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Genetic Research of Sheep-Goats and Cattle in Kazakhstan: A Review of Research in 2025

A comprehensive review of molecular genetic and genomic studies on Kazakhstani livestock populations, based on Scopus-indexed publications in 2025.

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Abstract

This review article analyzes recent molecular genetic and genomic studies conducted on Kazakhstani populations of sheep, goats, and cattle, based on scientific publications indexed in the Scopus database in 2025. The review examines research on genetic diversity, population structure, selection signatures, and genomic associations with economically important traits. Particular attention is given to studies utilizing modern technologies such as SNP genotyping and whole-genome sequencing. The results demonstrate significant achievements in understanding the genetic architecture of Kazakhstani livestock breeds and provide a foundation for implementing genomic selection programs.

Keywords: livestock production; genomics; SNP genotyping; whole-genome sequencing; GWAS; genetic diversity; adaptability; genomic selection

Introduction

Livestock farming plays a crucial role in ensuring food security in the Republic of Kazakhstan, sustainable development of the agricultural sector, and preserving the socio-economic potential of rural areas. Local breeds of agricultural animals adapted to harsh continental climate conditions — characterized by high temperature fluctuations and limited feed resources — represent valuable genetic resources. These breeds have formed over centuries through natural and artificial selection under specific environmental conditions and possess unique adaptive characteristics.

In recent years, advanced approaches in molecular genetics and genomics have fundamentally expanded the methodological capabilities for studying agricultural animals. Single nucleotide polymorphism (SNP) genotyping and whole-genome sequencing (WGS) technologies enable comprehensive analysis of genetic diversity, identification of selection signatures, detection of genomic associations with economically important traits, and assessment of inbreeding levels.

The purpose of this article is to provide a comprehensive review of the current state and development trends of genetic research on livestock in Kazakhstan, based on publications in scientific journals indexed in the Scopus database published in 2025. Special attention is given to studies of sheep, goats, and cattle populations — traditional and economically significant sectors of animal husbandry in the country.

I. Genetic Research on Sheep and Goats

Population Structure and Genetic Diversity

Sheep farming is one of Kazakhstan's traditional and economically important sectors. The fat-tailed coarse-wooled sheep breeds widely distributed in the country have formed under long-term selection in specific environmental conditions and possess unique adaptive characteristics.

A comparative analysis of the genetic structure of fat-tailed coarse-wooled sheep breeds by Dossybayev et al. (2025) [1] aimed to study the genetic characteristics of local fat-tailed coarse-wooled sheep populations in Kazakhstan using modern genomic technologies. The study used SNP genotyping data from 501 samples representing three main Kazakhstani sheep breeds: Kazakh fat-tailed coarse-wool (n=497), Edilbay (n=2), and Hissar (n=2).

Genomic research results demonstrate the unique genetic identity and high level of genetic diversity of sheep breeds raised in Kazakhstan, particularly the Edilbay breed. The Edilbay breed showed the highest level of genetic diversity (He=0.382), while the Kazakh fat-tailed coarse-wool sheep showed an average level (He=0.359). Principal component analysis revealed clear differences between Kazakh fat-tailed coarse-wool, Edilbay, and Hissar breeds, indicating distinct genetic origins and independent evolutionary paths despite phenotypic similarities (Fig. 1).

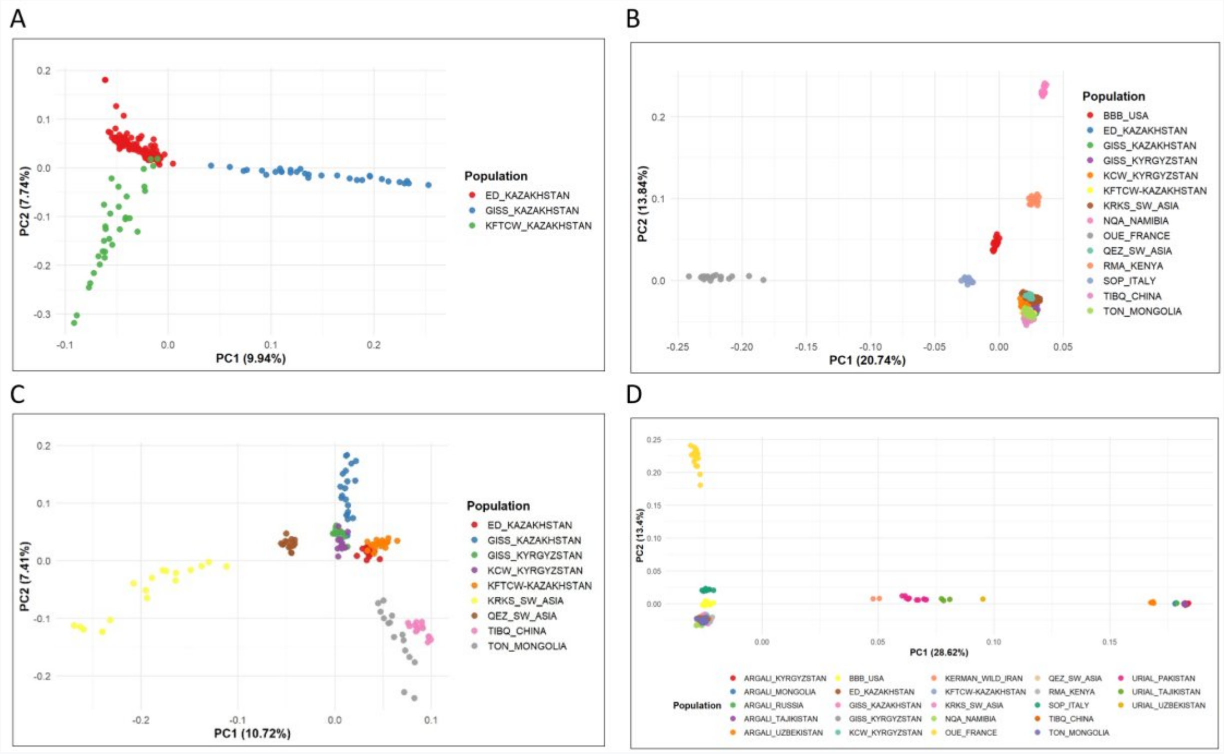

Figure 1. Principal Component Analysis (PCA) of studied sheep populations. (A) Three studied sheep populations from Kazakhstan. (B) Studied world domestic sheep breeds. (C) Studied Asian domestic sheep breeds. (D) Extended PCA including wild and domestic sheep from Central Asia, Mongolia, China, and Africa. PCA analysis clearly demonstrates the genetic differentiation between the studied breeds.

Genome-Wide Association Studies (GWAS)

In recent years, genome-wide association studies (GWAS) have become widely used in sheep farming. Akhatayeva et al. (2025) [2] conducted a GWAS study on Kazakh fat-tailed coarse-wool sheep to identify genetic variants associated with body conformation traits. The study analyzed associations with 12 morphometric parameters including live weight (LW), wither height (WH), rump height (RH), chest width (ChW), chest depth (ChD), chest girth (ChG), body length (BL), pelvis width (PW), cannon bone circumference (CBC), tail width (TW), tail length (TL), and tail weight.

The study identified 25 genome-wide significant single nucleotide polymorphisms (SNPs) associated with various body measurements. These SNPs are located on different chromosomes and are linked to genes involved in skeletal development, muscle growth, and metabolic regulation. Candidate genes identified include MSTN, NCAPG, LCORL, HMGA2, and others known for their role in controlling growth and development in mammals. Fig. 2 presents Manhattan plots for nine of the twelve body conformation traits analyzed.

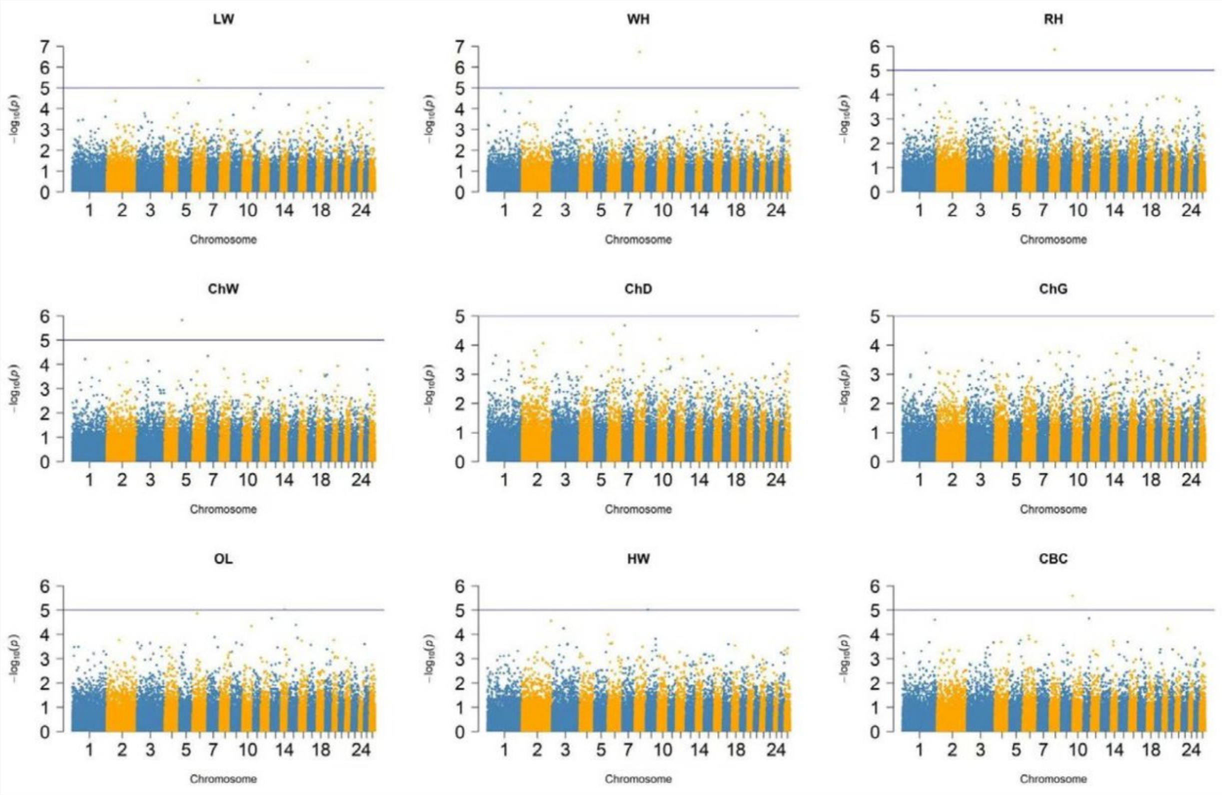

Figure 2. Manhattan plots of GWAS for body conformation traits in Kazakh fat-tailed coarse-wool sheep. Each point represents a SNP, with the y-axis showing –log■■(p-value) and the x-axis showing chromosome position. The horizontal line indicates the genome-wide significance threshold. Traits: LW – live weight; WH – wither height; RH – rump height; ChW – chest width; ChD – chest depth; ChG – chest girth; OL – body length; HW – pelvis width; CBC – cannon bone circumference.

Runs of Homozygosity (ROH) Analysis — Breed Characterization

Kozhakhmet et al. (2025) [3] used Runs of Homozygosity (ROH) analysis to assess the level of genetic diversity, relatedness, and identify selection signatures in the Kazakh fat-tailed coarse-wool sheep breed. ROH are continuous stretches of homozygous genotypes in the genome that indicate regions where an individual inherited identical DNA segments from both parents. The study found that short ROH segments (1–2 Mb) predominate, indicating ancient inbreeding that occurred many generations ago. The genomic inbreeding coefficient (F_ROH = 0.047) suggests a moderate level of inbreeding in the population (Fig. 3).

These results can be applied in breeding programs and genetic diversity monitoring in sheep farms across the country. The identified ROH-concentrated regions and candidate genes provide important information for developing genomic selection strategies.

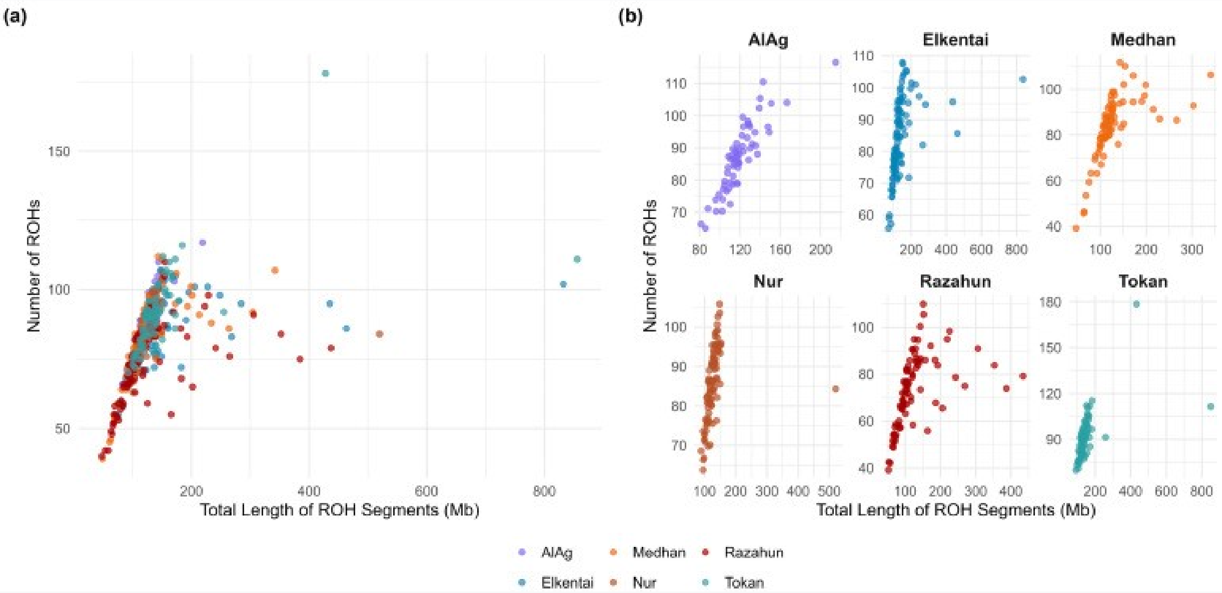

Figure 3. ROH distribution in Kazakh fat-tailed coarse-wool sheep. (a) Scatter plot showing the number of ROH segments versus their total length (Mb) for all 497 individuals, coloured by breed. (b) Per-breed scatter plots for six breed groups (AlAg, Elkentai, Medhan, Nur, Razahun, Tokan), revealing breed-specific inbreeding patterns.

Comparative Inbreeding Across Five Kazakhstani Sheep Breeds

Khamzina et al. (2025) [4] studied homozygosity regions in five local sheep breeds: Edilbay (ED, n=10), Kazakh fine-wool (KFW, n=10), Kazakh coarse-wool (KC, n=10), Semirechensk (SR, n=9), and Kazakh fat-tailed coarse-wool (KFC, n=497). The data show that the Kazakh fine-wool and Edilbay breeds have low genomic inbreeding levels (F_ROH = 0.039 and 0.037 respectively), indicating limited consanguineous mating. Relatively higher F_ROH values were recorded for Semirechensk (0.075), Kazakh coarse-wool (0.063), and Kazakh fat-tailed coarse-wool (0.047) breeds (Fig. 4).

Identified candidate genes in ROH regions include genes associated with meat productivity (MSTN, GDF8), wool quality (FGF5, PDGFD), and adaptation to environmental conditions (TSHR, KITLG). Indicators are not excessively high, indicating that genetic diversity has not been completely lost, and further selective work can be effectively conducted.

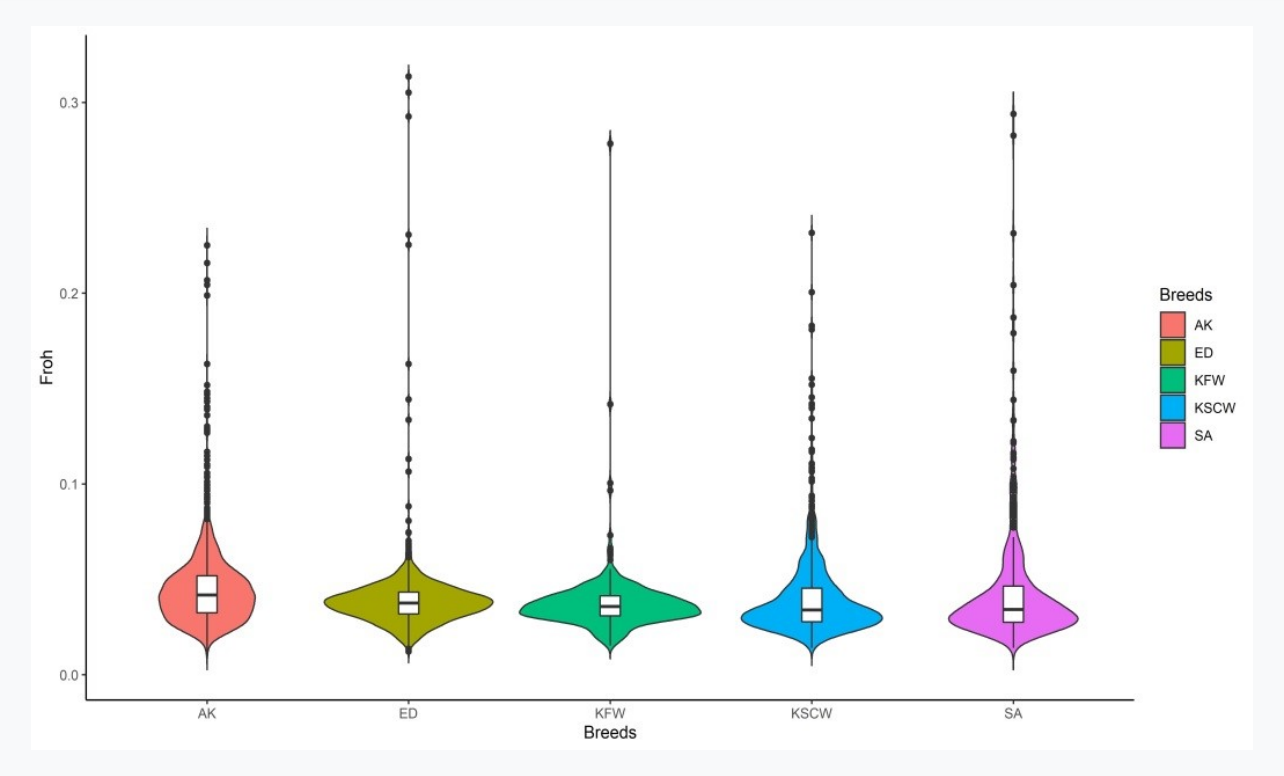

Figure 4. Genomic inbreeding coefficients (F_ROH) for five Kazakhstani sheep breeds: AK – Akjayik, ED – Edilbay, KFW – Kazakh fine-wool, KSCW – Kazakh semi-coarse-wool, SA – South Altai. Violin plots show the distribution of individual F_ROH values. Lower values indicate higher genetic diversity and less inbreeding.

Goat Genetic Research

Kichamu et al. (2025) [5] conducted genome-wide analysis to understand the genetic structure of local goat populations in Kazakhstan. The study used 120 samples from six settlements in five regions and analyzed 778,044 SNPs. Samples were collected from: Ushterek (Kostanay), Kosseit (Kyzylorda), Shokpar and Kundyzdy (Turkestan), and Darbaza (Zhetysu).

Analysis revealed significant variation in genetic diversity between populations. Samples from Shokpar and Kundyzdy showed predominant excess heterozygosity, while those from Kosseit and Darbaza had high inbreeding levels. Ushterek samples showed a balanced structure with moderate diversity. Selection signature analysis using iHS (integrated haplotype score) identified genomic regions under positive selection related to climate adaptation and disease resistance (Fig. 5).

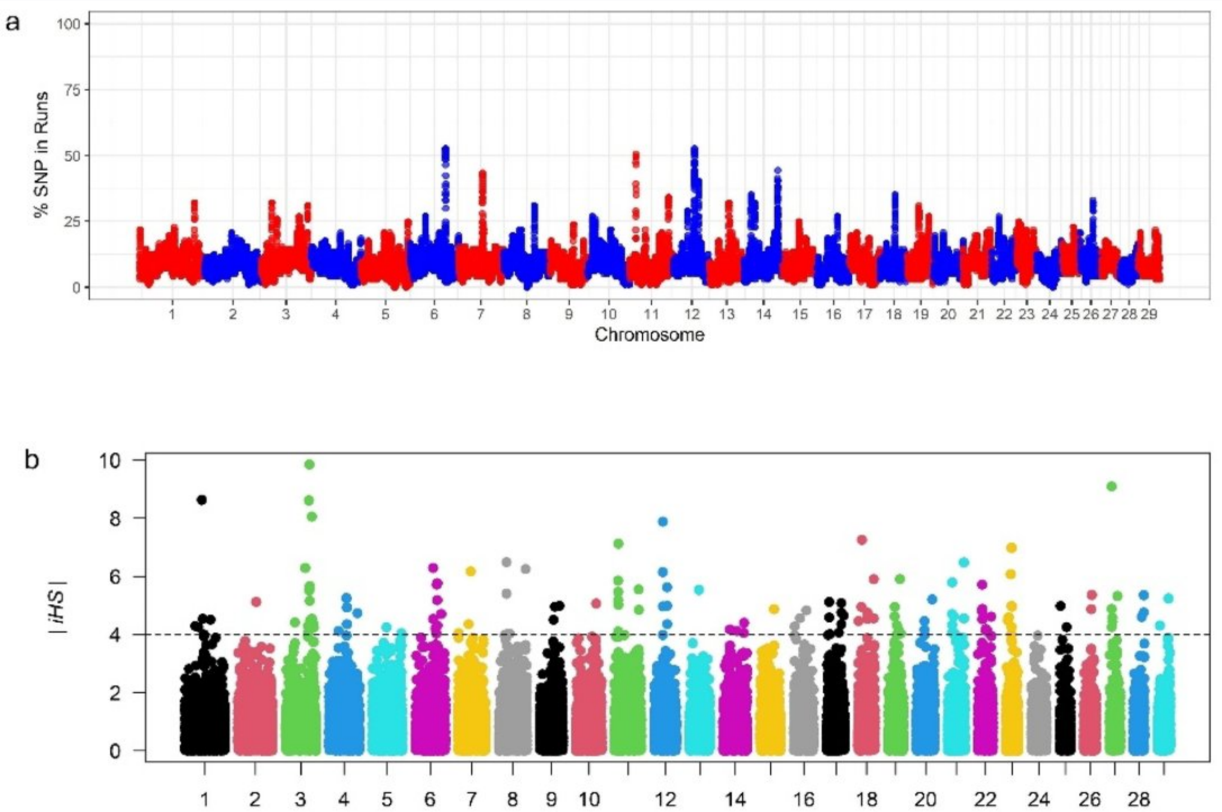

Figure 5. Manhattan plots showing (a) percentage of SNPs per chromosome in Runs of Homozygosity and (b) distribution of integrated haplotype score (|iHS|) across chromosomes. Peaks indicate genomic regions under positive selection in Kazakhstan local goat populations. The dashed line in (b) marks the significance threshold (|iHS| = 4).

II. Genetic Research on Cattle

Cattle farming occupies a leading position in Kazakhstan's agro-industrial complex and plays an important role in forming the country's food security and export potential. The Kazakh Whiteheaded cattle breed is one of the main beef breeds raised in the country, characterized by high adaptive qualities to continental climate conditions.

Selection Signatures in Kazakh Whiteheaded Cattle

Khamzina et al. (2025) [6] examined the genetic structure and ancestral breed composition of Kazakh Whiteheaded cattle using whole-genome resequencing. The research revealed that the Kazakh Whiteheaded cattle genome consists of genetic contributions from three breeds: Hereford (45%), Altai (30%), and Kalmyk (25%). Through principal component analysis (PCA) and ancestry determination, genomic analysis revealed significant selection signatures in genes associated with meat productivity, adaptation to climate conditions, and disease resistance (Fig. 6).

A genome-wide association analysis identified the KIT gene region on chromosome 6 as a major locus controlling coat colour, with admixture tracks showing distinct haplotype blocks in the four breed-forming groups (ALT, HER, KAL, KWH). These findings provide important information for developing genomic selection programs for Kazakh Whiteheaded cattle.

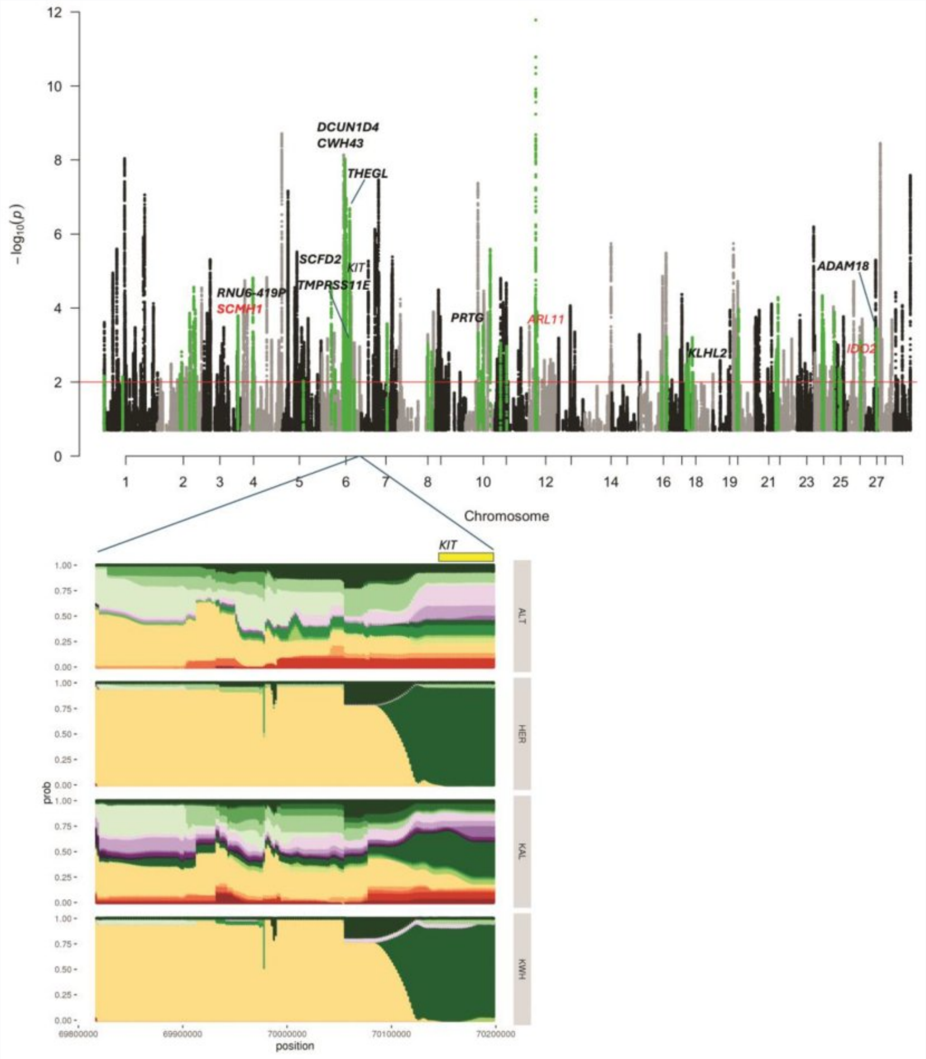

Figure 6. Selection signatures detected in four breed-forming groups of Kazakh Whiteheaded cattle. Top: Manhattan plot of genome-wide association across all 27 autosomes; annotated genes include KIT, THEGL, DCUN1D4, SCMH1, ARL11, KLHL21, and ADAM18. Bottom: Ancestral admixture tracks for a 400 kb window around the KIT locus on chromosome 6, shown separately for ALT (Altai), HER (Hereford), KAL (Kalmyk), and KWH (Kazakh Whiteheaded) groups.

Genetic Architecture and Origins of Kazakhstani Cattle

Niyazbekova et al. (2025) [7] characterized the genetic composition and origins of cattle breeds in Kazakhstan using whole-genome sequencing of 100 samples from six different Kazakhstani cattle populations, achieving an average sequencing depth of 30×. The study included three Kazakh local breeds (Kazakh local breed, Alatau, and Kazakh white-headed), analysed alongside 13 breed groups spanning North Europe, East Europe, West Europe, Central-South Europe, Northeast Asia, Xizang China, North-Central China, South China, Africa indicine, and India-Pakistan (Fig. 7).

PCA and ADMIXTURE analyses at K=2 and K=5 revealed that Kazakhstani cattle share the dominant Eurasian taurine component with European breeds, but also contain a distinct Northeast Asian component and traces of indicine ancestry (Fig. 7C). The phylogenetic tree suggests that the East Asian taurine lineage may represent the initial genetic contribution, subsequently displaced by migration of Eurasian cattle. The study identified several genomic regions under selection related to adaptation to harsh climatic conditions, disease resistance, and productivity traits.

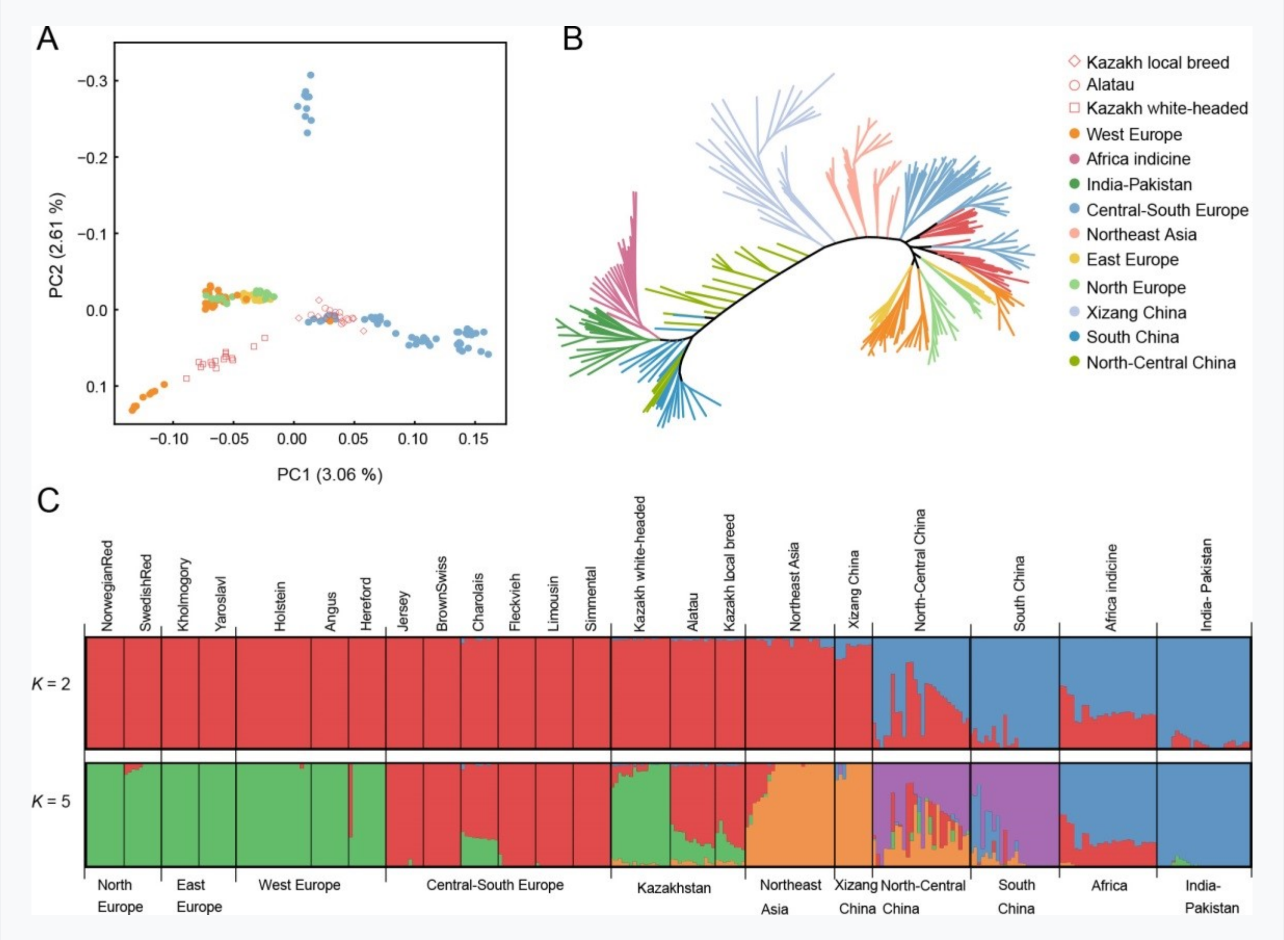

Figure 7. Phylogenetic relationships and population structure of Kazakhstani cattle. A: Principal Component Analysis of taurine cattle from various geographical regions, highlighting Kazakh local breed (■), Alatau (■), and Kazakh white-headed (■). B: Phylogenetic tree based on genome-wide SNP data, with branches coloured by breed group. C: ADMIXTURE bar plots at K=2 and K=5, showing the proportion of ancestral components for each population. The analysis reveals the complex genetic history of Kazakhstani cattle populations.

Conclusions

This review, based on scientific publications on genetic research of sheep, goats, and cattle breeds published in 2025, examines the current state and development trends in this field. The analyzed studies demonstrate significant progress in understanding the genetic architecture, population structure, and adaptive characteristics of Kazakhstani livestock breeds. Key findings include: (1) the Edilbay breed possesses the highest genetic diversity among studied sheep breeds (He=0.382); (2) GWAS identified 25 genome-wide significant SNPs for body conformation traits; (3) ROH analysis confirmed moderate inbreeding levels (F_ROH 0.037–0.075) across five sheep breeds; (4) local goat populations show strong regional differentiation and positive selection signatures; (5) Kazakh Whiteheaded cattle carry ancestry from Hereford (45%), Altai (30%), and Kalmyk (25%) breeds; (6) Kazakhstani cattle populations reveal East Asian taurine origins subsequently displaced by Eurasian cattle migration. The obtained results form a solid foundation for developing modern breeding programs based on genomic technologies and contribute to preserving the genetic diversity of valuable local breeds adapted to harsh continental climate conditions.

Future Research Directions and Recommendations

While the review shows significant scientific progress, several methodological, infrastructural, and organizational priorities can be identified for further research:

- **Expansion of genomic databases:** Creating a unified national genomic database for all major livestock breeds, standardizing phenotypic and genotypic data collection protocols.
- **Development of genomic selection programs:** Implementing genomic prediction methods for economically important traits and training specialists in genomic technologies.
- **Study of adaptation mechanisms:** Detailed investigation of genetic mechanisms of adaptation to climate change and research on disease resistance genes.
- **International collaboration:** Participation in international genomic research consortia, exchange of genetic material and data with foreign scientific centers.
- **Infrastructure development:** Creating modern genotyping and sequencing centers, establishing cryobanks for genetic resources.
- **Regulatory framework:** Developing regulations for genomic selection use in breeding and establishing standards for genetic material quality and certification.

References

1. Dossybayev K., et al. Genome-Wide SNP Analysis Reveals the Unique Genetic Characteristics of Kazakh Fat-Tailed Coarse-Wooled Sheep. *Biology.* 2025;14(11):1478. https://doi.org/10.3390/biology14111478

2. Akhatayeva Z, Dossybayev K, Kozhakhmet A, et al. Genome-Wide Association Study for Body Conformation Traits in Kazakh Fat-Tailed Coarse-Wool Sheep. *Genes.* 2025;16(9):1023. https://doi.org/10.3390/genes16091023

3. Kozhakhmet A, Akhatayeva Z, Dossybayev K, et al. Genomic Characterization of the Kazakh Fat-Tailed Coarse-Wool Sheep Breed Using ROH Analysis. *Animals (Basel).* 2025;15(18):2714. doi:10.3390/ani15182714

4. Khamzina A., Smagulov D., Dossybayev K., Kantanen J., Khamzin K. Assessing runs of homozygosity reveals production traits of Kazakh sheep breeds. *Brazilian Journal of Biology,* 85:2025. https://doi.org/10.1590/1519-6984.292980

5. Kichamu N., Wanjala G., Dossybayev K., Bagi Z., Bekmanov B., Kusza S. Genome-wide analysis provides insight into the genetic diversity and adaptability of Kazakhstan local goats. *Sci Rep* 15, 19327 (2025). https://doi.org/10.1038/s41598-025-02427-8

6. Khamzina AK, Igoshin AV, Muslimova ZU, et al. Resequencing Composite Kazakh Whiteheaded Cattle: Insights into Ancestral Breed Contributions, Selection Signatures, and Candidate Genetic Variants. *Animals.* 2025;15(3):385. https://doi.org/10.3390/ani15030385

7. Niyazbekova Z, Xu Y, Qiu M, et al. Whole-genome sequencing reveals genetic architecture and selection signatures of Kazakh cattle. *Zoological Research,* 46(2):301–311 (2025). https://doi.org/10.24272/j.issn.2095-8137.2024.235

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