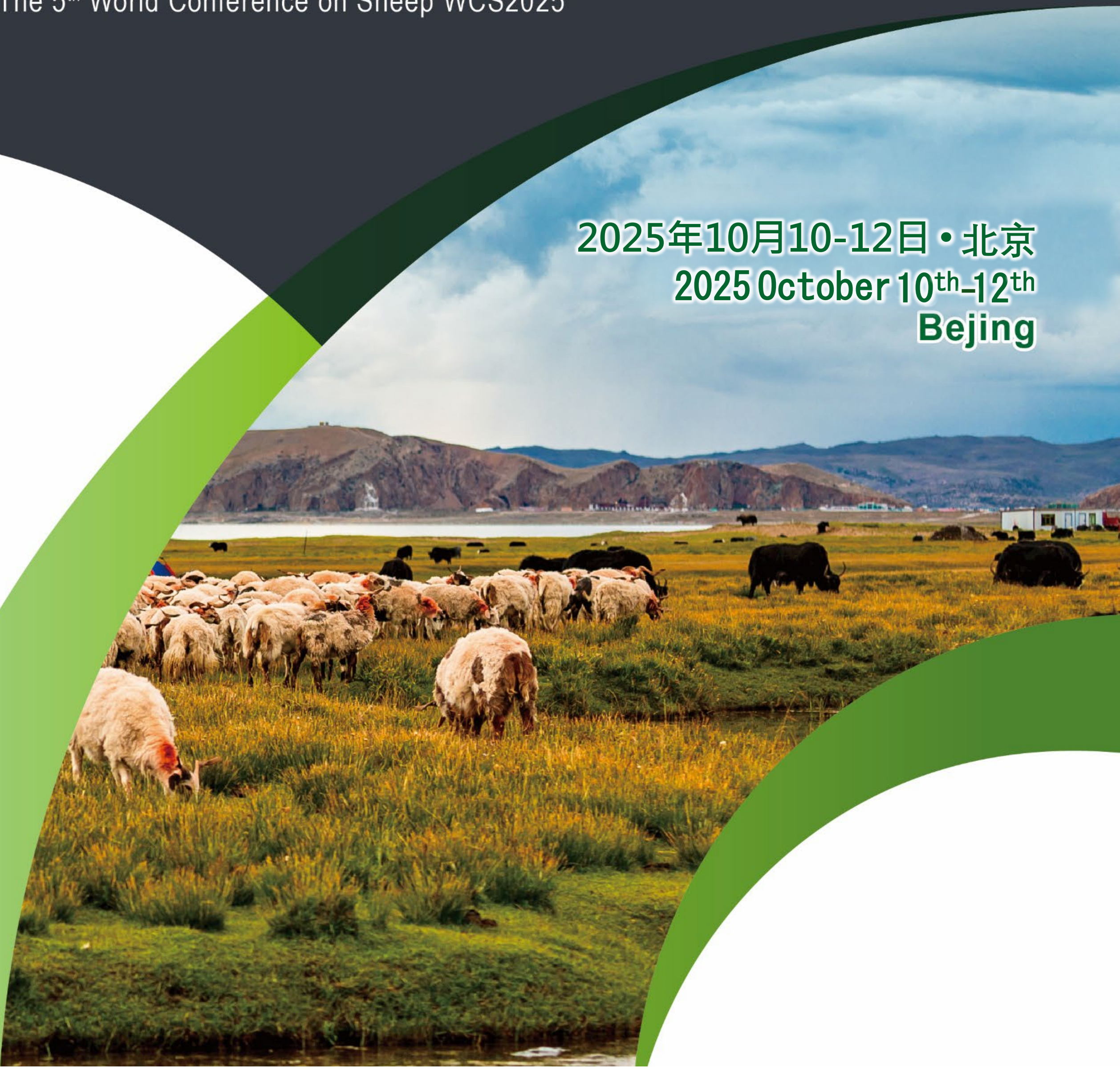
报告摘要

Abstract of the Reports

第五届世界绵羊大会

The 5th World Conference on Sheep WCS2025



2025年10月10-12日 • 北京

2025 October 10th-12th

Bejing

主会场

Meta-analysis of the genomic diversity of sheep

J.A. Lenstra[1], Shannon Clarke[2], Pam Wiener[3], Anne Da Silva[4], Stephen Hall[5] and the Sheep SNP Diversity Consortium
[1]Utrecht Univ, Netherlands; [2]AG Research, New Zealand; [3]Roslin Institute, Edinburgh, UK; [4]Univ. Limoges, France; [5]Estonian Univ. Life Sci., Tartu, Estland

The most common approaches for studying the genomic diversity of individuals or populations are whole-genome sequencing and genotyping of SNPs distributed over the genome on bead arrays. The last approach has the advantage of an even coverage for both alleles of all SNPs. However, most diversity studies have a restricted geographic scope and show only the relationships within a regional or national panel of breeds. We show the added value of a meta-analysis of published 50K SNP genotypes from several different sources. We illustrate this approach for (1) wild sheep species, (2) African sheep, and (3) European sheep.

(1) We present a preliminary comparison of domestic sheep, the feral European mouflons and the wild Asian mouflons, which are the wild ancestors of domestic sheep, with the wild urial and argali sheep. This shows a large diversity of both the Iranian mouflons and the urial, which is at least partially explained by gene flow between these species. We will quantify this per individual and look for interactions between wild and domestic sheep.(2) A meta-dataset for 59 African breeds from 22 different sources allowed in combination with archaeological evidence a reconstruction of the prehistoric immigration of thin-tailed domestic sheep into Africa and the later introductions of fat-tailed sheep. Contrary to current beliefs, fat-tailed sheep were introduced into Egypt only during the Ptolemaic period. (3) Merging 35 published datasets with novel data for 39 British breeds allows a meta-analysis of 215 European breeds. A preliminary phylogenetic network of local breeds indicates clustering and breed relationships across Europe with a high level of breed-level differentiation in North Europe. We also identified English Longwool, English Down or Spanish Merino ancestry of several continental breeds. These and other introgressions will be quantified using the f3 coancestry and the f4 admixture coefficients.

数字绵羊构建与繁殖性状解析
Construction of Digital Sheep and Analysis of Reproductive Traits

刘永斌 研究员，内蒙古农业大学
Prof. Yongbin Liu, Inner Mongolia Agricultural University

绵羊作为全球重要的农业资源与反刍动物模型，其高效育种对畜牧业可持续发展具有战略意义。然而，传统育种模式存在周期长、性状度量效率低、基因与环境互作机制解析困难等瓶颈，严重制约了遗传进展与产业效益的提升。此背景下，绵羊”的数字构建成为推动其科学研究与产业变革的革命性工具。团队通过整合多组学（泛基因组、单细胞转录组、蛋白组、宏基因组）及环境大数据，构建绵羊个体的全方位数字孪生体，实现对复杂经济性状的精准解析与动态预测。具体以“微生物-宿主-性腺轴”为例，了解数字技术在深度挖掘控制关键繁殖性状的遗传位点与调控网络，靶向调控微生物组以精准干预繁殖性能、推动羊育种进入“微生物精准营养”新阶段的重要性。因此，开展数字绵羊构建是突破传统育种瓶颈的必由之路，对提升我国绵羊种业核心竞争力与畜牧业现代化水平具有至关重要的意义。

Sheep, as an important global agricultural resource and a model for ruminant animals, it's efficient breeding is strategic for the sustainable development of animal husbandry. At present, traditional breeding patterns are characterized by the long cycles, low efficiency in trait measurement, and difficulties in parsing the mechanisms between gene and environment interactions. These limitations severely restrict genetic progress and industrial benefits. Therefore, the "digital construction" of sheep has become a revolutionary tool for promoting scientific research and industrial transformation in sheep breeding. Our research team has constructed a comprehensive digital twin of sheep by integrating multi-omics (pan-genome, single-cell transcriptome, proteome, metagenome) and environmental data, consquently, it can improve the precise analysis and dynamic prediction of complex economic traits. Taking the “microbiota-host-gonad axis” as an example, the study highlights the importance of digital technology in deeply exploring genetic loci and regulatory networks that control key reproductive traits, and in targeting the microbiome for precise intervention in reproductive performance. This approach ushers sheep breeding into a new era of “microbiota precision nutrition.” Therefore, the construction of digital sheep is an essential pathway to break through the bottlenecks of traditional breeding. It is of vital importance for enhancing the core competitiveness of China’s sheep breeding industry and advancing the modernization of animal husbandry.

Integration of genomic data into genetic evaluations: an example from the New Zealand Sheep Industry.

Prof. Michael Lee, University of Otago

Breeding values, derived from genetic evaluation, underpin genetic improvement (increased profitability) of most commercial species. New technologies can allow improved predictions from genetic evaluation and hence faster genetic gain. One example of this is the inclusion of genomic data into genetic evaluations allowing more accurate breeding values and earlier selection decisions giving faster genetic gain. In the New Zealand Sheep Industry, since 2018, a transition has been made from pedigree-only best linear unbiased predictions (BLUP) to multi-step genomic evaluations to single step genomic BLUP (ssGBLUP) and to a multi-breed ssGBLUP. This presentation will give a background and overview of this transition.

The SheepGTEx resource for sheep genetics and genomics research

房灵昭 助理教授，奥胡斯大学
Asst.Prof. Lingzhao Fang, Aarhus University

Genetic mutation and drift, coupled with natural and human-mediated selection and migration, have produced a wide variety of genotypes and phenotypes in farmed animals. Characterizing how genomic variants affect genome function to ultimately influence complex traits in farmed animals is essential for the development of sustainable precision agriculture and comparative genomics. Here, as part of the Farm animal Genotype-Tissue Expression (FarmGTEx) project, we present the pilot phase of the SheepGTEx resource through analyzing 6,761 RNA-sequencing samples of 51 primary tissues in a multi-breed population of sheep. We identify millions of regulatory variants associated with seven types of molecular phenotypes, and fine-map 322,467 primary and 113,968 non-primary effects, revealing a high degree of regulatory allelic heterogeneity. We systematically characterize the pleiotropic effects of these variants on molecular phenotypes, assess their context-specific regulatory patterns across tissues, breeds, sexes, and developmental stages, as well as explore their evolutionary constraints across mammals. Finally, we demonstrate the substantial potential of the SheepGTEx resource (https://sheepgtex.farmgtex.org), by providing examples of regulatory mechanisms underpinning complex traits, population divergence between European and Asian breeds, and adaptive evolution in sheep over the past ten millennia.

解析与优化绵羊胃肠道微生物组与功能
Understanding and optimizing gastrointestinal microbiome and function in sheep

王佳堃 教授，浙江大学
Prof. Jiakun Wang, Zhejiang University

绵羊在全球农业中扮演着关键角色，为人类提供肉奶制品。其胃肠道微生物组（尤其是瘤胃微生物组）对消化难分解饲料（如植物细胞壁物质）至关重要。可将饲料分解产生挥发性脂肪酸这一绵羊主要能量来源。瘤胃微生物组还是反刍动物代谢蛋白质（微生物生物质）、必需维生素和氨基酸的主要供给源。此外，胃肠道微生物组可影响绵羊免疫系统、肠道病原菌增殖及消化道健康。近几十年来，科学家在解析和优化绵羊复杂胃肠道微生物组（特别是瘤胃微生物组）功能方面取得重大进展。胃肠道微生物组的早期定植与组装动态过程同时受确定性和随机性因素影响，共同塑造其最终组成、结构与功能。部分胃肠道微生物具有遗传性，表明宿主基因对微生物组存在影响。在断奶前，胃肠道微生物组更具可塑性，此时干预措施效果更显著。日粮补充（如开食料、优质牧草和益生菌）对调控微生物组发育具有潜力。此外，瘤胃微生物移植已成为重构胃肠道微生物组的新型手段，该方法还有助于改善肠道健康、增强免疫力并减少腹泻。总体而言，现有证据表明绵羊多样化且动态变化的胃肠道微生物组通过与宿主和日粮的多维度互动，对其营养吸收、生产性能、肉奶品质、健康状况及甲烷排放产生深远影响。

Sheep play a vital role in global agriculture, supplying meat and milk for human consumption. The sheep gastrointestinal (GI) microbiome, particularly the rumen microbiome, is crucial for digesting otherwise indigestible feed (i.e. plant cell wall materials), producing volatile fatty acids (VFAs), which are the primary source of energy for sheep. The rumen microbiome is also the primary source of metabolizable protein (microbial biomass), essential vitamins, and amino acids of ruminants. Moreover, the GI microbiome can influence the sheep’s immune system, proliferation of enteric pathogens, and GI health. In recent decades, scientists have made substantial progress in understanding and optimizing the intricate GI microbiome and its functions, particularly the rumen microbiome of sheep. The dynamic processes of early colonization and assembly of the GI microbiome are influenced by both deterministic and stochastic forces, which collectively shape its eventual composition, structure, and functionality. Some GI microbes demonstrate heritability, suggesting a genetic influence from the hosts on their GI microbiome. Before weaning, the GI microbiome is more amenable to interventions, making early interventions more effective. Dietary supplementation, such as starter feeds, high-quality forage, and probiotics, holds some potential in shaping the GI microbiome development. Furthermore, rumen microbiome transplantation has emerged as a promising approach for reprogramming GI microbiome assembly. This method also has the potential to improve gut health, strengthen immune systems, and reduce diarrhea. Overall, the evolving evidence suggests that sheep's diverse and dynamic GI microbiome interacts in many ways with hosts and diets, playing a vital role in influencing sheep nutrition, productivity, quality of meat and milk, health, and CH4 emissions.

Ancient Sheep of the North Europe: Genomic and Isotopic Insights

Prof. Juha Kantanen, Natural Resources Institute Finland, 31600 Jokioinen, Finland (ORCID 0000-0001-6350-6373)

Sheep have played a central role in Northern European subsistence economies since their introduction during the Neolithic period. In this review presentation, genomic and isotopic evidence is integrated to explore the long-term continuity and adaptation of sheep populations in the region. Whole-genome sequencing (up to 11.6X) of five ancient sheep from the Baltic islands of Gotland and Åland, dating from ~4100 calBP to ~1600 CE, reveals strong genetic affinities with modern North European short-tailed breeds. These findings suggest a remarkable degree of genetic continuity over millennia, although a decline in genetic diversity in recent centuries points to bottlenecks associated with modern breed formation.

Complementing the genomic data, stable isotope analysis ($\delta^{13}C$ and $\delta^{15}N$) of 43 archaeological sheep and cattle remains from Finland and northern Fennoscandia (c. 200 - 3 700 years old archaeological bones) provides insights into changing feeding practices. The results indicate a gradual increase in forest-based fodder use over time. The isotopic variation reflects not only environmental and cultural shifts but also physiological and sampling factors beyond what is recorded in historical sources.

Together, these multidisciplinary findings illuminate the deep history of sheep in Northern Europe, highlighting both the resilience and transformation of their genetic and dietary landscapes over long periods of prehistorical and historical time.

分论坛1

11日下午

家畜环境适应性与体型性状遗传调控机制
Genetic Regulatory Mechanisms of Environmental Adaptation and Body Size Traits in Livestock

蒋琳 研究员，中国农业科学院北京畜牧兽医研究所
Prof. Lin Jiang, Institute of Animal Science of CAAS

中国是全球畜禽种质资源最丰富的国家，拥有1090个畜禽遗传资源，多样性优势尤为显著，其中抗逆性与体型性状最为突出，而这两类性状恰恰是家畜育种的主要目标性状。研究聚焦家畜低氧适应性与体型发育两大关键科学问题，充分发挥我国地方家畜资源的独特禀赋，以群体基因组学为核心切入点，系统整合分子进化学、古DNA学、细胞生物学等多学科技术方法，揭示了藏区家畜耐低氧性状的生理生化基础及遗传调控机制，解析了家畜体高、体长率、体组成等体型性状的主效基因和形成机制，为家畜抗逆性和体型的育种改良提供了理论基础。

China has one of the world’s richest livestock and poultry genetic reservoirs, with 1,090 documented resources underscoring its remarkable diversity. Among these, traits related to stress resistance and body size—key targets in livestock breeding—are especially pronounced in local breeds. This study focuses on two fundamental scientific questions: hypoxic adaptation and the genetic basis of body size development in livestock. Building on the unique advantages of local genetic resources, we employed population genomics as the key technique, complemented by multidisciplinary approaches from evolutionary biology, ancient DNA analysis, and cell biology. We systematically elucidate the physiological and genetic regulatory mechanisms underlying hypoxic adaptation in Tibetan livestock, and identify key genes and developmental pathways shaping body size traits such as stature, body proportions, and composition. These findings provide a solid theoretical foundation for enhancing stress resistance and body conformation in livestock breeding.

绵羊多组织表观遗传调控图谱绘制及应用
Mapping and application of multi-tissue epigenetic regulation atlas in sheep

张德印 博士后，兰州大学
Dr. Deyin Zhang, Lanzhou University

表观遗传调控图谱是解析复杂性状遗传调控机制和鉴定功能突变位点的基础底盘图谱和基因组功能导航图谱。但目前仍缺乏对绵羊基因组功能元件的系统注释。在本研究中，生成了9种代表性的92个转录组和表观基因组数据集，以及来自全球29个品种的2357个个体的全基因组数据，和尾脂重性状相关的4006条表型数据。基于功能元件、染色质状态及其功能等绘制出绵羊多组织表观遗传调控图谱，对绵羊基因组进行了系统注释，共鉴定出753723个功能元件，包括846058个开放染色质区域、40606个潜在启动子和158677个潜在增强子，其中60%以上为首次发现。同时探讨了功能元件在解释绵羊驯化和改良过程中表型变异方面的作用，发现与感知能力和免疫反应相关的组织特异性启动子和增强子在受驯化影响的基因组区域中高度富集，而背最长肌组织特异性活性增强子和尾脂组织特异性活性启动子在受选育影响的基因组区域中高度富集。此外，基于多维组学数据，鉴定出影响绵羊尾脂沉积的关键基因（BMP2）及因果变异（Chr13:51760995 A > C）。综上，本研究通过多组学数据集的整合为未来研究绵羊复杂性状提供了基础资源和成功案例。

Epigenetic regulation atlas serves as the fundamental chassis atlas and the genomic function navigation atlas for deciphering the genetic regulatory mechanisms of important complex traits and identifying functional mutation sites. However,yet systematic functional annotation of the sheep genome is lacking. Here, we generated 92 transcriptomic and epigenomic datasets from nine major tissues, along with whole-genome data from 2357 individuals across 29 breeds worldwide, and 4006 phenotypic data related to tail fat weight. We constructed the first multi-tissue epigenome atlas in terms of functional elements, chromatin states and their functions. A total of 753,723 non-redundant functional elements, including 846,058 open chromatin regions, 40,606 potential promoters and 158,677 potential enhancers, with over 60% being novel. Meanwhile, the explored the utility of the functional elements in interpreting phenotypic variation during sheep domestication and improvement. It was found that tissue-specific promoters and enhancers related to sensory abilities and immune response that were highly enriched in genomic regions influenced by domestication, while longissimus dorsi tissue-specific active enhancers and tail fat tissue-specific active promoters were highly enriched in genomic regions influenced by breeding and improvement. In addition, based on multi-dimensional omics data, the key gene (BMP2) and causal variation (Chr13:51760995 A > C) that affect the tail fat deposition in sheep were identified. Overall, this research provides foundational resources and a successful case for future investigations of complex traits in sheep through the integration of multi-omics datasets.

基于多组学探究绵羊对F17 大肠杆菌抗性的遗传调控机制

Multi-omics Investigations for Genetic Mechanism underlying E. coli F17 Susceptibility of Sheep

陈炜昊 博士后，扬州大学
Dr. Weihao Chen, Yangzhou University

羔羊腹泻病是绵羊饲养生产过程中最为常见的问题，F17大肠杆菌（E.coli F17）则是导致羔羊腹泻病的主要病原菌之一，其在世界各地广泛传播且呈现较高的检出率、致死率和耐药性特征。前期研究发现，湖羊品种内部存在F17大肠杆菌易感和拮抗两种类型个体，且二者在转录表达模式和基因组结构上存在显著差异，因此，从遗传角度解析绵羊对F17大肠杆菌的抗性机制，可能是解决绵羊F17大肠杆菌腹泻病的最优解。本研究利用多组学联合分析结合机器学习算法，构建F17大肠杆菌易感/拮抗个体遗传调控中肠道菌群、代谢物、宿主转录表达间的互作网络，并围绕互作网络中的关键lncRNA——DRB1-AS1开展了一系列体外验证实验，明确了DRB1-AS1通过miR-3957-5p/TFF2/CXCR4轴影响绵羊对F17大肠杆菌抗性的具体分子调控机制，为绵羊腹泻病的防治和抗病育种工作提供新的理论依据。

Lamb diarrhea is a common problem in large-scale sheep farms and causes serious economic losses for the sheep industry. Epidemiological surveys have shown that E. coli F17 is one of the major pathogens causing lamb diarrhea and characterized with high morbidity and mortality in farm lambs globally. Besides, the high prevalence of antibiotic resistance in E. coli F17 provides a renewed sense of urgency for E. coli F17 infection, which also indicated that it’s an effective solution to enhance the host E. coli F17 susceptibility from a genetic basis. In our previous study, we found that individuals with different E. coli F17 susceptibility exist in Hu sheep breed, and the in-depth research indicated that certain genetic variations may be the underlying reason for the difference resistance of the E. coli F17 susceptibility. In the present study, we systematically elucidate the regulatory mechanism of E. coli F17 susceptibility of sheep from the perspective of the gut microbiota-metabolite-host transcriptome interaction based on multi-omics data and machine learning approach. Based on which, we revealed a ceRNA regulatory network of DRB1-AS1, which can enhance the E. coli F17 susceptibility via the miR-3957-5p/TFF2/CXCR4 axis in sheep intestinal epithelial cells and mice. Our present study can contribute to the basic understandings of the prevention and control of sheep diarrhea, and provide necessary theoretical references for sheep breeding.

军垦肉羊新品种培育与繁殖性状的遗传解析
Genetic Analysis of Breeding and Reproductive Traits in a New Variety of Junken Mutton Sheep in China

杨华 研究员，新疆农垦科学院
Prof. Hua Yang, Xinjiang Academy of Agricultural and Reclamation Sciences

绵羊是世界范围内分布广泛的重要家畜，既为人类提供肉食也产羊毛。绵羊品种的培育始于亚洲绵羊被引入欧洲之后，主要在西欧和西南亚地区发展。过去十年中国成功培育出多个绵羊新品种，如鲁西黑头羊、华蒙肉羊、天华肉羊以及军垦肉羊新品种。其中军垦肉羊以萨福克羊为父本，湖羊和阿勒泰羊为母本，以体重、生长速度和繁殖率为核心选育指标，通过三元杂交、BLUP育种值评估、多胎基因标记辅助选择等现代育种技术构建三级育种体系，历经杂交创新、横交固定和选育提高三个阶段，历时24年于2025年成功培育。该品种初情期为5-6月龄，经产母羊产羔率达202.90%。公羊和母羊断奶重分别为30.98 kg和27.74 kg，周岁体重达79.4 kg和62.86 kg，成年体重分别为118.68 kg和69.00 kg。12月龄公羊和母羊屠宰率分别为59.00%和58.00%。育种和生产实践证明该品种具有体型大、生长快、肉用性能好、繁殖率高、遗传稳定等优点，适应新疆寒冷干旱地区的放牧、半舍饲及舍饲等多种养殖模式。进一步通过全基因组重测序获得20×有效测序深度，采用FST和H方法分析军垦肉羊、萨福克羊和湖羊的基因组多样性、群体结构及选择信号。结果显示获得5,236.338G高质量基因组数据及28,767,952个SNP位点。鉴定出99个覆盖候选基因的选择信号，其中23个基因与繁殖、生长、免疫和代谢相关的通路及GO条目显著关联。发现ARHGEF4、CATIP、CCDC115等主要基因，以及mTOR信号通路、黑色素生成、Hippo信号通路等关键通路与繁殖性状显著相关。这些结果为理解军垦肉羊的人工选择进化及新品种繁殖性状的候选基因提供了重要依据。

Sheep are an important livestock species distributes throughout the world, providing both meat and wool for human consumption. Sheep breed development took place in the Western Europe and Southwest Asia after import of sheep from Asia to Europe. Many new sheep breeds have been bred in in China in the past decade, such as Luxi Black Head sheep, Huameng mutton sheep, Tianhua mutton sheep and a new variety of Junken mutton sheep, which were successfully cultivated through grading hybridization by using Suffolk sheep as the paternal line and Hu sheep and Altay sheep as maternal lines, with body weight, growth rate, and reproductive efficiency as core selection criteria, a three-level breeding system was established through modern breeding techniques including three-way crossbreeding, BLUP breeding value estimation, and marker-assisted selection for fecundity genes. Over 24 years, spanning three phases-hybrid innovation, crossbreeding stabilization, and breeding improvement. A new meat sheep breed, "Junken Mutton Sheep", was successfully developed in 2025. The Junken Mutton Sheep breed exhibits a puberty onset at 5-6 months of age and a lambing rate of 202.90% in multiparous ewes. Weaning weights for rams and ewes are 30.98 kg and 27.74 kg, respectively, with yearling weights reaching 79.4 kg for rams and 62.86 kg for ewes. Adult weights attain 118.68 kg for rams and 69.00 kg for ewes. The dressing percentage at 12 months of age is 59.00% for rams and 58.00% for ewes. Breeding and production practice have proven that this breed is characterized by large body size, rapid growth, excellent meat performance, high reproductive efficiency, and genetic stability. It demonstrates strong adaptability to various farming systems in Xinjiang's cold and arid regions, including grazing, semi-intensive, and intensive management models.Furthermore, the effective sequencing depth of 20× were carried out by whole-genome re-sequencing, the genomic diversity and population structure, and selection signatures were investigated in Junken Mutton Sheep, Suffolk sheep and Hu sheep by FST and H methods. The results revealed 5,236.338G high-quality genome data and 28,767,952 SNPs of Junken Mutton Sheep were obtained. Moreover, 99 selection signals spanning candidate genes were identified, 23 genes were significantly associated with pathways and GO terms related to reproduction, growth, immunity and metabolism. ARHGEF4, CATIP and CCDC115, etc. major genes, and mTOR signaling pathway, melanogenesis, Hippo signaling and other key signaling pathways were significantly correlated with reproductive traits. These results provided understanding of artificial selection evolution of Junken Mutton Sheep and candidate genes of reproduction in new sheep breeding.

Signatures of selection and copy number variants (CNVs) in genomes of native Russian sheep breeds

Dr. Nikolay Yudin, Institute of Cytology and Genetics, Siberian Branch of the Russian Academy of Sciences

Domestication and selective breeding have changed genomes of sheep breeds to respond to environmental challenges and human needs. The genomes of local breeds are valuable sources of genomic variants to be used in selection programs. We identified signatures of selection and CNVs in the genomes of native Russian sheep breeds using a high-density genotyping. Then resequencing data for Tuva, Baikal, Altai Mountain and Buryat breeds was used for localization of genes and genetic variants related to environmental adaptation and economically important traits. More than 50% of the regions under putative selection in whole dataset matched with intervals identified in previous scans for selective sweeps in sheep genomes. These regions contain candidate genes related to morphology, domestication, wool traits, environmental adaptation etc. We identified genes associated with high-altitude adaptation, thermal perception, fat storage, body size etc. in putatively selected regions in the Altai Mountain breed, and genes related to body size, coat colour, fat-tail phenotype, polledness etc. in the Buryat breed using resequencing data. High-frequency missense mutations on top of selection peaks were found in genes related to immunity in the Baikal breed and wool traits, cell differentiation and fat deposition in the Tuva breed. Genes found under selection owing to haplotype frequency changes were related to wool traits, parasite resistance, insulin receptor pathway and DNA repair in the Baikal breed, and vision in the Tuva breed. We characterized the signatures of selection and CNV makeup in genomes of local sheep breeds from the Russia and found a lot of candidate genes and genetic variants that could have a role in local adaptation and contribute to economically important traits. This work forms a basis for developing highly productive sheep breeds, better suited to diverse Eurasian environments.

Sheep Genomics in Kazakhstan: SNP-Based Insights into Diversity, Inbreeding, and Trait-Associated Genes

Dr. Kairat Dossybayev, Kazakh, Scientific Research Institute of Animal Husbandry and Forage Production, Kazakhstan

Sheep breeding is a key sector of livestock production in Kazakhstan, where fat-tailed coarse-wool breeds such as Kazakh, Edilbay, Hissar, and Saryarka sheep are highly valued for their adaptability to harsh environments, early maturity, and production of high-quality meat, fat, and wool. Despite their economic and cultural importance, the genomic diversity and evolutionary background of these breeds remain insufficiently characterized.

In a series of genome-wide studies, we applied medium- to high-density SNP genotyping (OvineSNP50 BeadChip) to more than 1,000 sheep representing major Kazakh breeds to investigate their genetic diversity, population structure, inbreeding levels, and candidate genes associated with economically important traits. Principal component analysis, population structure analysis, and phylogenetic inference revealed a clear differentiation among local breeds and demonstrated that Edilbay sheep, in particular, possess high genetic diversity and form a distinct genetic cluster. Evidence of historical gene flow was detected among populations, emphasizing their shared evolutionary history and genetic connections to ancient domestic sheep lineages.

Runs of homozygosity (ROH) analysis across the genome identified over 41,000 ROH segments, predominantly short (1-4 Mb), providing insights into demographic history and recent inbreeding. A strong correlation between FROH and FGRM confirmed the reliability of ROH-based approaches. Regions with high ROH density revealed signatures of selection associated with muscle development, wool characteristics, fat metabolism, and reproductive traits. Notable candidate genes included *MYF5, PRDM16, TGM3, SLC26A4, SMAD5, BMP2, BMPR2, CLOCK, and KDM2B.* Additionally, genome-wide association studies (GWAS) identified several loci linked to body conformation traits such as live weight, chest width, and cannon bone circumference. Genes including *VCAN, IGFBP6, ST7, DTNBP1, SCD5, KYNU, FGF12*, and *FTO* were associated with growth, body size, and fat deposition, providing potential molecular markers for marker-assisted selection (MAS).

Collectively, these results represent the first comprehensive genomic characterization of native Kazakh sheep breeds. They highlight their unique genetic resources, reveal key genomic regions underlying productivity traits, and provide essential tools for breeding, conservation, and genomic selection programs. This research lays the foundation for future advances in sustainable sheep production and contributes to our understanding of sheep domestication and genetic evolution in Central Asia.

绵羊图结构泛基因组与全变异插补参考面板的构建
Development and Construction of a Sheep Graph Pangenome and a Comprehensive Variant Imputation Reference Panel

姜雨 教授，西北农林科技大学
Prof. Yu Jiang, Northwest A&F University

Sheep (Ovis aries) are among the earliest domesticated livestock species, and China has a long history of sheep farming, with sheep production playing a significant role in the agricultural economy. To further advance the sheep breeding industry, it is essential to construct a comprehensive map of genetic variation in sheep to elucidate functional variants underlying important economic traits. Although numerous genomic studies in sheep have been published, the majority have focused on single nucleotide variants (SNVs) and short insertions/deletions (indels; 1–49 bp) detected relative to a single linear reference genome—variants that are readily identifiable using high-throughput short-read DNA sequencing (next-generation sequencing). In contrast, larger-scale structural variations (SVs) have been less studied due to limitations in detection methods and higher costs. Recent advances in long-read DNA sequencing technologies (third-generation sequencing), particularly PacBio HiFi sequencing, have now made it feasible to construct accurate genome-wide SV maps. Our study fully utilized the 61 third-generation HiFi sequencing datasets, as well as 4,718 second-generation population-scale high-depth genomic datasets of major breeds spanning Asia, the Middle East, Europe, and Africa, which accumulated by the research group and from public databases. A total of 255,861 high-quality SVs suitable for genotyping were identified. Moreover, a sheep graph-based pangenome covering major breeds worldwide and a comprehensive variant imputation reference panel were constructed. The panel includes 59.08 million SNPs, 7.82 million Indels, and 182,041 SVs. Using this reference panel, we will impute missing genotypes in larger populations with low-coverage whole-genome sequencing data, thereby estimating the frequency and distribution of each variant across populations. By integrating multi-dimensional data including complex phenotypic records and transcriptomic profiles, we will further perform expression quantitative trait locus (eQTL) analyses to uncover variant-gene regulatory relationships. This will enable the establishment of functional links between multi-type genetic variations and gene expression, ultimately contributing to a better understanding of the genetic mechanisms underlying important traits in sheep.

绵羊单细胞表达图谱构建及其应用
Construction and Applications of Sheep Single-Cell Expression Atlas

储明星 研究员，中国农业科学院北京畜牧兽医研究所
Prof. Mingxing Chu, Institute of Animal Science of CAAS

测序技术与算法快速发展使解析细胞层面关键基因与通路的调控机制、阐明绵羊复杂性状分子基础成为可能。本研究整合了自有小尾寒羊胚胎期（16种组织）和成年期（40种组织）的单细胞转录组数据，以及公共数据库中湖羊数据（8种组织），每种组织至少两个生物学重复，构建了覆盖绵羊42种组织（包括消化、生殖、神经等系统）的单细胞图谱。共捕获146万个细胞，鉴定出129种细胞类型，归属于7个主要谱系。揭示了细胞通讯、基因表达模式及调控网络的动态变化在组织内和组织间的细胞异质性，发现绵羊与人类基因表达特征高度保守。通过整合普通转录组数据推断了细胞类型组成比例，鉴定出ieGenes。本成果为解析绵羊复杂性状的遗传机制提供了重要资源与理论依据。

Rapid advancements in sequencing technologies and computational algorithms have enabled precise dissection of key genes and pathway regulations at cellular resolution, facilitating the elucidation of molecular mechanisms underlying complex traits in sheep. In this study, we integrated single-cell transcriptome data from in-house Small Tail Han sheep at embryonic (16 tissues) and adult stages (40 tissues), supplemented with public data from Hu sheep (8 tissues), with at least two biological replicates for each tissue, to construct a comprehensive single-cell atlas encompassing 42 tissue types (including digestive, reproductive, neural, and other systems) in sheep. Our analysis captured 1.46 million cells and identified 129 distinct cell types categorized into 7 major lineages. This research uncovered cellular heterogeneity of dynamic variations in cell communications, gene expression patterns, and regulatory networks within and between tissues. This research demonstrated high evolutionary conservation of gene expression features between sheep and human. Through integration of bulk RNA-seq data, we inferred cell-type composition proportions and identified ieGenes. These findings provide critical resources and a theoretical foundation for deciphering the genetic mechanisms governing complex traits in sheep.

绵羊多胎性状的机制解析研究
Molecular Mechanisms of Prolificacy Traits in Sheep: Research Insights and Application Prospects

张艳丽 教授，南京农业大学
Prof. Yanli Zhang, Nanjing Agricultural University

繁殖效率，尤其是多胎性状，是决定绵羊产业经济效益的核心要素。本报告旨在系统综述绵羊多胎性状的分子遗传调控机制，重点阐述已知主效基因及其相关信号通路在调控卵巢功能与排卵率中的作用，并介绍基于基因组学、转录组学等高通量技术新近发现的候选基因及调控网络。此外，报告还将探讨表观遗传调控机制以及营养与环境因素对多胎性状的影响。最后，将讨论如何将上述基础研究成果应用于分子标记辅助选择及基因组育种，以加速高繁殖力绵羊新品种（系）的选育进程，为推动绵羊产业的可持续发展提供理论支持与技术路径。

Report Abstract: Reproductive efficiency, particularly prolificacy, is a critical determinant of economic returns in the sheep industry. This report systematically reviews the molecular genetic regulatory mechanisms underlying prolificacy traits in sheep, with a focus on the roles of known major genes and their associated signaling pathways in regulating ovarian function and ovulation rate. It also highlights candidate genes and regulatory networks recently identified through high-throughput technologies such as genomics and transcriptomics. Furthermore, the report discusses the influence of epigenetic regulation as well as nutritional and environmental factors on prolificacy. Finally, it explores the application of these foundational research findings in molecular marker-assisted selection and genomic breeding programs, aiming to accelerate the development of new sheep breeds or lines with high reproductive performance and to provide scientific support and technical pathways for the sustainable development of the global sheep industry.

分论坛2

11日下午

Effect of Zilpaterol Hydrochloride in Egyptian Fat-Tailed Sheep Differing in Breed Type

Asst.Prof. Mahmoud M Abdelsattar, South Valley University

β-adrenergic agonists such as zilpaterol hydrochloride (ZH) are widely used to redirect nutrients toward muscle accretion, yet breed-specific responses in fat-tailed sheep remain poorly quantified. Differences in muscle and adipose composition in Egyptian local breeds could result in different responses to ZH. We hypothesized that Ossimi (heavy, high-fat) and Barki (light, lean) lambs would exhibit divergent tissue repartitioning when fed 0, 0.10 or 0.15 mg ZH kg^{-1} BW for 30 days. Sixty intact males (10 mo) were individually fed a concentrate: wheat-straw (80:20) diet. Data on growth, blood metabolites, carcass traits and meat quality were analyzed as 2 × 3 factorial. ZH linearly increased ADG and improved feed conversion, but the magnitude was greater in Barki. Dressing percentage rose in Barki yet fell in Ossimi at the high dose, reflecting a reduction in shoulder, flank, ribs, and longissimus muscle of Ossimi but increases in Barki. Conversely, kidney fat and omental fat declined in Barki while increased in Ossimi. Meat pH and protein content increased linearly with ZH, whereas shear force dropped, indicating improved tenderness. Hematologically, ZH raised hemoglobin, hematocrit, red blood cells, and neutrophils. Plasma total protein, insulin-like growth factor 1, triiodothyronine, and thyroxine, and glucose were elevated, while cholesterol and triglycerides decreased. Results demonstrate that ZH efficacy is breed-dependent with lean-type Barki lambs channel extra energy into muscle and maintain low visceral fat than Ossimi lambs. These findings provide decision-making tools for precision dosing of β-agonists in diverse fat-tailed breeds, maximizing carcass value while maintaing quality carcasses.

中国羊肉量质协同提升研究进展
Research Progress on the Coordinated Improvement of Quality and Quantity of Sheep & Goats Meat in China

罗海玲 教授，中国农业大学
Prof. Hailing Luo , China Agricultural University

中国一直是全球羊肉产量最大的国家，从 2013 年的 408 万吨增加到 2024 年的 518 万吨，同时羊肉的质量也发生了变化。在中国，羊肉生产有三种饲养方式，包括放牧、限制放牧加补饲以及舍饲。不同饲养方式导致了产量和肉质的变化，特别是肉质的改变，例如羔羊肉中肌内脂肪沉积增加，特别是ω-6 多不饱和脂肪酸含量过高，而ω-3 多不饱和脂肪酸含量过低。一般来说，当羔羊从放牧牧场转为集中饲养并投喂精饲料时，其肉中的ω-6 与ω-3 脂肪酸的比例会从 1 增加到 20。我们证明，对于断奶的滩羊，限制放牧时间分别为 0 小时、2 小时、4 小时、8 小时和 12 小时，其ω-6/ω-3 比值逐渐降低，分别为 20.23、9.74、6.18、4.99 和 4.28；而对于断奶的乌珠穆沁羊，其数值分别为 5.75、3.8、3.67、3.94、3.45 和 1.26，这是因为它们在不同牧场摄入的草种类不同。然而，尽管采食相同的饲料，湖羊肌肉中的ω-6/ω-3 比值显著低于滩羊和杜波羊。羔羊的脂肪酸组成可以通过营养调控得到改善，在饲料中添加维生素 E 可以减少肉的滴水损失，降低硬脂酸和与"羊肉气味"相关的支链脂肪酸的含量，同时提高肌肉中 CLA 和不饱和脂肪酸的含量。在饲料中添加不同类型油脂对羔羊肉中的脂肪酸有显著影响。大豆油和菜籽油将ω-6/ω-3 比例从 9.59 提高到 14.23，而鱼油则将该比例显著降低至 1.70。添加苜蓿皂苷可将 ω-6/ω-3 比例从 6.45 降低到 5.60。舍饲海南黑山羊的日粮中添加假蒟提取物提高了肉中具有增香作用的化合物的含量，包括与鲜味相关的氨基酸（如谷氨酸）以及中链脂肪酸，同时减少了海南黑山羊饲料中具有促氧化作用的 n-6 多不饱和脂肪酸。上调了与果香/蜡质风味相关的长链酯类，下调了与青草/草本风味相关的醛类和醇类。

总之，改变放牧方式为舍饲对肉质特别是脂肪酸组成产生了不利影响。然而，通过放牧+补饲、或者全舍饲中使用不同的添加剂可以改善这种不利影响以达到养羊生产的量质协同提升。

China has been the world's largest producer in mutton from 4.08 million ton in 2013 to 5.18 million ton in 2024, meanwhile the quality has been changed. There are three kinds of feeding methods for mutton production including grazing, restricted grazing time plus supplementary feeding and house-feeding in China. The different feeding methods led to the variations in yield and meat quality, with a particular emphasis on the changes in meat quality, such as intramuscular fat deposits increasing in lamb meat, specifically over-rich in ω-6 polyunsaturated fatty acids but low in ω-3 polyunsaturated fatty acids. Generally, the ratio of ω-6 to ω-3 fatty acids in meat increases from 1 to 20 when lambs are switched from a grazing pasture to house-feeding with concentrate. We proved that the ω-6/ω-3 ratio with restricted grazing time of 0 hr, 2 hr, 4 hr, 8 hr and 12 hr was decreasing gradually with 20.23, 9.74, 6.18, 4.99 and 4.28 for the weaned male Tan lambs, and with 5.75, 3.8, 3.67, 3.94, 3.45 and1.26 in the weaned male Ujumuqin lambs, since the different kinds of grass were intake in different pasture between them. However, the ω-6/ω-3 ratio in the muscle of Hu sheep was significantly lower than that of Tan sheep and Duper sheep by feeding the same diet.The fatty acid composition of lamb can be improved by feed additives. The addition of vitamin E to the diet reduce the drip loss of meat and the content of stearic acid and branched-chain fatty acids related to the "mutton odor", but improve the content of CLA and unsaturated fatty acids in muscle. Feeding different types of oil in diet had a significant effect on the fatty acids in lamb meat. The soybean oil and canola oil increased the ω-6/ω-3 ratio from 9.59 to 14.23, but fish oil decreased the ratio to 1.70 significantly. The addition of alfalfa saponins, a compound that regulates lipid metabolism, reduced the ω-6/ω-3 ratio from 6.45 to 5.60. Piper sarmentosum enhanced the accumulation of flavor-enhancing compounds, including umami-related amino acids (e.g., glutamic acid) and medium-chain fatty acids, while reducing pro-oxidative n-6 PUFAs in meat of Hainan Black Goat which house feeding. Notably, it upregulated long-chain esters associated with fruity/waxy notes and downregulated aldehydes and alcohols linked to green/herbal notes.

In summary, there has been an adverse effect on the composition change of fatty acids in lamb meat by changing grazing system to housing feeding.

However, this adverse effect can be improved by either grazing regime plus concentrate feeding or house feeding by different additives to achieve the coordinated improvement of both quantity and quality in sheep farming production.

玉米加工方式调控山羊和绵羊瘤胃发酵及有效能的营养生理学机理
Corn Processing Methods Modulate Rumen Fermentation Dynamics and Energy Utilization by Host-Microbiome Metabolic Cross-talk in Goats and Sheep

曹阳春 教授，西北农林科技大学
Prof. Yangchun Cao, Northwest A&F University

反刍动物胃肠道不同部位对淀粉的消化和利用效率不同。谷物的加工方法会影响其在反刍动物消化道的降解位置，从而影响反刍动物对谷物能量的利用效率。整粒玉米提高奶山羊对淀粉、NDF、ADF和CP的表观消化率，显著降低粪能、热增耗和总产热量，因而显著提高DE、ME和NE。网瓣胃孔对食糜尺寸的选择性通过效应是玉米加工方式调控瘤胃代谢的关键生理机制。整粒玉米由于粒径较大难以通过奶山羊网瓣胃孔，而滞留在瘤网胃中通过反刍、咀嚼逐步释放淀粉，有利于瘤胃内环境的稳定。这一发现明晰了瘤胃是奶山羊高效利用整粒玉米的核心调控位点。在整粒玉米日粮中添加RP-Leu或RP-Amy未能改善奶山羊淀粉和能量利用效率。整粒玉米主要在瘤胃中被缓慢降解，到达小肠淀粉较少，增加小肠淀粉酶无法发挥作用。整粒玉米通过淀粉在瘤胃中的逐步释放，改善山羊瘤胃微生物区系，增加碳水化合物与氨基酸代谢水平实现瘤胃能氮高效利用，并增强瘤胃上皮吸收功能，降低炎症反应。

The digestive and utilization efficiency of starch varies in different parts of the gastrointestinal tract of ruminants. The processing methods of grains will affect the degradation location of grains in ruminants, thereby influencing the utilization efficiency of grain energy by ruminants. Over the past decades, our research group conducted a lot of studies to explore the effects of corn processing methods on the production performance and nutrient metabolism of goats and sheep. Overall, whole corn has a positive effect on the production performance of goats and sheep compared to ground corn. Whole corn grain diet increases the apparent digestibility of starch, NDF, ADF, and CP in dairy goats, and significantly improves DE, ME, and NE values of diet and corn grain, because of the decreased fecal energy loss, heat increasement and total heat production. The selective function of the reticulo-omasal orifice on chyme particle size is crucial for the ruminal degradation of corn with different particle sizes. Whole corn grain prolongs starch degradation time in the rumen, optimizes ruminal fermentation patterns, maintains the stability of rumen environment, and reduces fecal energy losses and heat increment, thereby improving ME and NE of diet and corn grain. Supplementing RP-Leu and RP-Amy in whole corn diets did not significantly improve starch digestibility and energy utilization efficiency in dairy goats. Whole corn, likely due to its large particle size, might be difficult to pass through the reticulo-omasal orifice into the small intestine, suggesting that the small intestine is not the primary site for efficient utilization of whole corn grain, and measures of stimulating amylase activity in small intestine can not increase starch digestibility in dairy goats. Feeding the diet with whole corn grain to goats could gradually release starch in the rumen, improve the rumen microbial community, increase the metabolism levels of carbohydrates and amino acids, enhance the absorption function of the rumen epithelium while reducing inflammatory.

羔羊瘤胃发育及营养调控
Rumen development and nutritional regulation in lambs

刘军花 教授，南京农业大学
Prof. Junhua Liu, Nanjing Agricultural University

研究利用起源江浙太湖流域的谱系清晰的湖羊为主要研究对象，建立了系统的"日粮营养—瘤胃微生物代谢—瘤胃上皮生理—动物健康生长"的研究思路和方法体系，阐明了瘤胃上皮发育的细胞学基础，创建了可模拟瘤胃上皮复杂形态和功能的类器官模型，发现了瘤胃上皮发育不良的细胞调控机制及关键驱动因子；鉴定出瘤胃假长双歧杆菌衍生的吲哚三甲醛和白色念珠菌衍生的前列腺素D2，发现了其促进瘤胃上皮及肌层发育的差异化作用和靶点；阐释了瘤胃稳态失衡及重塑的微生物学机制，提出靶向营养调控新策略。相关研究结果为解密瘤胃黑匣子及实现肉羊高效健康养殖提供了重要理论依据。

The Hu sheep, a breed with a well-documented pedigree originating from the Taihu Lake region of Jiangsu and Zhejiang, was selected as the primary research subject. A systematic research approach and methodology were established, encompassing the following areas: "dietary nutrition, rumen microbial metabolism, rumen epithelial physiology, animal health and growth." The work elucidated the cytological basis of rumen epithelial development, created an organoid model capable of simulating the complex morphology and function of rumen epithelium, and identified cellular regulatory mechanisms and key drivers underlying rumen epithelial dysplasia. The present study identified indole-3-carboxaldehyde, a metabolite derived from Bifidobacterium pseudolongum, and prostaglandin D2, a hormone produced by Candida albicans. These findings elucidate the differential roles and targets of these compounds in promoting the development of the rumen's epithelial and muscular layers. The present study elucidated the microbiological mechanisms underlying rumen homeostasis disruption and remodeling, and proposed novel strategies for targeted nutritional regulation. The findings of the present study provide crucial theoretical foundations for deciphering the rumen black box and achieving efficient, healthy sheep farming.

育肥绵羊适应高淀粉日粮机制研究
Adaptation Mechanism of Fattening Sheep to High-Starch Diets

李飞 教授，兰州大学
Prof. Fei Li, Lanzhou University

饲喂高谷物饲粮是提高反刍动物生产性能的有效手段，但由于有效纤维含量不足通常易引发亚急性瘤胃酸中毒（subacute rumen acidosis，SARA）等代谢性疾病，进而损害瘤胃功能。但生产中发现，长期饲喂高淀粉或高谷物日粮并不会对育肥绵羊造成负面影响，这表明绵羊在采食高淀粉日粮过程生理状态存在适应，本研究在对绵羊饲喂不同时长（0天、21天、42天和63天））高淀粉日粮，研究其对动物生产性能、养分消化及瘤胃微生物影响，揭示绵羊适应高淀粉日粮的机制，结果表明随着高淀粉日粮饲喂时间延长，育肥绵羊生长性能提高、养分消化率改善，瘤胃中Ruminococcaceae bacterium R-25和Ruminococcus albus等纤维降解菌相对丰度线性增加，瘤胃微生物结构和功能重塑以实现对高淀粉饲粮的逐渐适应。

Feeding high-grain diets is an effective approach to improving the production performance of ruminants. However, due to the insufficient content of effective fiber, such diets often lead to metabolic disorders such as subacute rumen acidosis (SARA), thereby impairing rumen function. Interestingly, in production practice, long-term feeding of high-starch or high-grain diets does not cause adverse effects in fattening sheep, indicating that sheep exhibit physiological adaptation when consuming high-starch diets. In this study, sheep were fed high-starch diets for different durations (0, 21, 42, and 63 days) to investigate the effects on growth performance, nutrient digestibility, and rumen microbiota, thereby elucidating the adaptive mechanisms of sheep to high-starch diets. The results showed that, with prolonged feeding of high-starch diets, fattening sheep exhibited improved growth performance and nutrient digestibility. Moreover, the relative abundance of fiber-degrading bacteria such as *Ruminococcaceae* bacterium R-25 and *Ruminococcus* albus increased linearly, and the rumen microbial structure and function were remodeled to gradually adapt to the high-starch diet.

绵羊全组织转录组数据库构建与肌肉组织间品质差异研究
Construction of the whole-tissue transcriptome database and exploration of quality differences among muscle tissues in sheep

王梦芝 教授，扬州大学
Prof. Mengzhi Wang, Yangzhou University

本研究首先整合了包括绵羊等7个物种、每个物种个体105个组织样品总计1642条自测序转录组数据及28710条公共转录组数据，构建了首个大规模设计性的草食动物全组织转录组数据库，为绵羊生物学性状差异调控通路分析提供了平台。而后检测了湖羊13个部位肌肉品质，发现理化性质及组织学性状在组织间均有显著差异，据表型对基因和代谢物关联分析，发现主要通过调控脂质代谢、能量供应等通路影响嫩度、脂肪沉积及风味。继而对4个部位肌肉的转录组比较，发现了富集于脂质代谢和氧化磷酸化等通路的，如*AMPK*，3,340个差异基因。并筛选了*CIDEC*、*FABP4*、*PLIN1*、*BDH1*等脂质调控关键基因，如*CIDEC*可能与周脂素和PPARγ等相互作用来调控脂质代谢与沉积，为提升肉品质提供了针对性的指导。

This study integrated 1,642 self-sequenced and 28,710 public transcriptomes from seven sheep species to construct the first large-scale, multi-tissue transcriptome database for herbivores, providing a platform for analyzing key regulatory pathways underlying biological traits. Analysis of thirteen anatomical regions of Hu sheep revealed significant differences in meat physicochemical properties and histological characteristics. Correlation and multi-omics analyses indicated that tenderness, fat deposition, and flavor were primarily influenced by lipid metabolism and energy supply pathways. Transcriptome comparison of four muscle regions identified 3,340 differentially expressed genes (DEGs), enriched in processes like muscle development, lipid metabolism, and oxidative phosphorylation. *AMPK* ensures energy homeostasis, directly influencing intramuscular fat deposition, lipid composition, and overall meat quality. Key candidate genes influencing lipid synthesis *included CIDEC, FABP4, PLIN1, BDH1.* Notably, *CIDEC* regulates energy balance by inhibiting lipolysis and promoting lipid deposition. It interacts with proteins such as perilipin and PPARγ, which control fat metabolism and storage. These findings offer valuable insights for targeted nutritional strategies to enhance meat quality in sheep.

膨化油菜秸秆替代花生秧对育肥羔羊生长、营养物质消化率、能量代谢、微生物粗蛋白合成、肉氨基酸及脂肪酸组成的影响

Effect of replacing peanut vine with extruded rape straw on growth, nutrient digestibility, energy metabolism, microbial crude protein synthesis, meat amino acid and fatty acid profiles of finishing lambs

马涛 研究员，中国农业科学院饲料研究所
Prof. Tao Ma, Institute of Feed Research of CAAS

膨化饲料是一种提高饲料适口性和消化率的工艺。本试验旨在研究膨化油菜秸秆替代花生秧这一常用的粗饲料原料对育肥羔羊生长性能、表观营养物质消化率、能量代谢、微生物粗蛋白（MCP）合成以及背最长肌（LT）氨基酸和脂肪酸组成的影响。试验选用24只2月龄、体重相近的湖羊公羔，分别以花生蔓（CON，n=12）和挤压油菜秸秆（TRT，n=12）作为唯一粗饲料来源。试验持续120天，包括30天的适应期，正试期每30天进行称重，第81-90天期间进行消化率试验。试验结束时屠宰采集瘤胃液和肉样。除粗脂肪表观消化率在TRT组更高（$P = 0.008$）外，两组间生长性能、营养物质表观消化率或能量利用效率均无差异，此外，TRT组羔羊的MCP（$P = 0.072$）有升高的趋势。两组羔羊LT样品中大多数氨基酸和脂肪酸的浓度没有差异，而TRT组羔羊LT样品中蛋氨酸（$P = 0.044$）的浓度升高，肉豆蔻酸（C14：1）（$P = 0.010$）、十七碳烯酸（C17：1）（$P < 0.001$）、反式亚油酸（C18：2n6t）（$P = 0.003$）和γ-亚麻酸（C18：3n6）（$P < 0.001$）浓度降低。综上，膨化油菜秸秆可以有效替代羔羊日粮中的花生秧，而不会损害羔羊健康或对营养的利用效率。

关键词：膨化油菜秸秆；花生秧；羔羊；生长；氨基酸；脂肪酸

Extrusion is a process to improve the palatability and digestibility of the feed. Here, we investigated the effects of replacing peanut vine with extruded rape straw on growth performance, apparent nutrient digestibility, energy metabolism, microbial crude protein (MCP) synthesis, and amino acid and fatty acid profiles in the longissimus thoracic (LT) of finishing lambs. Twenty-four 2-month-old male Hu lambs of similar body weight (19.5 ± 1.0 kg) were fed two diets containing either peanut vine (CON, n = 12) or extruded rape straw (TRT, n = 12) as the only roughage source. The experiment lasted 120 days, including a 30-day adaptation period. Lambs were weighed every 30 d. Digestibility trial was conducted during the 81-90 days of the experiment. At the end of the experiments, lambs were slaughtered for ruminal fluid and meat sample collection. No difference in growth performance, apparent digestibility of nutrients, or energy utilization efficiency was observed, except for the apparent digestibility of ether extract, which was greater ($P = 0.008$) for lambs in the TRT group. In addition, the MCP estimated using urinary purine derivatives ($P = 0.072$) tended to be greater in the lambs of the TRT group. The concentration of most amino acids and fatty acids was not different in the LT sample of two groups of lambs, while the concentration of Met ($P = 0.044$) was greater, and that of myristoleic acid (C14:1) ($P = 0.010$), heptadecenoic acid (C17:1) ($P < 0.001$), trans-linoleic acid (C18:2n6t) ($P = 0.003$) and gamma-linolenic acid (C18:3n6) ($P < 0.001$) were lower in the LT sample of lambs from TRT group. In conclusion, extruded rape straw can effectively replace peanut vine in the diet of lambs without compromising health or nutrient utilization.

Keywords: Extruded rape straw; peanut vine; lamb; growth; amino acid; fatty acid

Comparative Genomic Insights into Tail Length and Abnormalities in Pigs and Sheep

Prof. Xuying Zhang, Justus Liebig University Giessen

Long tails in pigs and sheep are associated with tail biting and increased susceptibility to flystrike, respectively. Tail docking has been widely used to mitigate these issues but increasingly conflicts with animal welfare regulations, highlighting the need for sustainable breeding strategies targeting tail length (TL) and abnormalities (TA). We investigated the genetic basis of tail traits using whole-genome sequencing (WGS)- based genome-wide association studies (GWAS) and comparative genomic analyses (CGA) in experimentallyselected populations of pigs and sheep. TL was measured at birth, and TA was assessed radiographically at 14 weeks. GWAS identified a significant locus in pigs and suggestive loci for TL in both species. The genomic windows of the significant locus on SSC18 in pigs and TL GWAS locus on OAR4 in sheep were found to be conserved, harboring six common genes with predicted functional variants. Additionally, eight species-specific putative functional candidate genes for TL were identified on OAR11, OAR21, and OAR23 in sheep, and five species-specific candidate genes on SSC1, SSC10, and SSC16 in pigs. For tail abnormalities, no conserved genomic windows were detected across species; five candidate genes were identified on OAR6, OAR14 and OAR25 in sheep, and three on SSC2 in pigs. Gene ontology and pathway analyses predicted shared biological processes and carbohydrate metabolism, as well as species-specific immune and inflammatory signaling, and pig-specific TGF-β signaling and endochondral ossification. These findings provide insight into the genetic mechanisms governing tail morphogenesis and perinatal tail development and suggest potential targets for selective breeding strategies to improve animal welfare while reducing the need for tail docking.

Multi-Modal Predictive Framework for Animal Health

Prof. Jie Kang, Sydney Univeristy

Animal diseases pose major challenges to productivity, animal welfare, and biosecurity across livestock industries. Traditional diagnostic approaches often rely on a single data source, limiting early detection and timely decision-making. We propose a multi-modal predictive framework that integrates diverse streams of information, including genomic data, sensor and imaging outputs, clinical records, and environmental variables, into a unified predictive model. By leveraging advanced statistical learning and machine learning methods, the framework captures complementary signals across data modalities to improve accuracy, robustness, and timeliness of disease prediction. Case studies demonstrate the framework’s ability to predict disease before clinical signs appear, identify which animals are at higher or lower risk, and identify key predictive biomarkers. Importantly, the modular design allows adaptation to specific production systems and diseases of interest, while supporting real-time monitoring and decision support for producers, veterinarians, and policymakers. This work highlights the potential of integrative, data-driven solutions to transform animal health management, reduce economic losses, and enhance sustainable production.

新型基因编辑底盘工具的研发与绵羊生物育种
Development of Novel Gene-Editing Chassis Tools and Their Application in Sheep Biobreeding

胡文萍 副研究员，中国农业科学院北京畜牧兽医研究所
Assoc. Prof. Wenping Hu, Institute of Animal Science of CAAS

International biobreeding technology has fully entered the era of molecular and whole-genome breeding, and is quickly moving forward into the era of gene-editing breeding. Gene editing stands as a leading technology in global biobreeding, relies on highly efficient editors that fit the core biological chassis of livestock and poultry—these editors are not only the basis of biological breeding, but also one of the key "bottleneck technologies" that restrict its development. Focusing on the main needs of livestock and poultry biological breeding, our team has developed new and original chassis gene editors, and created new germplasm in sheep by using multi-gene and multi-trait aggregated editing. We used bioinformatics and evolutionary genomics analysis to screen four new Cas12a and TnpB editors, and tested their editing efficiency in mammalian cells; the results showed this efficiency is similar to that of the well-known LbCas12a and ISDra2-TnpB, which initially proves the practical value of these new and original chassis editing tools. Additionally, we have established an efficient somatic cell nuclear transfer platform for sheep, optimized in vitro oocyte maturation methods, and significantly improved oocyte quality and cloning efficiency. Furthermore, we have optimized the multi-gene editing strategies, and created the world's first 3-gene-edited cloned sheep. This provides high-quality resources for sheep genetic improvement and empowers the industrialization of livestock biobreeding.

Technology for increasing the productivity of meat sheep

Dr. Madrahimov Shodlik, Samarkand State Veterinary Medicine Livestock and Biotechnology University

The study presents data on the live weight and meat productivity of first-generation (F1) crossbred lambs obtained from crossing Jaidari breed ewes with Hisar breed lambs, which is a scientific basis for increasing the meat productivity of tailed sheep breeds in the natural and climatic conditions of the Republic of Karakalpakstan. It was established that at the age of 18 months, the second-group (purebred Hissar) and third-group (Hissar x Jaidar) lambs of the first generation (F1) surpassed their peers of the first group (purebred Jaidar) in live weight by 6.0 kg or 9.2% ($P<0.001$) and 4.4 kg or 6.7% ($P<0.01$) respectively. This indicates the high genetic potential of these animals in the formation of live weight and meat productivity, as well as their good adaptability to the external environment and the high potential of breeding rams.

As well as on the main absolute and relative indicators of slaughter results. Group II (pure Hissar breed) and Group III (½ Hissar x ½ Jaidar) crossbred first-generation (F1) rams compared to their peers in group I (pure Jaidar breed) respectively by 15.6 kg or 33.5% ($P<0.001$) and 5.6 kg or 12.0% ($P<0.01$), uncooled carcass weight by 9.4 kg or 47.7% ($P<0.001$) and 5.2 kg or 26.4% ($P<0.01$), slaughter weight by 13.5 kg or 59.5% ($P<0.001$) and 6.8 kg or 29.9% ($P<0.01$), and slaughter yield in rams by 48.8; 58.3 and 56.7%, respectively, which is 9.5 and 7.9% higher than the peers of the I group (pure Jaidari).

Thus, based on the scientific basis for increasing the meat productivity of tailed sheep breeds in the natural and climatic conditions of the Republic of Karakalpakstan, the first-generation (F1) crossbred lambs obtained as a result of crossing purebred Hissar and Jaidar sheep with Hissar sheep showed high live weight and meat productivity indicators, which testifies to the high genetic potential of feeding them with complete and rationed feeds in pasture conditions.

分论坛1

12日上午

糖基化酶介导的碱基编辑器的开发及其在绵羊分子育种中的应用
Development of glycosylase-mediated base editors and their application in sheep molecular breeding

魏迎辉 教授，西北农林科技大大学
Prof. Yinghui Wei, Northwest A&F University

Developing glycosylase-based base editors (gBEs) to broaden the editing scope is highly desirable for biomedical research and agricultural applications. However, the off-target effects and applicability of gBEs need further investigation. We employ GOTI to detect rare DNA off-target events in mouse embryos injected with N-methylpurine glycosylase-based AYBE and gGBE. Transcriptome-wide RNA analysis reveals that TadA8e-V106W, derived from AYBE, induces low-frequency RNA off-target editing. Both base editors efficiently induce A/G-to-Y editing in mouse and sheep embryos, and in newborn lambs. The robust efficiency and specificity of AYBE and gGBE underscore their potential for clinical applications and genetic improvement in livestock.

从杂合子优势角度看地方绵羊品种多羔性状的选育
Genetic improvement of fecundity traits in indigenous sheep breeds: leveraging heterozygote advantage

方超，曹行，马海玉，刘玲玲，陈秋明，刘武军 新疆农业大学动物科学学院 中国 新疆 乌鲁木齐 830052
Cao Fang, Hang Cao, Haiyu Ma, Lingling Liu, Qiuming Chen, Wujun Liu College of Animal Science, Xinjiang Agricultural University, Urumqi 830052, Xinjiang, China

缺乏多羔性能，其遗传机制尚不明确。本研究以多浪羊为对象，收集147只产单羔和150只产双羔个体的全基因组重测序数据，分析发现双羔组的核苷酸多样性和观测杂合度显著低于单羔组。通过全基因组关联分析，共鉴定到18个加性数量性状位点（QTL）和27个显性QTL，其中3个QTL同时表现出加性与显性效应。基因功能注释表明，BMP5和MTNR1B等与生殖调控相关的基因可能在产羔数调控中发挥重要作用，且相关关键位点的基因型已通过桑格测序验证。在显性效应QTL中，部分位点表现为杂合子优势，部分则为杂合子劣势。结合团队前期研究及已有文献，推测杂合子效应的复杂性可能是导致地方品种多羔性能缺失的原因之一。本研究为多浪羊及其他地方品种在多羔性状选育方面提供了理论依据。

Litter size is a key economic trait in sheep, yet the genetic mechanisms underlying the limited multi-lambing capacity of many indigenous breeds remain poorly understood. Focusing on Duolang sheep, this study sequenced whole-genome sequences from 147 single-lamb and 150 twin-lamb individuals. We found significantly lower nucleotide diversity and observed heterozygosity in the twin-lamb group compared to the single-lamb group. Through genome-wide association analysis, we identified 18 additive quantitative trait loci (QTLs) and 27 dominant QTLs, three of which exhibited both additive and dominant effects. Functional annotation indicated that genes such as *BMP5* and *MTNR1B*, associated with reproductive regulation, likely influence litter size, with key loci validated by Sanger sequencing. Among the dominant QTLs, some displayed heterozygote advantage, while others showed heterozygote disadvantage. Drawing on our previous researches and existing literatures, we propose that the complexity of heterozygote effects may explain the limited multi-lambing performance in local breeds. These findings provide a theoretical basis for selective breeding to enhance multi-lambing traits in Duolang sheep and other indigenous breeds.

面向绵羊智慧养殖的激光牧草高效种植关键技术研究
Research on key technologies of efficient laser forage planting for smart sheep farming

杨明来 教授，吉林农业大学
Prof. Minglai Yang, Jilin Agricultural University

报告阐述激光技术特点及在农业应用情况，重点介绍激在绵羊养殖中，有关牧草高效种植关键技术研究进展，包括：
1、激光应用于牧草种植增产提质；
2、激光辐照增强种子活性，促进增产；
3、激光促进育苗的分子生物学表现等。

The report elaborated on the characteristics of laser technology and its applications in agriculture, focusing on the research progress of key technologies related to efficient forage cultivation in sheep farming. These technologies included:
1. Application of lasers to increase yield and improve quality in forage cultivation;
2. Laser irradiation to enhance seed viability and promote yield increases;
3. Molecular biological manifestations of laser-assisted seedling cultivation.

绵羊组学数据分析工具构建与应用
Construction and Application of a Sheep Omics Data Analysis Platform

张俊 副研究员，国家农业信息化工程技术研究中心
Assoc. Prof. Jun Zhang, National Agricultural Informatization Engineering Research Center

绵羊作为重要的经济动物，其遗传改良是推动畜牧业发展的关键。随着高通量测序技术和高精度表型检测技术的协同进步，基因组学、转录组学、蛋白质组学、代谢组学以及表型组学已广泛应用，形成了“基因型—表型—环境”多维数据体系。然而，现有分析方法面临两大瓶颈：一是多组学数据来源多样、结构不一，缺乏统一的整合接口；二是普遍缺少表型组数据的标准化处理模块，导致“表型—组学”关联分析效率低下，难以系统解析“基因—表型”调控网络。开发一种能够整合表型组的绵羊多组学数据分析工具，不仅可实现“表型引导组学解析”的研究新范式，高效管理与整合海量数据，还可通过多维度关联分析揭示复杂性状的遗传基础，为绵羊分子育种提供从“表型预测”到“基因验证”的全链条技术支撑。

As an important economic animal, the genetic improvement of sheep is crucial for the development of the livestock industry. With the synergistic advancement of high-throughput sequencing technologies and high-precision phenotyping techniques, genomics, transcriptomics, proteomics, metabolomics, and phenomics have been widely applied, forming a multi-dimensional "genotype-phenotype-environment" data system. However, current analytical tools face two major bottlenecks: firstly, multi-omics data come from diverse sources with varied formats, lacking a unified integration interface; secondly, there is a general absence of standardized modules for phenomics data, leading to inefficient "phenotype-omics" association analysis and hindering the systematic exploration of "gene-phenotype" regulatory networks. Developing an integrated sheep multi-omics data analysis tool that incorporates phenomics would not only enable a "phenotype-guided omics analysis" research paradigm and facilitate the integrated management of massive datasets but also reveal the genetic mechanisms underlying complex traits through multi-dimensional correlation analysis. This would provide comprehensive technical support for sheep molecular breeding, spanning from "phenotype prediction" to "gene validation."

人工智能赋能农牧业：从视觉到大模型应用
Artificial Intelligence for Livestock Farming: From Computer Vision to Large Model Applications

黄栋 副教授，华南农业大学
Assoc. Prof. Dong Huang, South China Agricultural University

报告将从智慧农业的背景出发，探讨人工智能如何从生产端、经营端、人才端赋能畜牧业，实现提质增效与智慧化管理。在生产端，结合计算机视觉技术实现畜禽生长监测、体重预估等，提升养殖效率，降低人工成本与疫病风险。在经营端，构建农牧企业大数据分析系统，提升农牧企业管理效率；并结合大模型技术，构建农牧企业财务智能体，推动传统企业向数据驱动的精细化运营迈进。在人才端，以农业特色人工智能通识必修课建设为例，分享人工智能赋能农林类人才培养的一些经验，并探讨其未来发展方向与挑战。

This talk begins with the background of smart agriculture to explore how AI empowers livestock farming across production, management, and education. This talk will discuss how AI achieves quality improvement, efficiency gains, and intelligent management. Specifically, for production, computer vision enables livestock growth monitoring and weight estimation, thereby enhancing breeding efficiency while reducing labor costs and disease risks. For management, this talk will detail the construction of big data analytics systems and financial intelligent agents powered by large models to advance traditional enterprises toward data-driven, refined operations. Finally, for education, this talk will share experiences in establishing general courses of AI for agricultural universities, discussing future directions and challenges in cultivating AI-empowered professionals.

技术链与产业链的双向赋能：工业互联技术驱动的智慧养殖架构融合与创新

Two-Way Empowerment of Technology Chains and Industrial Chains: Integration and Innovation in Smart Aquaculture Architecture Driven by Industrial Internet Technologies

杨松 副教授，北京理工大学
Assoc. Prof. Song Yang, Beijing Institute of Technology

智慧养殖的数字化转型需突破“数据采集 - 传输 - 处理 - 决策”全链路的技术协同与产业链贯通难题。本报告围绕流媒体转发技术、边缘计算网络、工业互联网分层架构与智慧养殖业务的耦合逻辑展开，结合实景采集装备的多源数据（视频、环境传感等）采集能力，阐释流媒体技术如何实现养殖场景音视频、监控数据的高效传输与多终端（场内 / 场外）分发；同时，依托工业互联“设备 - 执行 - 控制 - 管理 - 企业”的分层互联架构，解析如何打通智慧养殖从种植、饲料、养殖到屠宰加工、物流零售的全产业链数据链路，通过“感、传、算、控”一体化体系，推动技术链与产业链双向赋能，为智慧养殖的透明化、智能化与全流程可追溯提供技术融合范式与落地路径参考。

The digital transformation of smart aquaculture demands overcoming challenges in technical collaboration and industrial chain integration throughout the entire "data collection-transmission-processing-decision-making" cycle. This report explores the coupling logic between streaming media forwarding technology, edge computing networks, industrial Internet hierarchical architecture, and smart aquaculture operations. Leveraging multi-source data (video, environmental sensing, etc.) acquisition by real-scene devices, it illustrates how streaming media enables efficient transmission and multi-terminal (on-site/off-site) distribution of aquaculture audio-visual and monitoring data. Additionally, relying on the industrial Internet's hierarchical interconnection (from "equipment-execution-control-management-enterprise"), it analyzes how to unify the entire industrial chain data flow in smart aquaculture (from planting, feed, and breeding to slaughtering, processing, logistics, and retail). Via an integrated "sensing-transmission-computing-control" system, the lecture highlights how technical and industrial chains mutually empower each other, offering a paradigm for smart aquaculture’s transparency, intelligence, and full-process traceability.

基于计算机视觉的智慧养羊实践研究
Enhancing Precision Livestock Management with Advanced Machine Vision and Deep Learning

王美丽 教授，西北农林科技大学
Prof. Meili Wang, Northwest A&F University

针对羊只行为基础数据不完善、智能化识别水平低等问题，提出了基于特征融合的羊只行为识别方法，通过对羊只站立、卧趴、进食、饮水、攻击、死亡等行为的识别，能够实现快速响应和预警防范。针对规模化养殖中羊只生长性能评估需求，搭建了羊只深度图像数据采集设备，提出了一种基于深度学习的体重估计方法。通过点云滤波、语义分割及重建获取羊只体尺参数，解决养殖场日常管理中的分栏分群问题，为智能化育种中快速表型数据获取奠定基础。通过对算法与硬件深度融合以及定制设备研究，实现了养殖过程中数据的全面感知与自动获取。

To address the issues of incomplete foundational data on sheep behavior and low levels of intelligent recognition, a behavior recognition method for sheep based on feature fusion has been proposed. This method enables rapid response and early warning prevention by identifying behaviors such as standing, lying down, eating, drinking, attacking, and death. To meet to the demand for performance assessment of sheep growth in large-scale breeding, depth image data collection equipment has been established, and a weight estimation method based on deep learning has been introduced. By using point cloud filtering, semantic segmentation, and reconstruction, the body size parameters of sheep can be obtained, resolving the challenges of pen allocation and flock grouping in daily management at the farm. This lays the groundwork for rapid acquisition of phenotypic data in intelligent breeding. Through the deep integration of algorithms and hardware, as well as the research of customized equipment, comprehensive sensing and automated data acquisition throughout the farming process have been achieved.

智能+ 在肉羊育种中的实践与探索
Practice and exploration of "Smart+" in mutton sheep breeding

刘志红 教授, 内蒙古农业大学
Prof. Zhihong Liu, Inner Mongolia Agricultural University

人工智能技术赋能畜牧业将是推动畜牧业的可持续发展的契机。在肉羊育种中开展智能化应用，一方面面临产业综合规模化率不足、育种周期长、育种有效数据不足、生物性状机制解析等产业本身的问题，另一方面传统生产模式与智能化生产间的差异，缺乏相关评价标准。研究在肉羊育种中的实践围绕育种大数据库建立、智能化性能采集与标准制定、机器视觉模型优化、自动化BLUP育种模型选择、智能化采集表型与基因组选育融合等方面开展，系统介绍了数字化、智能化在肉羊育种中的实现和应用。

Practice and exploration of "Smart+" in mutton sheep breeding
Empowering the livestock industry with artificial intelligence technology will be an opportunity to promote its sustainable development. The application of intelligent technology in mutton sheep breeding faces inherent challenges, including insufficient scale, long breeding cycles, insufficient effective breeding data, and lack of understanding of biological trait mechanisms. Furthermore, there are differences between traditional production models and intelligent production, and a lack of relevant evaluation standards. This study of practical applications in mutton sheep breeding focuses on the establishment of a large breeding database, intelligent performance acquisition and standardization, machine vision model optimization, automated BLUP breeding model selection, and the integration of intelligent phenotyping and genomic selection. It systematically introduces the implementation and application of digitalization and intelligence in mutton sheep breeding.

聚焦智慧养羊技术在全球羊业转型升级中的应用实践与创新
Application Practices and Innovations of Smart Sheep Farming Technology in the Global Transformation and Upgrading of the Sheep Industry

唐骏启 博士，安徽哈泰智能科技有限公司
Dr. Junqi Tang, Anhui Hatai Intelligent Technology Co., Ltd.

针对传统养殖中效率低、资源浪费、疫病防控滞后等问题，系统梳理物联网、人工智能、大数据等技术的融合应用，建立智慧养羊体系。

利用智能化技术，监测并采集羊只的运动量、采食量、环境、体尺、繁殖周期等关键生物信息，依托大数据平台结合AIGC，优化育种，实现系谱改良；优化饲喂配方，实现精准饲喂；建立疫病预警模型，实现常见传染病提前预警，动态治理生物环境，使羔羊成活率提升8%-12%；发病率降低20%以上；饲料损耗减少15%，养殖成本下降10%-15%，通过智能化设备投入及技术革新，提升技术养羊收益。探讨溯源技术在羊业溯源中的应用前景，及未来需进一步突破小规模养殖、适配性技术研发、多技术协同融合、绿色低碳养殖模式构建等关键问题。

推动智慧养羊技术向规模化与精细化并重、效率与生态兼顾的方向发展，为全球羊业可持续发展提供技术支撑。

Addressing the issues of low efficiency, resource waste, and lagging disease prevention in traditional sheep farming, this report systematically reviews the integrated application of technologies such as the Internet of Things, artificial intelligence, and big data to establish a smart sheep farming system. By leveraging intelligent technologies, key biological data including sheep activity levels, feed intake, environment, body measurements, and reproductive cycles are monitored and collected. Combined with a big data platform and AIGC, this approach optimizes breeding for pedigree improvement, refines feeding formulas for precise feeding, and establishes disease early-warning models to predict common infectious diseases in advance. It also enables dynamic management of the biological environment, increasing lamb survival rates by 8%-12%, reducing disease incidence by over 20%, decreasing feed loss by 15%, and lowering farming costs by 10%-15%. Through investments in intelligent equipment and technological innovations, profitability in sheep farming is enhanced. The report also explores the application prospects of traceability technology in the sheep industry and discusses key challenges for future breakthroughs, including small-scale farming, adaptive technology development, multi-technology integration, and the establishment of green, low-carbon farming models. It promotes the development of smart sheep farming toward a balance of scale and precision, efficiency, and ecological sustainability, providing technical support for the sustainable development of the global sheep industry.

数智驱动绵羊全产业链高质量可持续发展
Digital and Intelligent-Driven High-Quality and Sustainable Development of the Entire Sheep Industry Chain

马志愤 博士，一牧数智（杭州）科技有限公司
Dr. Zhifen Ma, EYIMU Digital Intelligence (Hangzhou) Technology Co., Ltd.

本演讲报告围绕“数智驱动绵羊全产业链高质量可持续发展”这一核心主题，深入探讨了如何将大数据、人工智能、物联网、区块链等新一代数字智能技术与绵羊产业的育种、养殖、加工、流通、消费等各个环节进行深度融合。报告旨在通过科技赋能，构建一个透明、高效、可追溯的现代化绵羊产业体系。

报告系统分析了当前绵羊产业面临的挑战，如生产效率、质量安全控制、资源环境压力及市场波动等。针对这些问题，报告提出了以数据为关键生产要素、以智能化决策为核心驱动力的全产业链解决方案。具体而言，数智技术将应用于智能育种、智慧养殖、智能屠宰加工、供应链优化和精准营销等领域，从而实现降本增效、提升羊肉品质与安全水平、减少环境足迹，并增强产业抗风险能力。

最终，展望了数智驱动下绵羊产业的未来图景：一个集成了绿色生产模式、高效资源配置与协同、全程质量安全和显著经济效益的高质量、可持续发展新模式，为保障国家粮食安全、促进乡村振兴和实现农业现代化提供重要支撑。

This speech delves into the core theme of "Digital and Intelligent-Driven High-Quality and Sustainable Development of the Entire Sheep Industry Chain." It explores the deep integration of new-generation digital and intelligent technologies—such as big data, artificial intelligence, the Internet of Things, and blockchain—into every segment of the sheep industry, from breeding and farming to processing, distribution, and consumption. The objective is to leverage technological innovation to build a transparent, efficient, and traceable modern industrial system.

The report provides a systematic analysis of the challenges currently facing the industry, including production efficiency, quality and safety control, resource and environmental pressures, and market volatility. In response, it proposes a comprehensive, data-driven, and intelligently managed solution for the entire chain. Specifically, digital and intelligent technologies will be applied in areas like precision breeding, smart farming, intelligent slaughtering and processing, supply chain optimization, and targeted marketing. This integration aims to reduce costs, improve efficiency, enhance the quality and safety of products, minimize the environmental footprint, and bolster the industry's resilience to risks.

Ultimately, the report envisions a future for the sheep industry underpinned by digital intelligence: a new model of high-quality and sustainable development characterized by green production practices, optimal resource allocation, end-to-end quality assurance, and significant economic benefits. This model is poised to make substantial contributions to ensuring national food security, promoting rural revitalization, and advancing agricultural modernization.

分论坛2

12日上午

开发非规范的引物编辑器，用于高效敲入/ 敲除绵羊受精卵中的基因
Development of non-canonical prime editors for efficient knock-in/knockout of genes in sheep zygotes

刘江怀 教授，南京大学
Prof. Jianghuai Liu, Nanjing University

The prime editor (PE) represents a recent key addition to the precise editing tools, offering significant potential for installing various types of small-sized genetic modifications. We have sought different strategies to improve the applicability of PE. In a 2023 study, we adopted an unconventional approach by focusing on a nuclease PE (PEn) platform that integrated the PE-specialized editing mechanism with Cas9's dsDNA nuclease activity. Via the use of a DNA repair-regulatory module, we established an uPEn platform that not only featured superior efficiencies for desirable edits, but also presented commendable editing purities. Subsequently, we and collaborators applied uPEn in Hu sheep zygotes, to concomitantly introduce Kozak motif knock-in at PPARG and to knock out MSTN, achieving effective bi-locus installation of programmed alleles. Most recently, to address the unidirectional editing pattern with uPEn, our collaborative team re-configured the template RNA architecture to enable opposite-direction editing and unfold uPEn's editable space. Altogether, our investigations establish uPEn as an effective and versatile editing platform for livestock genetic improvements and beyond.

解码绵羊配子的冷冻损伤：多组学和纳米材料
Decoding Cryodamage in Ovine Gametes：Multi-Omics & Nanomaterial

傅祥伟 副教授， 中国农业大学
Assoc. Prof. Xiangwei Fu , China Agricultural University

本报告主要介绍了解析绵羊配子冷冻损伤机制的多组学联合分析方法，以及为提升冷冻卵母细胞质量而开发的新型防护策略，对提升绵羊体内外胚胎生产效率、遗传资源保护与品种改良具有重要意义。通过多组学联合分析，系统揭示了精子与卵母细胞冷冻过程中与冷冻损伤相关的关键通路及生物标志物。通过实验验证发现，下调膜蛋白FCGR1A会降低冷冻精子受精能力；而促进肌动蛋白聚合与维生素B6代谢可改善冷冻卵母细胞质量。研究还评估了羟基磷灰石（HA）和聚乳酸-羟基乙酸共聚物-白藜芦醇（PLGA-RES）两种纳米材料对卵母细胞的保护作用，组学结合验证实验发现，HA通过粘着斑通路缓解氧化应激，PLGA-RES则通过内吞作用及PI3K/AKT/mTOR通路，提升绵羊冷冻卵母细胞质量。

This report primarily introduces a multi-omics integrated analysis approach to elucidate the mechanisms of cryodamage in sheep gametes, as well as novel protective strategies developed to enhance the quality of cryopreserved oocytes. These advancements hold significant importance for improving the efficiency of in vivo and in vitro embryo production in sheep, along with genetic resource conservation and breed improvement. Through multi-omics integrated analysis, key pathways and biomarkers associated with cryodamage during sperm and oocyte cryopreservation were systematically revealed. Experimental validation demonstrated that downregulation of the membrane protein FCGR1A reduced the fertilization capacity of cryopreserved sperm, while promoting actin polymerization and vitamin B6 metabolism improved the quality of cryopreserved oocytes. The study also evaluated the protective effects of two nanomaterials—hydroxyapatite (HA) and poly(lactic-co-glycolic acid)-resveratrol (PLGA-RES)—on oocytes. Integrated omics and validation experiments revealed that HA alleviated oxidative stress through the focal adhesion pathway, whereas PLGA-RES enhanced the quality of cryopreserved sheep oocytes via endocytosis and the PI3K/AKT/mTOR pathway.

绵羊全周期睾丸发育动态图谱绘制及分子机制解析
Dissecting the molecular regulatory mechanism based on a dynamic atlas of testicular development throughout the entire cycle in sheep

周扬 教授，内蒙古大学
Prof. Yang Zhou, Inner Mongolia University

种公羊优良的精液品质与精子质量是提高母羊受胎率的关键因素，但目前绵羊全周期睾丸发育的遗传调控机制研究匮乏，制约着绵羊种质创制选育进程。睾丸发育是一个复杂且动态的过程，是决定雄性哺乳动物繁殖性能的关键基础。我们将运用多组学联合分析技术体系，构建绵羊全周期睾丸发育多组学动态图谱，实现绵羊睾丸发育轨迹的高分辨率解析，建立绵羊睾丸发育多组学数据库；基于多组学整合数据充分挖掘绵羊睾丸发育相关基因，特别是决定精子质量的关键基因，并系统解析其分子机制。

The superior semen quality and sperm viability of breeding rams are pivotal factors influencing the conception rates of ewes. However, the genetic and molecular mechanisms governing the entire-cycle testicular development in sheep remain poorly understood, which hinders the progress of sheep germplasm innovation and breeding. Testicular development is a highly complex and dynamic biological process, serving as the fundamental basis for male mammalian reproductive performance. To address this critical knowledge gap, we propose a multi-omics-based analytical framework to systematically construct a multi-omics dynamic atlas of entire-cycle testicular development in sheep. This will enable high-resolution profiling of ovine testicular developmental trajectories and establish the multi-omics database on sheep testicular development. By leveraging the integrated multi-omics data, we will thoroughly identify genes associated with ovine testicular development, particularly those critical for determining sperm quality, and systematically elucidate their molecular mechanisms.

家畜多能干细胞建系及其应用
Establishment and Application of Stable Pluripotent Stem Cell Lines in Livestock

郅明雷 副教授，中国农业大学
Assoc. Prof. Minglei Zhi , China Agricultural University

多能干细胞在临床医学和动物育种中具有广阔的应用前景，然而自1981年第一例胚胎干细胞系在小鼠上获得成功以来，只有在人、大鼠、猴子上获得了稳定的胚胎上胚层来源的干细胞系，虽然各国学者在家畜动物上进行了大量研究，始终未能建立稳定的胚胎干细胞系，直到本团队建立稳定的猪原肠化前上胚层干细胞。我们通过构建家畜动物早期胚胎发育图谱，从胚胎多能性发育调控分子机制入手，解析上胚层不同多能性状态的调控信号通路，成功建立了稳定的猪、牛、羊上胚层干细胞分离和培养体系。所建立的细胞系能够维持胚胎上胚层多能性状态，具有典型干细胞特征（表达特异干细胞标记分子、具有多向分化潜能），在长期传代过程中保持基因组的稳定。这些家畜干细胞具有良好的应用前景和技术优势，在细胞培养肉领域，可作为细胞产品的底盘种子细胞；在家畜优良品种培育领域，将干细胞定向分化为配子，可以在实验室中完成优良家畜胚胎的批量生产和选择；在医学研究领域，将干细胞与基因编辑技术结合,可用于构建多基因编辑的复杂动物模型；在基础研究领域，通过将家畜、人、小鼠等不同物种间的干细胞进行比较，解析物种间调控的差异性和保守性, 可以为干细胞的应用提供理论依据。

Pluripotent stem cells (PSCs) hold broad prospects in clinical medicine and animal breeding. Since embryonic stem cells first established in mice in 1981, stable epiblast-derived PSCs have only been obtained in humans, rats, and monkeys. Despite of ongoing extensive research efforts, the establishment of stable PSCs in livestock remained elusive until we derived stable pre-gastrulation epiblast stem cell lines from pigs. Based on the insights of constructing transcriptional atlases of early embryo development and elucidating the molecular mechanisms governing pluripotency, we deciphered the signaling pathways regulating different pluripotency states of the epiblast, which led us develop culture systems for derivation of stable epiblast stem cells from early embryos in pigs, cattle, and sheep. These established PSCs maintain pluripotency of the epiblast and exhibit stem cells characteristic properties, including expression of specific marker genes and multidirectional differentiation potential, and preserving genomic stability during long-term passage. Stable livestock PSCs possess significant application potential and technical advantages. In the field of cultured meat, PSC can serve as foundational seed cells for cellular products. For livestock breeding, the directed differentiation of PSCs into gametes enables the large-scale production and selection of high-quality embryos in laboratory. In medical research, combining stem cells with gene-editing technologies facilitates the creation of complex animal models with multiple genetic modifications. Finally, in basic research, comparative studies of PSCs across species can reveal the conserved and divergent regulatory mechanisms, which provide theoretical foundation for the application of PSCs.

反刍动物早期胚胎发育的调控
Regulation of early embryonic development in ruminants

张坤 研究员，浙江大学
Prof. Kun Zhang, Zhejiang University

牛早期胚胎发育研究具有重要的科学价值与产业应用意义。一方面，该研究是现代生物育种技术的重要基础。结合基因组选择、基因编辑或干细胞育种等体外胚胎技术，可显著提升动物育种的效率与精准性。另一方面，奶牛养殖业长期面临早期胚胎丢失率高的生产问题。牛早期胚胎在发育第一周内尤其脆弱，是胚胎死亡的高发期，该阶段伴随基因组激活和首次细胞谱系分化等关键生物学事件。浙江大学张坤课题组以牛早期胚胎为模型，长期聚焦这些事件的分子调控机制。通过单细胞转录组测序技术，团队首次明确牛第一次细胞谱系分化发生于早期囊胚阶段，并鉴定出SOX2等转录因子在此过程中的核心作用，其功能机制与模式动物小鼠存在显著差异。进一步借助单碱基编辑技术，课题组系统解析了谱系特异性转录因子的互作网络。这些研究成果深化了对牛早期发育规律的认识，为解决繁殖障碍、优化育种策略提供了关键理论依据和潜在的分子靶点。

Research on early bovine embryonic development is of significant scientific value and holds considerable industrial application potential. One perspective posits that it functions as a foundational element for contemporary animal breeding technologies. The integration of in vitro embryo techniques with genomic selection, gene editing, or stem cell breeding has the potential to enhance the efficiency and precision of livestock breeding significantly. Conversely, the dairy industry is confronted with a significant challenge in the form of high rates of early embryonic loss. The first week of bovine embryonic development represents a critical period, characterized by a high incidence of embryo mortality. Concurrently, this period is marked by significant biological events, including embryonic genome activation and the first lineage specification event. The research team led by Dr. Zhang Kun at Zhejiang University employs the early bovine embryo as a model to investigate the molecular regulatory mechanisms underlying these crucial events. Utilizing single-cell RNA-seq technology, they were the first to reveal that the first lineage specification event in cattle occurs at the early blastocyst stage. The transcription factor SOX2 and others were identified as playing a central role in this process and its functional mechanism significantly differs from that observed in model organisms such as mice. Furthermore, the team applied base editing technology to systematically analyze the interaction network of lineage-specific transcription factors. These findings serve to deepen our understanding of early developmental regulation in cattle, and provide crucial theoretical support and molecular targets for addressing reproductive disorders and optimizing breeding strategies.

Towards cost-effective conservation of genetic diversity in native Finnish small ruminant breeds

Prof. Peippo Jaana, Natural Resources Institute

Indigenous Nordic farm animals breeds represent centuries of adaptation to the northern latitudes with extreme weather conditions. These hardy breeds display characteristics that may also be crucial for the sustainable food production in our unpredictable future. Farms raising indigenous breeds rely on natural matings and subsequently face challenges in the ability to exchange breeding materials due to differences in disease statuses or geographical distances between farms. To maintain genetic diversity in these native animal populations of small ruminant species, conservation of rare dam and sire lineages is crucial. Due to lack of optimized assisted reproductive technologies (ARTs) in small ruminant species only very limited number of sires are used in breeding schemes and large amount of genetic diversity is lost in each generation. Subsequently, there is a need to optimize cost-effective ARTs also for these small ruminant species. Artificial insemination (AI) is a cost-effective method to exchange genetic material between farms without compromising on-farm disease status or animal welfare. Collection of epididymal sperm is a cost-effective method to collect sperm for AIs and in vitro embryo production (IVP). Ability to use embryo culture medium from IVP instead of embryo biopsy for genotyping of desired traits improves post-thaw viability of embryos and maintains their export status. Optimization of AI and non-surgical embryo transfer in small ruminant species will remain as future challenges.

ADAFSA's Strategic Role in Advancing Small Ruminant Health and Sustainable Livestock Management

Dr. Mohammed Albreiki, Abu Dhabi Agriculture and Food Safety Authority (ADAFSA)

Small ruminants are essential for food security and sustainable agriculture in the United Arab Emirates (UAE). The Abu Dhabi Agriculture and Food Safety Authority (ADAFSA) has developed a comprehensive strategy to enhance small ruminant health and productivity through surveillance, innovation, and sustainable management.

ADAFSA implements active and passive surveillance programs to monitor animal health trends and detect emerging and endemic diseases such as PPR and brucellosis. Annual vaccination campaigns are conducted across the emirate, supported by post-vaccination evaluation studies to assess immune response and program effectiveness. The Authority also leads One Health (OH) initiatives integrating human, animal, and environmental health to address zoonotic threats collaboratively.

In addition, ADAFSA launched the Abu Dhabi Agri-Genome Program for sheep and goats to improve genetic diversity, productivity, and disease resistance through advanced genomic tools. These efforts are complemented by research partnerships and farmer engagement to promote sustainable feeding systems, animal welfare, and reduced antimicrobial use.

Collectively, these initiatives strengthen livestock resilience, support national food security goals, and advance the UAE's vision for sustainable and science-driven livestock management.

布鲁氏菌分泌蛋白BPE005 调控胎盘炎症机制的研究
Study on the mechanism of secreted protein BPE005 of *Brucella* regulate placental inflammation

邓兴梅 副教授，石河子大学
Assoc. Prof. Xingmei Deng, Shihezi University

胎盘炎症是布鲁氏菌引起动物流产的主要原因，布鲁氏菌T4SS分泌蛋白参与调控布鲁氏菌胞内生存及宿主免疫应答，为了探索布鲁氏菌分泌蛋白调控母体胎盘炎症及致流产机制，研究以胚胎发育的关键因子GPR126为研究对象，通过酵母双杂交、免疫共沉淀筛选鉴定与GPR126布鲁氏菌T4SS系统分泌蛋白BPE005，通过构建BPE005基因缺失株与回补株，在细胞水平证实，布鲁氏菌BPE005通过调控GPR126-cAMP-CREB信号通路促进TNF-α产生并抑制IL-10的产生，促进母体胎盘炎症进而导致流产，进一步揭示布鲁氏菌分泌蛋白参与母体胎盘的炎症调控机制。

Placental inflammation is the primary cause of animal abortion induced by *Brucella. Brucella* T4SS secreted proteins are involved in regulating Brucella intracellular survival and host immune response. To explore the mechanism of placental inflammation abortion induced by secreted proteins of Brucella, our study focuses on GPR126, a key factor in embryonic development as the research object, the protein BPE005 interacted with GPR126 of the T4SS system of Brucella was screened and identified through yeast two-hybrid and co-immunoprecipitation, by constructing BPE005 gene deletion and complementation strains, It was confirmed that Brucella BPE005 promotes TNF-α production and inhibits IL-10 production by regulating the GPR126-cAMP-CREB signaling pathway to promote maternal placental inflammation and at the cellular level, Our study Further reveal the mechanism by which *Brucella* secreted proteins participate in the inflammatory regulation of the maternal placenta.

One Health 背景下羊产气荚膜梭菌病的流行与耐药性研究 Epidemiology and Drug Resistance of Sheep Clostridium perfringens Disease in the Context of One Health

王娟 副教授，西北农林科技大大学
Assoc. Prof. Juan Wang, Northwest A&F University

羊产气荚膜梭菌病是由产气荚膜梭菌引发的一类以急性死亡、肠毒血症、坏死性肠炎为主要特征的重要细菌性传染病，广泛流行于全球养羊主产区，对养羊业经济效益造成严重冲击。在“同一健康”（One Health）理念框架下，该疾病的流行传播与耐药性问题已突破单一动物健康范畴，形成了“动物-环境-人”多维度交叉影响的复杂公共卫生挑战，因此亟需系统性探究与防控。本研究围绕One Health核心维度，综合采用流行病学调查、微生物分离鉴定、分子分型及药物敏感性检测等技术方法，系统分析了我国多省份羊产气荚膜梭菌病的流行现状、优势血清型分布及环境定植特征，以及本团队在产气荚膜梭菌快速检测与防控技术方面的研究进展。

Sheep *Clostridium perfringens* disease is an important bacterial infectious disease caused by *Clostridium perfringens*, characterized mainly by acute death, enterotoxemia, and necrotic enteritis. It is widely prevalent in major sheep-raising areas around the world and causes a severe impact on the economic benefits of the sheep industry. Under the framework of the "One Health" concept, the epidemic spread and drug resistance of this disease have transcended the scope of single animal health, forming a complex public health challenge with multi-dimensional cross-impacts among "animals-environment-humans". Therefore, systematic investigation and prevention are urgently needed. Centering on the core dimensions of One Health, this study comprehensively adopted technical methods such as epidemiological investigation, microbial isolation and identification, molecular typing, and drug susceptibility testing to systematically analyze the epidemic status, distribution of dominant serotypes, and environmental colonization characteristics of sheep *Clostridium perfringens* disease in multiple provinces of China, as well as the research progress of the research team in the rapid detection and prevention technologies of *Clostridium perfringens*.

棘球蚴病的全球流行现状和种群演化历史
The Global Epidemiological Status and Population Evolutionary History of Echinococcosis

闫鸿斌 副研究员，中国农业科学院兰州兽医研究所
Assoc. Prof. Hongbin Yan, Lanzhou Veterinary Research Institute of CAAS

棘球蚴病，即包虫病，是一种严重的人畜共患寄生虫病，对全球畜牧业和人类健康构成重大威胁。我们对我国、巴基斯坦和尼日利亚流行的棘球蚴病进行了分子流行病学调查，探讨了患病率、病原物种、基因型分布和种群结构特征等信息，并综述了世界各地的包虫病流行现状。我们观察到在不同地区的棘球绦虫属（Echinococcus）物种和基因型分布存在显著差异，一些物种或基因型的地理范围呈扩展趋势。此外，我们对我国境内细粒棘球绦虫狭义种（Echinococcus granulosus sensu stricto，即G1和G3基因型）进行了全基因组遗传多态性分析。结果显示，G1和G3基因型之间存在线粒体-核基因组不一致的现象，这可能是由于历史上的地理隔离和后来的融合所致。种群历史和基因流分析反映了细粒棘球绦虫从新疆传播到青藏高原的传播路径，及二次接触后的基因渗透。多个基因组证据证实了细粒棘球绦虫的杂交是普遍存在的。基因变异突显了其对寄生生活方式的适应性进化特征。这些发现为我们提供了有关细粒棘球绦虫复杂的遗传动力和适应性策略的认识。这些研究为全球包虫病的预防和控制奠定了基础，强调了国际合作和全面控制措施的重要性。

Echinococcosis, i.e., Hydatid Disease, is a serious zoonotic parasitic disease, posing significant threats to global livestock and human health. We conducted molecular epidemiological investigations of echinococcosis prevalent in China, Pakistan and Nigeria, exploring details such as prevalence rates, pathogen species, genotype distributions, and population structure characteristics, and reviewed the worldwide epidemiological status of echinococcosis. We observed significant differences in the species and genotype distributions of *Echinococcus* across different regions, with some species or genotypes showing an expanding trend in their geographic range. Additionally, we performed a genome-wide genetic polymorphism analysis of *Echinococcus granulosus* sensu stricto (*E. granulosus*, G1 and G3 genotypes) in China. The results revealed mitochondrial-nuclear discordance between G1 and G3 genotypes, possibly arising from historical geographic separation and subsequent fusion. Demographic history and gene flow among populations reflected the transmission route of *E. granulosus* from Xinjiang to the Qinghai–Tibet Plateau, which is followed by introgression from secondary contact. Multiple genomic evidence confirmed that cross-fertilization in *E. granulosus* is prevalent. Genetic variations highlighted adaptive evolutionary features in response to parasitic lifestyle. These insights provided valuable understanding of the complex population dynamics and adaptive strategies of *E. granulosus.* These studies provided the basis for global echinococcosis prevention and control, underscoring the importance of international collaboration and comprehensive control measures.

Isolation and Characterization of *Pasteurella spps* from Pneumonic Cases in selected province of Ethiopia: Evidence of Differences between Field and Vaccine Biotypes

Adehanom Baraki Tesfaye, Doctoral student, Lanzhou Veterinary Research Institute of CAAS

Ethiopia is the largest livestock producer in Africa, But still in burden of endemic and epidemic disease. Pneumonic pasteurellosis is the leading cause of recurrent morbidity and mortality in ruminants. Its control is mainly done using an annual vaccination with a monovalent whole broth culture of *Pasteurella multocida*. However, the multiplicity of the serotypes circulating in the field and lack of cross-protective immunity hinder the effectiveness of the vaccination program warranting the development of a vaccine with better efficacy. To this effect, the identification, and characterization of the strains from different regions of the country is necessary. In this paper, Pasteurella organisms collected from camels, cattle, goats, and sheep with respiratory signs suggestive of pasteurellosis in three selected provinces were isolated, and characterized. From clinically pneumonic cases, 793 nasal swabs (286 goats, 276 sheep, 168 camels, and 63 cattle) were collected aseptically and cultured. Bacteria pathogens were identified at the species level by biochemical tests. Culture positivity was 29.3%. The isolation frequencies of *B. trehalosi, M. haemolytica*, and *P. multocida* were 47.7%, 43.2%, and 9.1%, respectively. A higher isolation rate was observed in sheep (37.4%), and the lowest in cattle (6.2%). Mixed infection with *B. trehalosi* and *M. haemolytica* was observed in sheep, goats, and camels. Despite the higher frequencies of isolation of *B. trehalosi* and *M. haemolytica* from all host species, the vaccine currently being used in Ethiopia consists of only *P. multocida* biotypes A for sheep and goats and biotype B for cattle. Moreover, camels are not considered in the pasteurellosis vaccination program in the country. Therefore, the result suggests the need to include *B. trehalosi* and *M. haemolytica* in the vaccine preparation as well as underlines the relevance of considering camels in the vaccination program, So far demanding a cross-protective vaccine development incorporating all Pasteurella species.

2025

第五届世界绵羊大会

The 5th World Conference on Sheep WCS2025

WC

202