quality and antioxidant capacity of frozen-thawed sperm were assessed to screen the optimal PCP treatment concentration. Meanwhile, untargeted metabolomics and proteomics were adopted to identify differential metabolites and proteins.

Results: Supplementation with various concentrations of PCP in the cryopreservation extender for goat semen improved the quality and antioxidant capacity of post-thaw sperm. The 400 mg/L PCP group showed significantly higher sperm motility, viability, acrosome integrity, plasma membrane integrity, and activities of superoxide dismutase (SOD) and catalase (CAT) than the control group ($P < 0.05$), along with a significantly lower malondialdehyde (MDA) level ($P < 0.05$). Metabolomic analysis identified 597 differential metabolites including diverse amino acids, glycerophosphocholine and N-acetyl-5-hydroxytryptamine, which were mainly enriched in pathways such as metabolic processes, pantothenate and CoA biosynthesis, C5-branched dibasic acid metabolism and multiple amino acid metabolisms. Meanwhile, proteomic analysis identified 335 differentially expressed proteins including ATP2B3, PFN2 and RAB35, which were predominantly enriched in pathways associated with energy metabolism and fatty acid metabolism. Integrated metabolomic and proteomic analysis revealed 28 shared differential pathways between the two groups, including the phosphatidylinositol signaling system, amino acid metabolism, cholesterol metabolism and apoptosis.

Conclusion: Supplementation with PCP in the freezing extender improved the quality and antioxidant capacity of frozen-thawed goat semen, and the optimal effect was obtained at 400 mg/L PCP. Proteomic and metabolomic analyses demonstrated that PCP significantly enhanced sperm quality and antioxidant capacity by regulating core molecules such as glycerophosphocholine, N-acetyl-5-hydroxytryptamine, ATP2B3 and PFN2, and activating three pivotal pathways: antioxidation, membrane protection and anti-apoptosis. These results provide a theoretical foundation for the industrial application of PCP as a natural cryoprotectant.

Keywords: Goat, Frozen Semen, *Poria Cocos* Polysaccharide, Metabolomics, Proteomics

***CSF1* Positively Regulates Endometrial Function via the P38-MAPK Pathways during Early Pregnancy in Goats (*Capra hircus*)**

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Abstract: Embryo implantation is a complex biological process whose success depends on synchrony between a competent embryo and a receptive endometrium. In this study, we investigated the regulatory role of Colony-Stimulating Factor 1 (CSF1) in modulating endometrial function during early pregnancy in goats. We observed that CSF1 expression was significantly upregulated during early gestation. Functionally, *CSF1* overexpression in goat endometrial epithelial cells (gEECs) markedly enhanced the expression of the epithelial-mesenchymal transition (EMT) markers Vimentin and N-cadherin, as well as in hormone-treated gEECs, *CSF1* affected *RSAD2* but not *ISG15* or *CXCL10*; conversely, *CSF1* silencing attenuated these effects. Transcriptomic analysis implicated the P38-MAPK signaling pathway as a downstream mediator of *CSF1*-induced endometrial receptivity. Mechanistic investigations revealed that *CSF1* treatment increased P38 phosphorylation and partial EMT marker expression. Notably, pharmacological activation of P38 using HY-B1204 rescued the downregulation of N-cadherin induced by *CSF1* silencing, but did not significantly rescue Vimentin. Collectively, these findings demonstrate that *CSF1* is involved in the activation of the P38-MAPK pathway, thereby regulating molecular characteristics associated with endometrial receptivity during early implantation in goats, providing new insights into CSF1-mediated mechanisms in ruminant reproduction.

Keywords: *CSF1*; hormone; goat endometrial epithelial cells; P38-MAPK; endometrial function

Heat Stress Induced Differential Expression of Reproductive Genes and the Modulatory Role of Herbal Supplementation in Indigenous Goats

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Objective: Heat stress is one of the major environmental factors that negatively affects the reproductive performance of livestock, especially in tropical regions. In this study, we examined how heat stress influences the expression of important reproductive function-related genes in the ovarian tissue of Nandidurga goat.

Methods: A total of 24 goats were randomly divided into six experimental groups consisting of control and heat-stressed animals, with or without herbal supplementation, and maintained under controlled environmental conditions throughout the study period. The expression of key reproductive genes, including FSHR, LHR, PGF2 α , Estradiol, PGE2, and COX-2, was analyzed using RT-qPCR in ovarian tissue samples collected at the end of the experiment.

Results: The results showed that heat stress significantly altered the expression pattern of several genes associated with reproductive function. In particular, the reduced expression of LHR and estradiol under heat stress suggests impaired follicular development and disrupted steroidogenesis. On the other hand, COX-2 expression was significantly increased, indicating enhanced inflammatory and cellular stress responses in ovarian tissue. Changes observed in PGF2 α expression may also indicate disturbances in luteal function, while FSHR and PGE2 expression remained relatively unchanged among the groups. Interestingly, goats receiving herbal supplementation during heat stress showed partial recovery in the expression of certain genes related to angiogenesis and antioxidant activity in the ovaries.

Conclusion: Overall, the findings indicate that heat stress interferes with important molecular pathways regulating reproduction, thereby reducing reproductive efficiency in goats. The study also highlights the sensitivity of ovarian function to thermal stress and suggests that herbal nutritional supplementation could serve as a supportive strategy to minimize the adverse effects of heat stress.

Keywords: Indigenous Goats; Ovary; Phytotherapy; Reproduction; Thermotolerance

AI-Enabled 2D-3D Fusion for Automated Body Measurement in Goats

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Objective: Accurate body measurement of goats is essential for genetic evaluation and precision management. However, traditional 3D sensors face challenges from multipath scattering caused by goat hair and significant errors induced by non-standard standing postures in unconstrained environments. We developed a 2D-3D cross-modal fusion framework with an active posture-scoring mechanism to achieve high-precision, non-contact measurement for goats.

Methods: A dual Time-of-Flight (ToF) camera system was constructed to reconstruct full-view 3D point clouds of goats. To bypass the noise from hair, a deep learning network was utilized to detect eight anatomical keypoints in 2D infrared images. These semantic coordinates were then mapped to the 3D space using camera intrinsic parameters, followed by local surface smoothing to enhance precision. Crucially, an AI-based topology model evaluated the goat's skeletal posture in real-time. The system automatically triggered data capture and geometric calculation only when the goat's posture met predefined standard thresholds. Linear parameters (height and length) and curve circumferences (chest girth) were subsequently calculated via Euclidean distance and B-spline integration.

Results: The AI posture-selection mechanism effectively reduced systematic errors by filtering out frames with bowed backs or turned necks. Compared to pure 3D geometric methods, the 2D-3D fusion architecture improved the measurement accuracy of body length and chest girth, achieving a mean relative error (MRE) of less than 3% ($P < 0.01$). The system demonstrated high efficiency, processing 15 frames per second on edge computing hardware.

Conclusion: This study provides a robust solution for goat phenotyping that overcomes the interference of hair and posture. The proposed method supports the digital transformation of the goat industry by providing precise, automated data for breeding and production management.

Keywords: Goat, 3D point cloud, AI posture recognition, Body measurement, Phenotyping

Regularized Canonical Correlation Analysis as the Preference Tool to Evaluate Multidimensional Breeding Linear Traits Underlying Fertility Phenotypes in Murciano-Granadina Does

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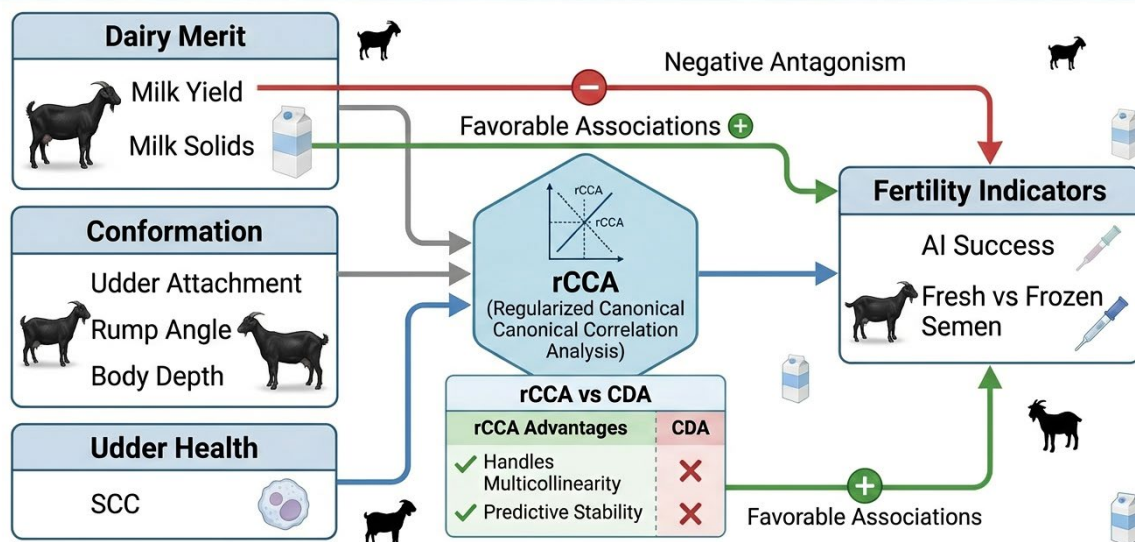
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Abstract: Fertility in dairy goats represents a multidimensional phenomic trait emerging from the interaction between production, morphostructural conformation, udder health, and reproductive physiology. Under these conditions, analytical approaches capable of integrating highly correlated biological dimensions are required to properly characterize the multivariate architecture underlying reproductive performance. The present study evaluated the suitability of Regularized Canonical Correlation Analysis (rCCA) as an integrative framework to investigate the relationships between breeding values for dairy merit and conformation traits with fertility indicators in Murciano-Granadina does, and compared its analytical performance with conventional Canonical Discriminant Analysis (CDA). Data from 21,757 does and 32,693 artificial insemination records collected over a 10-year period were analyzed. Predicted breeding values for milk yield, milk composition, somatic cell count, and 17 linear appraisal traits were jointly evaluated against fertility indicators associated with insemination day, buck batch, and semen type. Regularized canonical correlation analysis identified structured latent covariance dimensions linking fertility performance with production and conformation traits while effectively controlling multicollinearity and overfitting. For linear appraisal traits, the first canonical dimension explained 66.23% of the shared variability with fertility, whereas the first two dimensions jointly accounted for 88.82% of the explained covariance. For milk yield and composition traits, the first and second canonical functions explained 57.14% and 30.03% of the shared variability, respectively, indicating a more multidimensional relationship between dairy merit and reproductive performance. Canonical correlations revealed a biologically relevant antagonism between milk yield breeding values and fertility indicators, while traits related to udder attachment, rump angle, body depth, and milk solids showed favorable associations with reproductive success. Fresh semen consistently outperformed frozen semen across fertility indicators, and buck-specific effects contributed substantially to fertility variation. Ten-fold cross-validation demonstrated high model robustness and predictive stability across the λ_1 – λ_2 regularization parameter space. In linear appraisal models, optimal predictive performance concentrated within intermediate λ_2 values (0.25–0.75), whereas very low λ_2 values generated higher prediction error due to overfitting. In contrast, milk yield and composition traits exhibited stable predictive performance across most regularization combinations, indicating a more homogeneous covariance structure. These findings confirmed that rCCA maintained reliable canonical relationships under high-dimensional and collinear biological conditions. Compared with CDA, rCCA proved superior for evaluating fertility phenomics because it models shared covariance structures between correlated biological trait blocks rather than relying on predefined categorical discrimination. Unlike CDA, which simplifies reproductive variability into discrete classes and is highly sensitive to multicollinearity, rCCA preserved the multidimensional continuity underlying fertility expression while improving biological interpretability and predictive stability. These results support the implementation

of rCCA as a preferable multivariate framework for integrated breeding strategies aimed at balancing productivity, structural functionality, udder health, and reproductive efficiency in Murciano-Granadina goats.

ANALYZING MURCIANO-GRANADINA DAIRY GOAT FERTILITY: A REGULARIZED CANONICAL CORRELATION ANALYSIS (rCCA) APPROACH



Keywords: reproductive efficiency; phenomics; breeding values; morphostructural traits; artificial insemination; reproductive resilience.

Relationships of short photoperiod and male effects with faecal 16S rRNA, metabolomic analysis, serum metabolites, and reproduction performance of dairy goats in non-breeding season

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Abstract: The seasonal oestrus patterns of Saanen dairy goats constrain the year-round continuity of milk supply. This study aimed to investigate the effects of short photoperiod and male effect on oestrus regulation in Xinong Saanen dairy goats in non-breeding season. Eighty healthy female dairy goats aged 2.5–3.5 years were randomly assigned to two groups during the non-breeding season (March to April): a control group (natural long photoperiod) and an experimental group (short photoperiod and male effect methods), with 40 goats per group and 10 goats per pen. In the experimental group, two bucks were additionally housed per pen, separated from the does by partitions. The trial lasted four weeks, and oestrus was monitored subsequently. Faecal and serum samples were collected weekly, and reproductive hormone levels (FSH, LH, E2, P4) were measured on days 7, 14, 21, and 28. On days 0 and 14 and at oestrus (experimental group), serum and faecal samples underwent metabolomic and the feces underwent 16S sequencing analyses, respectively. By integrating gut microbiota, serum metabolomics, and production performance data, the study systematically evaluated the synergistic regulation of dairy goat oestrus by short photoperiod and male effects. Results indicated that short photoperiod treatment combined with the male effect significantly influenced the dynamic changes in serum reproductive hormones, with marked increases in E2 and FSH levels ($p < 0.05$). Faecal microbial 16S rRNA analysis revealed altered microbial community structures at phylum and genus levels in the treatment groups, with the *Bacteroidetes* and *Firmicutes* phyla becoming dominant. β -diversity analysis demonstrated significant differences in microbial composition between groups. Metabolomic analysis suggested that this treatment significantly altered the serum and faecal metabolite profiles. KEGG pathway enrichment analysis indicated that differentially abundant metabolites were primarily associated with reproduction-related pathways, including steroid hormone synthesis and gonadotropin-releasing hormone signalling. Correlation analysis further revealed significant associations between specific bacterial genera and hormones/metabolites, notably a significant positive correlation between *Bifidobacterium* and oestradiol (E2) ($p < 0.001$). In summary, short photoperiod treatment combined with male effect synergistically promotes oestrus in dairy goats by regulating the endocrine system, gut microbiota, and metabolic networks.

Keywords: Xinong Saanen dairy goats, short photoperiod, male effect, faeces, serum metabolites

***STC1* Gene Polymorphism and Its Effect on Ovarian Granulosa Cell Function in Dazu Black Goats**

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Abstract: Stanniocalcin-1 (*STC1*) is a multifunctional glycoprotein involved in various physiological processes, including reproduction, and plays an important regulatory role in ovarian growth and development. However, whether *STC1* can serve as a molecular marker for marker-assisted breeding (MAS) in goats remains unclear. Our previous study found that miR-495-3p can affect the function of goat ovarian granulosa cells. Based on this, the present study used transcriptome sequencing combined with a dual-luciferase reporter assay to confirm that *STC1* is a direct target of miR-495-3p (Figure 1). Functional studies revealed that *STC1* is predominantly expressed in ovarian granulosa cells and promotes granulosa cell proliferation while inhibiting apoptosis. Further Sanger sequencing screening revealed that among the three SNP loci identified in *STC1*, the g.70801961C>T locus was significantly associated with litter size. Moreover, this mutation significantly enhanced the ability of *STC1* to promote cell proliferation and inhibit apoptosis. Overall, these findings indicate that *STC1* promotes cell proliferation and inhibits apoptosis in goat ovarian granulosa cells, and that its g.70801961C>T locus can serve as an effective candidate molecular marker for litter size trait in Dazu black goats.

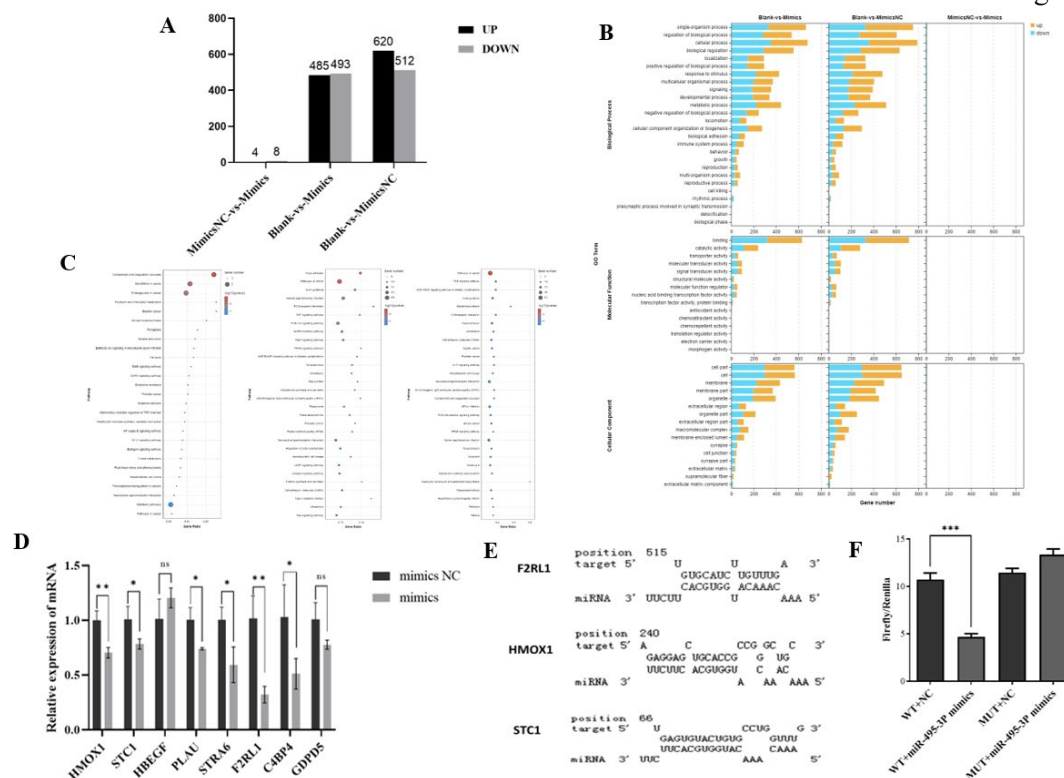


Figure 1 Transcriptome sequencing screening and validation of the key gene *STC1*

Keywords: Goats; granulosa cells; *STC1*; SNPs

Ubiquitination properties of skin tissue in Inner Mongolia cashmere goats based on 4D label-free quantitative ubiquitinomics

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Objective: Post-translational modification by ubiquitination plays an important role in modulating protein stability and various biological activities. Nevertheless, few studies have been performed on how ubiquitination contributes to regulation in the skin of Inner Mongolia cashmere goats and the production of cashmere fiber. In this study, we attempted to determine the ubiquitinome of skin in Inner Mongolia cashmere goats.

Methods: Skin samples were obtained from three cashmere goats of Inner Mongolia and three Boer goats. The ubiquitinated peptides were isolated by employing anti-di-glycine lysine affinity beads and further analysed by using 4D label-free quantitative ubiquitinomics with timsTOF Pro2 mass spectrometry. Differentially ubiquitinated sites were recognized according to the fold change >1.5 or ≤ 0.6667 with a p-value ≤ 0.05 . In addition, motif analysis, functional enrichment, subcellular localization, and protein-protein interaction networks were conducted to explore the biological implications of differential modifications.

Results: In total, 2,734 ubiquitinated proteins, with 8,606 ubiquitination sites, were detected. Among these ubiquitination sites, 160 were differentially expressed in the two groups; there were 10 upregulated and 150 downregulated ubiquitination sites in cashmere goats. Several conserved ubiquitination motifs, such as K....K and KGP.V..., were highly enriched. The main biological functions associated with differentially expressed ubiquitination proteins included keratin intermediate filament formation, cytoskeleton organization, skin barrier formation, cell adhesion, and protein degradation. The interaction network revealed KRT1, KRT5, KRT10, KRT14, VIM, and ACTA1 as major hub proteins.

Conclusion: In this study, the identification of the ubiquitin proteome in cashmere goat skin for the first time indicates that the lower levels of ubiquitination of keratin and cytoskeletal proteins might result in stabilization of these proteins to increase the functions of secondary hair follicles and synthesis of cashmere fibers.

Overview of breeding and reproduction of dairy goats in China

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Abstract: The dairy goat industry in China developed rapidly with the estimated population of more than 10 million heads. Due to the increasing market of goat milk, dairy goat farming has brought considerable profits to farmers in China. At present there are more than 50 famous varieties and breeds of dairy goats in the world, the use of these breeds for pure breeding and crossbreeding in many country and regions had also produced new breeds adapted to local ecological environments. With the progress of modern molecular technology and reproductive technology, the breeding technology of dairy goats has made great progress. Except for traditional breeding methods, advanced breeding methods such as molecular marker assisted selective breeding, genomic selective breeding, nuclear transfer and transgenic technology are widely used. The multiple ovulation and ET (MOET) program combined with ES and AI significantly increase annual genetic progress by decreasing the generation interval. The technique of sexed semen to produce more progeny of the desired sex based on X and Y sperm physical, physiological, and immunological characteristics is a revolutionary technology for goat breeding. Sexed sperm sorting technology greatly reduces farm costs and increases milk production. Moreover, the use of sexed semen increases herd genetic gain compared with use of normal semen. The effects of protein and energy levels on reproduction have been proved, although the exact mechanisms between ovarian function and dietary composition are obscure. Reproduction in goats regarded as seasonal, the estrus is affected by many factors such as photoperiod, breed, and climate, and among which photoperiod is the crucial factor. The reproductive physiology of seasonal reproduction in goats has been extensively studied, especially the pineal gland and the hypothalamus-pituitary-ovarian (HPO) axis involved in the conversion of light signals to reproductive signals, as well as hormone secretion characteristics. In non-breeding season, hormone scheme based on progesterone and eCG is a common method to induce estrus and ovulation. Induction of estrus at different location and time varied with photoperiod, nutrition and buck effect etc.. Although the reproductive performance is not as good in the non-breeding season as in the breeding season, these estrus induction programs are still effective, trying to guarantee milk long-term availability satisfying the year-round market demands. In summary, the overview of dairy goat breeding and reproductive management in China will illustrate the future perspectives of global dairy goat industry.

Keywords: overview, dairy goat, breeding and reproduction, perspectives

Dietary Quercetin Enhances Ovulation and Corpus Luteum Formation in Ewes via Improving Antioxidant Capacity and Follicular Development

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Objective: Improving ovulation efficiency and corpus luteum (CL) formation is essential for enhancing reproductive performance in goat production systems. However, the physiological mechanisms by which dietary phytochemicals regulate ovarian function remain unclear. This study investigated whether dietary quercetin supplementation improves ovarian activity in goats by modulating follicular development, endocrine function, and systemic antioxidant status.

Methods: Sixty healthy ewes were randomly assigned to four groups: control (Con), 2 g/d (Q2), 4 g/d (Q4), and 8 g/d (Q8) quercetin supplementation. Estrus synchronization was performed using progesterone sponges combined with prostaglandin injection. Serum samples and ovarian tissues were collected during the follicular phase. Follicle classification and corpus luteum counts were determined by morphological observation and histological analysis. Serum antioxidant indices, including total superoxide dismutase (T-SOD), malondialdehyde (MDA), glutathione peroxidase (GSH-Px), and total antioxidant capacity (T-AOC), were measured using commercial assay kits. Reproductive hormone levels were also quantified.

Results: Dietary quercetin significantly improved ovarian activity in ewes. Compared with the control group (1.00 ± 0.00 CL), corpus luteum numbers increased significantly in Q2 (2.50 ± 1.22), Q4 (3.50 ± 1.05), and Q8 (3.17 ± 0.75) groups ($P < 0.001$), with the highest ovulatory response observed in Q4. Histological analysis showed increased developing follicles and more active ovarian structures in quercetin-treated groups compared with controls. Serum biochemical analysis indicated improved antioxidant status after quercetin supplementation. MDA levels were significantly reduced, while GSH-Px activity and T-AOC levels were significantly increased ($P < 0.05$). In addition, FSH concentration was significantly elevated in the Q8 group (49.64 ± 8.89 mIU/mL vs. 37.00 ± 4.40 in control, $P < 0.01$), whereas most other reproductive hormones remained stable across groups.

Conclusion: Dietary quercetin supplementation enhances ovulation performance and corpus luteum formation in ewes by promoting follicular development and improving systemic antioxidant capacity, without disrupting overall endocrine homeostasis. These findings suggest that quercetin is a promising natural feed additive for improving reproductive efficiency in production systems.

Keywords: Quercetin, goat, corpus luteum, follicular development, antioxidant status

CRTC2 Promotes Goat Intramuscular Preadipocyte Differentiation and Lipid Metabolism via Interaction with CLTC

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Objective: *CREB-regulated transcription coactivator 2 (CRTC2)* has been implicated in lipid metabolism in several species, yet its role in goat intramuscular preadipocyte differentiation and lipid deposition remains unknown. This study aimed to elucidate the regulatory effects of *CRTC2* on intramuscular adipocyte differentiation and lipid metabolism in goats and to explore the underlying protein interaction mechanism.

Methods: Goat intramuscular preadipocytes were isolated and induced for adipogenic differentiation with oleic acid. A *CRTC2* overexpression plasmid (*OE-CRTC2*) and a *CRTC2*-specific small interfering RNA (*Si-CRTC2*) were transfected into the cells. Lipid droplet accumulation was evaluated by Oil Red O and Bodipy staining, and triglyceride (TG) content was measured. The mRNA and protein levels of adipogenic markers (*C/EBPα*, *C/EBPβ*, *PPARγ*) and lipid metabolism-related genes (*SREBP1*, *FASN*, *ACC*, *AP2*, *DGAT1*, *ATGL*, *LPL*, *HSL*) were detected by real-time quantitative PCR (RT-qPCR) and Western blotting (WB). Immunoprecipitation-mass spectrometry (IP-MS) was performed to identify *CRTC2*-interacting proteins, followed by protein-protein interaction (PPI) network analysis and molecular docking.

Results: Overexpression of *CRTC2* significantly promoted lipid droplet accumulation and increased TG content ($P < 0.05$). It up-regulated the mRNA and protein expression of *C/EBPα* ($P < 0.01$) and enhanced the mRNA levels of lipogenic genes as well as lipolytic genes ($P < 0.01$), while decreasing *ATGL* and *LPL* protein levels. Conversely, *Si-CRTC2* reduced lipid droplet size, down-regulated *C/EBPβ* ($P < 0.01$) and *PPARγ* ($P < 0.05$), suppressed both lipogenic and lipolytic gene mRNA expression ($P < 0.01$), and increased *ATGL* and *LPL* protein content. IP-MS identified 42 proteins specifically interacting with *CRTC2*, and PPI network analysis revealed that clathrin heavy chain 1 (*CLTC*) is a potential interacting partner. Molecular docking confirmed multiple interaction sites between *CRTC2* and *CLTC*.

Conclusion: *CRTC2* promotes goat intramuscular preadipocyte differentiation and lipid metabolism. The interaction between *CRTC2* and *CLTC* may mediate this regulatory process. These findings provide a novel mechanistic insight and a potential target for molecular breeding to improve goat meat quality.

Keywords: Goat; *CRTC2*; Intramuscular preadipocyte; Lipid metabolism; *CLTC*; Adipocyte differentiation

Integrated Single-Cell Transcriptomics and Multi-Omics Analyses Identify EGR1 as a Master Regulator of Androgen Biosynthesis in Goat Theca Cells

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Objective: The ovary is a critical female reproductive organ responsible for producing steroid hormones and mature oocytes, thereby maintaining endocrine homeostasis and female fertility. Among ovarian somatic cells, theca cells (TCs) are the primary source of androgen biosynthesis, which provides essential substrates for estrogen production. However, the molecular mechanisms governing steroidogenesis in ovarian theca cells remain poorly understood.

Methods: Ovarian tissues were collected from Dazu Black Goat individuals with different ovarian reserves for single-cell transcriptome sequencing. GO, GSEA, Monocle3, and SCENIC analyses were performed to screen and identify key regulatory factors involved in ovarian development. Subsequently, primary theca cells from Dazu Black Goat were cultured in vitro and transfected with EGR1 overexpression and knockdown vectors to evaluate androgen synthesis levels in theca cells. Integrated ChIP-seq and RNA-seq analyses were then conducted to identify key target genes transcriptionally regulated by EGR1 that influence androgen synthesis. Finally, Sanger sequencing was used to identify polymorphisms in the EGR1 gene, and association analyses were performed between EGR1 SNPs and kidding number as well as kidding interval.

Results: Single-cell transcriptomic profiling generated a comprehensive cellular atlas of goat ovaries across different ovarian reserve stages and revealed that theca cells were highly enriched for pathways associated with steroid hormone biosynthesis. SCENIC analysis identified EGR1 as a central transcriptional regulator in theca cells. Overexpression and knockdown experiments demonstrated that the EGR1 gene functions as a negative regulator involved in androgen synthesis in theca cells. Integrated ChIP-seq and RNA-seq analyses revealed that EGR1 directly binds to the promoter regions of key steroidogenic genes, including HSD3B, HSD11B1, and HSD17B2, thereby promoting androgen biosynthesis. Furthermore, population genetic analysis showed that the EGR1g.1487C>A polymorphism was significantly associated with reproductive traits in Dazu Black goats.

Conclusion: This study identifies EGR1 as a critical transcriptional regulator of androgen biosynthesis in goat theca cells and provides mechanistic insights into the transcriptional control of ovarian steroidogenesis. These findings provide a theoretical foundation for elucidating the molecular mechanisms underlying reproductive performance in Dazu Black goats and offer valuable insights for future genetic improvement and gene-editing strategies.

Keywords: Goat, Androgen Synthesis, Theca Cells, EGR1.

PART 9: Other Products

Traditional Value-Added Products of the Changthang Pastoralist of Ladakh – A Way Forward

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Abstract: Ladakh, a high-altitude cold desert in northern India, relies heavily on pastoral livestock rearing for livelihood security, cultural identity, and rural economy. Among the most important livestock are Changthangi sheep, Changthangi Cashmere goats and Ladakhi Yaks, which are uniquely adapted to the extreme climate of the Changthang region of Ladakh. These livestock contribute substantially to their income through sale of pashmina/cashmere fiber, wool, milk, meat, hides, and manure. Despite their importance, much of the animal production practices are traditional methods and lacks scientific intervention with low value addition, limiting income potential for pastoral households. The present study highlights the practices and improvement in traditional value-added products derived from Changthangi sheep, Changthangi Cashmere goats and Ladakhi Yaks of Ladakh which include pashmina shawls and accessories, woolen garments, carpets, footwear, dried and smoked meat products, dairy preparations, and leather goods. It also examines the socio-economic role of these products in sustaining nomadic livelihoods, preserving cultural heritage, and supporting food security in remote mountain communities. The paper identifies major constraints like poor infrastructure, limited processing facilities, weak market linkage, lack of modern skills, and youth migration away from pastoralism. To address these challenges, recommendation like strengthening of local processing units, improving quality control and branding, promoting product diversification, building artisan capacity, and supporting sustainable and ethical value chains. Enhancing value addition in sheep and goat products can significantly improve profitability, preserve traditional knowledge, and contribute to inclusive and sustainable development in Ladakh.

Keywords: Ladakh, Changthangi sheep and goats, pashmina, pastoralism, value addition, wool, meat products, dairy products, livelihoods

Melatonin alleviates skin aging and improves cashmere production performance in aged cashmere goats via the gut-skin axis

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Objective: Skin aging impairs barrier function and hair follicle microenvironment, limiting cashmere production in aged goats. The gut-skin axis provides a new perspective. We previously found that exogenous melatonin improves cashmere yield and remodels gut microbiota. This study aims to investigate melatonin's alleviation of skin aging and verify the causal mechanism of gut microbiota via the gut-skin axis.

Methods: Experiment I (Cashmere goat experiment): Six-year-old aged Inner Mongolian cashmere goats were selected and received subcutaneous implantation of slow-release melatonin twice in late April and late June (2 mg/kg each time, releasing for approximately 60 days). Two-year-old goats served as young controls. Back skin, blood, rumen fluid, and feces were collected. Skin tissue structure was examined; antioxidant capacity, inflammatory factors, and matrix metalloproteinase levels were measured in both skin and blood; 16S rRNA sequencing was performed to analyze rumen and gut microbiota; untargeted metabolomics was used to detect metabolites in serum and feces.

Experiment II (Mouse validation experiment): An aging mouse model was induced by daily intraperitoneal injection of D-galactose, with simultaneous melatonin intervention. An antibiotic-treated group was included to deplete the gut microbiota. Additionally, fecal microbiota transplantation (FMT) was conducted: young, naturally aged, and melatonin-treated aged mice served as fecal donors, and their feces were transplanted into young recipient mice via gavage for two consecutive months. Skin tissue structure, as well as antioxidant capacity, inflammatory cytokine levels, and matrix metalloproteinase levels, were assessed in the recipient mice.

Results: Compared with young controls, aged cashmere goats showed significant skin aging: epidermal thickness significantly decreased, dermal collagen fibers were loosely and disorderly arranged, type I/III collagen ratio significantly increased; secondary hair follicle density and cashmere quality decreased. Oxidative stress, inflammatory factors, and matrix metalloproteinase levels in skin and blood were significantly elevated. Melatonin significantly improved all these aging indicators and enhanced cashmere quality. Moreover, melatonin significantly shifted gut microbiota composition of aged goats toward a younger-like profile. Metabolomics showed melatonin reversed aging-associated upregulation of protein and mineral metabolism pathways, shifting metabolic status toward youth. In mice, melatonin significantly ameliorated D-galactose-induced skin aging, but this protection was significantly weakened by antibiotic depletion of gut microbiota. Fecal transplantation from naturally aged mice induced skin aging in young recipients; whereas transplantation from melatonin-treated aged mice did not cause obvious aging, and all indicators remained close to young control levels.

Conclusion: From the perspective of the gut-skin axis, this study demonstrates that exogenous melatonin effectively alleviates skin aging and improves cashmere production performance in aged cashmere goats by enhancing antioxidant and anti-inflammatory capacities, remodeling the gut microbiota structure, and regulating its metabolites. Mouse fecal microbiota transplantation experiments further clarified the role of the gut microbiota in melatonin-mediated alleviation of skin aging, and indicated that the microbiota remodeled by melatonin no longer possesses the ability to induce skin aging.

Keywords: Melatonin, Aged cashmere goats, Skin aging, Gut-skin axis, Gut microbiota

Effects of *Artemisia annua* polysaccharide and different zinc sources on antioxidant capacity, immune function, intestinal tissue morphology and fecal trace element content in cashmere kids goats

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Abstract: The objective of this study was to study the effects of *Artemisia annua* polysaccharide and different zinc sources on the antioxidant capacity, immune function, intestinal tissue morphology and fecal trace element content of cashmere goats. Fifty cashmere goat lambs with similar body weight (16.20 ± 1.24 kg) were randomly divided into five groups, with 10 replicates in each group and 1 sheep in each replicate. The groups were divided into control group (basic diet, group C), T1 group (basic diet + ZnSO₄ 480 mg/piece/d), T2 group (basic diet + Zn-Gly 345 mg/piece/d), T3 group (basic diet + ASKP 3 g/piece/d+ZnSO₄ 480 mg/piece/day), and T4 group (basic diet + ASKP 3 g/piece/d+Zn-Gly 345 mg/piece/day). The test lasted for 75 days, including 15 days for the preliminary test and 60 days for the main test. Compared with group C, the serum CAT activity in the T3 and T4 groups was significantly increased ($P < 0.05$), and the serum levels of IgG and IgM in the T1, T3 and T4 groups were significantly increased ($P < 0.05$). The results of intestinal tissue morphology showed that there were no significant differences in villus height, crypt depth and villus height/crypt depth among the lambs in each group ($P > 0.05$). Compared with group C, the zinc content in the feces of each experimental group was significantly higher ($P < 0.05$), and the zinc content in the stool of the T3 and T4 groups was significantly higher than that of the T1 group ($P < 0.05$). (Conclusion) The mixed addition of ASKP and different zinc sources in the diet could improve the antioxidant capacity, immune function and zinc content in the feces of cashmere goats to varying degrees.

Key words: *Artemisia annua* polysaccharides; zinc source; Lamb; antioxidant capacity; immune function; Morphology of intestinal tissue

Insights into goat milk exosomes: endogenous loading and roles in alleviating colitis

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Abstract: Goat milk exosomes, as promising natural nanocarriers with superior biocompatibility, low immunogenicity and favorable biological stability, have garnered extensive research interest in the fields of functional food innovation and translational biomedicine over recent years. This study systematically characterized the proteomic profile of goat milk-derived exosomes and comprehensively evaluated their potential preventive and therapeutic functions against intestinal inflammatory diseases. First, comparative proteomics was applied to dissect and compare the protein compositions of exosomes isolated from goat milk, dairy goat peripheral plasma, and dairy goat mammary epithelial cells (GMECs). Quantitative analysis indicated that approximately 30% of exosomes circulating in goat milk are derived from GMECs. Importantly, we identified a novel protein-loading motif CLDN4, which can effectively enhance the endogenous cargo loading efficiency of GMEC-derived exosomes prior to their secretion into milk. Second, we investigated the *in vivo* preventive efficacy of goat milk exosomes against dextran sulfate sodium (DSS)-induced chronic colitis. Functional validation revealed that goat milk exosomes significantly attenuate intestinal inflammatory damage, mainly through inhibiting the activation of NF- κ B and Jun signaling pathways, as well as modulating the community structure of gut microbiota and regulating the production of key microbial metabolites. Collectively, this study elucidates the proteomic characteristics and CLDN4-dependent endogenous loading mechanism of goat milk exosomes, demonstrates their great application potential in the intervention of chronic intestinal inflammation, and provides solid theoretical basis and practical guidance for further development and utilization of goat milk exosomes in functional foods and biomedical delivery systems.

Keywords: Exosomes, dairy goat mammary epithelial cells, chronic colitis, fatty liver, functional foods

Multivariate authentication of chevon (*Capra hircus*) against beef, buffalo and chicken using physicochemical, textural and electronic-nose fingerprinting

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Objective: Goat meat (chevon) strengthens food security and smallholder livelihoods in tropical and subtropical systems, aligning with SDGs 2, 8, and 12. The higher price in many markets, creating a persistent incentive for adulteration with cheaper beef, buffalo or chicken meat. Molecular speciation methods are authoritative but resource-intensive. We aimed to test whether a parsimonious multivariate fingerprint built from routine quality, instrumental texture and electronic-nose measurements can authenticate chevon against beef, buffalo meat and chicken with accuracies relevant to food-control practice.

Methods: Longissimus thoracis et lumborum (chevon, beef, buffalo) and pectoralis major (chicken) samples were collected within 24 h post-mortem ($n = 12$ per species; total $N = 48$). Twenty-five variables were measured per sample: ultimate pH, CIE $L^*a^*b^*$ colour, drip and cooking loss, Warner–Bratzler shear force, six texture-profile descriptors (hardness, adhesiveness, springiness, cohesiveness, gumminess, chewiness), proximate composition (moisture, protein, fat, ash; AOAC) and the response of an eight-channel metal-oxide electronic-nose array. Autoscaled data were analysed by one-way ANOVA with Tukey HSD, principal component analysis (PCA), Ward-linkage hierarchical cluster analysis (HCA), linear discriminant analysis (LDA), partial least squares discriminant analysis (PLS-DA) and Random Forest. PLS-DA was validated by $R^2X(\text{cum})$, $R^2Y(\text{cum})$, leave-one-out $Q^2(\text{cum})$, 1000 random permutations of the species label and a CV-ANOVA F-test. Classifier accuracy was estimated by leave-one-out cross-validation.

Results: ANOVA detected significant species effects for all 25 variables ($P < 0.05$). PCA explained 59.9% of total variance in two components; chevon occupied a tight, isolated region of the score space, defined by intermediate redness, low hardness and a distinct E-nose response (Sensor 8; $P = 0.006$) (**Figure 1**). Ward-linkage HCA recovered the four species without misassignment. LDA reached 97.9% leave-one-out accuracy, with chevon classified at 100% sensitivity and specificity. The four-component PLS-DA model gave $R^2X(\text{cum}) = 0.766$, $R^2Y(\text{cum}) = 0.897$ and $Q^2(\text{cum}) = 0.849$; the 1000-permutation empirical p-values for both R^2Y and Q^2 were < 0.001 , and the CV-ANOVA was $P < 0.001$. PLS-DA and Random Forest both achieved 100% leave-one-out accuracy. Variable importance in projection (VIP) scores identified protein, moisture, ash, fat, redness (a^*), springiness and lightness (L^*) as the most informative predictors ($VIP > 1$).

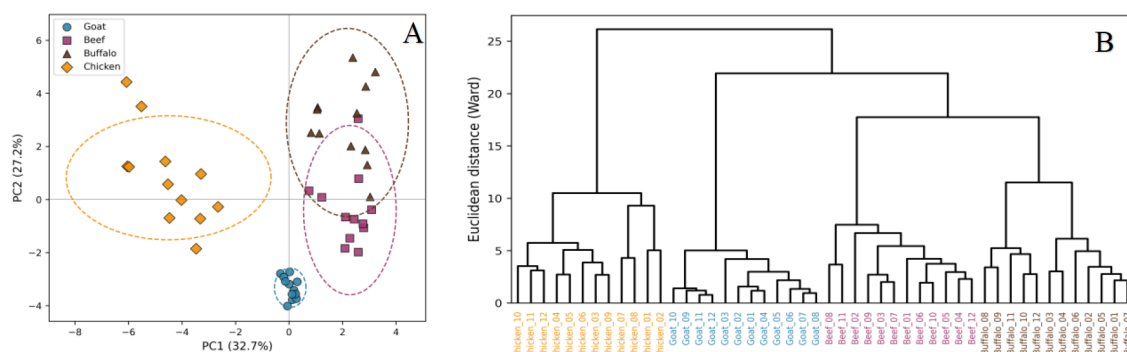


Figure 1. PCA scores plot (A) and Ward-linkage hierarchical-clustering dendrogram (B) of meat samples.

Conclusion: A 25-variable fingerprint comprising routine quality, textural, proximate and odor traits separate chevon from beef, buffalo and chicken at chevon-class sensitivity and specificity of 100%, with a PLS-DA model that is highly significant by both 1000-permutation testing and CV-ANOVA, good-fitted and predictive. The approach is directly implementable in standard meat-quality laboratories as a first-line authentication tool. The approach supports food-fraud prevention and supply-chain traceability.

Keywords: Chevron authentication, Meat quality, Chemometrics, Electronic nose, Goat, Food security