



## Population structure of Kyrgyz Mountain Merino sheep: Analysis of nuclear locus variability

### Tyrgoot Chortonbaev

Doctor of Agricultural Sciences, Professor  
Kyrgyz National Agrarian University named after K.I. Skryabin  
720005, 68 Mederov Str., Bishkek, Kyrgyz Republic  
<https://orcid.org/0000-0001-9820-2337>

### Zhaynagul Isakova

Doctor of Medical Sciences, Professor  
Kyrgyz Research Institute of Molecular Biology and Medicine  
720040, 3 Tologol Moldo Street, Bishkek, Kyrgyz Republic  
<https://orcid.org/0000-0002-3681-6939>

### Esenbek Belek uulu\*

Postgraduate Student  
Kyrgyz National Agrarian University named after K.I. Skryabin  
720005, 68 Mederov Str., Bishkek, Kyrgyz Republic  
<https://orcid.org/0000-0002-5590-1354>

**Abstract.** The relevance of the study is determined by the need to preserve local, unique and highly adapted breeds of farm animals in the context of global climate change and a reduction in the number of breeding stock. The Kyrgyz Mountain Merino is a valuable genetic resource, highly adaptable to mountain conditions, with high-quality wool and efficient use of scarce feed. However, a limited gene pool and increasing inbreeding pose risks to the breed's productivity and adaptability. The aim of the study was to analyse the population structure of the Kyrgyz Mountain Merino based on an assessment of nuclear locus variability. To achieve this goal, sheep were genotyped using a panel of highly polymorphic microsatellite markers (SSR) recommended by the International Society for Animal Genetics (ISAG). Allele diversity indices, observed and expected heterozygosity,  $F_{IS}$  fixation coefficients, Nei genetic distances were calculated, and population structure analysis was performed using cluster analysis, PCA and STRUCTURE model methods. The results of the study showed a high level of allelic diversity at most loci (number of alleles per locus 6-14, effective number of alleles  $N_e$  3.41-6.21,  $PIC > 0.69$ ). The observed heterozygosity ( $H_o = 0.68-0.73$ ) practically corresponded to the expected ( $H_e = 0.70-0.74$ ), and the  $F_{IS}$  coefficients remained low (0.012-0.028), indicating the absence of pronounced inbreeding. Genetic differentiation between groups was weak ( $F_{ST} = 0.018-0.032$ ), Nei's genetic distances were minimal (0.038-0.051), and STRUCTURE analysis revealed two conditional genetic clusters with uniform distribution across groups, confirming the integrity of the population. The practical value of the study lies in identifying the current state of the Kyrgyz Mountain Merino gene pool, which allows for the development of recommendations for controlled selection work, the preservation of unique alleles, and the maintenance of genetic diversity of the breed, ensuring its resistance to adverse environmental conditions

**Keywords:** genetic diversity; microsatellite markers; population structure; heterozygosity; fixation coefficient; allelic diversity; Kyrgyz sheep

**Suggested Citation:** Chortonbaev, T., Isakova, Zh., & Belek uulu, E. (2025). Population structure of Kyrgyz Mountain Merino sheep: Analysis of nuclear locus variability. *Bulletin of the Kyrgyz National Agrarian University*, 23(4), 63-71. doi: 10.63621/bknau./4.2025.63.

\*Corresponding author



Copyright © The Author(s). This is an open access article distributed under the terms of the Creative Commons Attribution License 4.0 (<https://creativecommons.org/licenses/by/4.0/>)

## Introduction

In the context of global climate change, intensification of livestock farming and expansion of the gene pool of strategic breeds, the conservation of local, unique and highly adapted breeds of farm animals is of particular importance. One such breed is the Kyrgyz Mountain Merino, a valuable genetic resource that has developed under the influence of the complex natural and climatic conditions of the high-altitude pastures of Kyrgyzstan (Zholborsov *et al.*, 2024). This breed is characterised by its resistance to hypoxia, pronounced adaptive mechanisms, high wool quality and ability to effectively utilise poor mountain feed. However, as noted by K. Iskakov *et al.* (2017), there has been a decline in the number of breeding stock, an increase in the level of inbreeding, and a narrowing of genetic diversity, which could potentially lead to a decrease in the adaptability and productivity of animals.

Modern science has a wide range of molecular genetic methods at its disposal that allow for an objective assessment of the state of breed populations. Studies of sheep are most often based on the analysis of mitochondrial DNA, as it is easier to isolate and provides information about the maternal line. However, according to A. Kawęcka *et al.* (2022), mitochondrial analysis does not reflect the full picture of genetic processes, does not allow for the assessment of paternal lineages, and does not characterise intrapopulation processes as a whole. Unlike mtDNA, the variability of nuclear loci provides comprehensive information about population structure, selection intensity, inbreeding levels, genetic heterogeneity, and the historical evolution of the breed (Li *et al.*, 2024). Nuclear markers – such as STR/SSR, SNP or microsatellite sequences – are highly polymorphic and allow for high-precision determination of allelic diversity, genetic distances and the degree of population differentiation. Studies of similar local sheep breeds in other countries, such as G. McKenzie *et al.* (2010) in New Zealand, show that the absence of a systematic selection policy, small effective population sizes and limited animal migration can lead to a decline in genetic diversity and the disappearance of unique alleles, especially in isolated mountain regions. Despite the practical importance of the Kyrgyz Mountain Merino, its gene pool has not been sufficiently studied to date. There is a lack of modern genetic studies using nuclear markers and reflecting the real structure of the breed. As pointed out by T. Odjakova *et al.* (2023), the lack of scientific data complicates the development of breeding programmes and strategies for preserving the gene pool, and also limits the possibilities for objective assessment of intraspecific variability and identification of unique genetic lines.

The relevance of the study is due to the need for a comprehensive analysis of the genetic diversity of the Kyrgyz Mountain Merino using modern molecular technologies. This will make it possible to identify the level of gene pool conservation, determine the degree

of genetic differentiation within the breed, establish existing genetic risks, and develop scientifically sound recommendations for breeding and selection work. The aim of the study was to obtain objective data on the genetic structure of the Kyrgyz Mountain Merino population by assessing the variability of nuclear loci and subsequently determining the levels of intrapopulation and intergroup variability. To achieve this goal, the following tasks were set: to determine the level of allelic diversity and the of polymorphism of nuclear markers; to calculate indicators of genetic heterozygosity and inbreeding coefficients; to identify the degree of genetic differentiation of the studied groups of animals. The study can not only supplement existing data on the genetic resources of sheep breeding in Kyrgyzstan, but also create a scientific basis for the development of long-term programmes for the conservation and rational use of the Kyrgyz Mountain Merino breed.

## Materials and Methods

The study was conducted in 2023 on Kyrgyz Mountain Merino sheep in the Naryn and Issyk-Kul regions (Naryn Breeding Farm and Issyk-Kul Breeding Farm). Laboratory analysis was carried out at the Research Institute of Molecular Biology and Medicine (Bishkek, Kyrgyzstan). A total of 36 animals were studied, divided into three groups according to age, sex, origin and absence of close kinship, as indicated in the work of A. Bekturov *et al.* (2023): Group 1 – 12 adult sheep, aged 2-3 years, females; Group 2 – 12 adult sheep, aged 2-3 years, males; Group 3 – 12 adult sheep, aged 3-4 years, females and males. The animals were kept on pasture with limited access to additional feed according to the standard breeding programme of the farms. All procedures were performed by veterinary specialists in accordance with animal welfare recommendations (Directive 2010/63/EU, 2010).

Five millilitre samples of whole blood were collected from the jugular vein using disposable sterile needles and vacuum tubes containing EDTA (ethylenediaminetetraacetic acid) as an anticoagulant. After sampling, the samples were immediately cooled and transported in a container with cooling elements at a temperature of 4-6°C. In the laboratory, the samples were frozen and stored at -20°C for no more than 4 weeks prior to analysis. Genomic DNA was extracted in two ways, depending on the quality of the source material: (1) using the standard phenol-chloroform method according to the protocol by J. Sambrook & D. Russell (2001) for samples without signs of haemolysis; (2) using the DNeasy Blood & Tissue Kit (Qiagen, Germany) for samples containing traces of haemolysis or having a reduced cell composition (Romanov, 2021). The quality and concentration of the isolated DNA were determined spectrophotometrically using Nanodrop 2000 (Thermo Scientific, USA) at wavelengths of 260/280 nm, as well as by

electrophoresis in 1.5% agarose gel to confirm the integrity of the genetic material. Loci were selected based on the criteria of polymorphism level, amplification stability, and informativeness for population analyses.

Microsatellite loci were analysed using a panel of 15 highly polymorphic STR markers included in the official ISAG/FAO recommended panel for sheep and widely used in population genetics studies (FAO, 2011) (Table 1).

**Table 1.** List of microsatellite loci used (n = 15)

No.	Locus	Chromosome (Oar_v4.0)	Allele range, bp
1	OarFCB20	2	90
2	MAF214	16	110-140
3	OarFCB304	17	140-170
4	INRA63	14	170-190
5	MAF65	15	110-130
6	MCM527	5	160-180
7	INRA023	3	200-220
8	OarAE129	6	130-160
9	SRCRSP8	1	210-240
10	MAF70	4	120-150
11	SPS113	11	130-160
12	CSRD247	14	210-250
13	INRA172	1	130-160
14	SRCRSP5	4	170-200
15	OarCP49	17	100-130

**Source:** compiled by the authors based on FAO (2011)

Marker amplification was performed by polymerase chain reaction (PCR) in a thermocycler according to optimised temperature conditions for each locus. PCR products were separated by capillary electrophoresis on an ABI 3130 automatic genetic analyser (Gootwine, 2020), after which allele sizes were determined using an internal molecular weight standard (Punuru *et al.*, 2025). Quality control of amplicons and visualisation of restriction patterns (if necessary) were performed by horizontal electrophoresis in 1.5-2.5% agarose gels stained with ethidium bromide and subsequent photography in a UV transilluminator. To minimise genotyping errors associated with non-specific fragments, the fluorescence intensity of individual bands of restriction patterns was additionally taken into account (Kulibaba *et al.*, 2023). Primary analysis of electropherograms was performed using GeneMapper v.5.0 (Applied Biosystems, USA), where each allele position was assigned a specific size in base pairs. Based on the obtained allele profiles, genetic diversity indices were calculated using GenAlEx v.6.5 (Peakall & Smouse, 2012; Gáspárdy, 2021) and Arlequin v.3.5 (Duncanson, 2025) software. The number of alleles per locus ( $N_a$ ) was determined as the total number of different alleles detected at each locus according to the standard population genetics methodology (Granero *et al.*, 2022). The effective number of alleles ( $N_e$ ) was calculated using formula (1):

$$N_e = \frac{1}{\sum p_i^2}, \quad (1)$$

where  $p_i$  is the frequency of the  $i$ -th allele at the locus (Nei, 1972).

Observed heterozygosity ( $H_o$ ) was calculated as the proportion of heterozygous genotypes in the total sample using formula (2):

$$H_o = \frac{N_{het}}{N}, \quad (2)$$

where  $N_{het}$  is the number of heterozygous individuals.

Expected heterozygosity ( $H_e$ ) was determined according to M. Nei (1978) using formula (3):

$$H_e = 1 - \sum P_i^2, \quad (3)$$

which reflects the probability of heterozygosity at Hardy-Weinberg equilibrium.

The fixation index ( $F_{IS}$ ) was calculated according to the formula by B. Weir & C. Cockerham (1984) (4):

$$F_{IS} = \frac{H_o}{H_e}, \quad (4)$$

which allows the level of inbreeding within groups to be assessed.

Locus polymorphism (PIC) was estimated according to D. Botstein *et al.* (1980) (5):

$$PIC = 1 - \sum p_i^2 - \sum \sum 2p_i^2 p_j^2, \quad (5)$$

where  $p_i$  and  $p_j$  are allele frequencies.

Genetic distances between the studied groups were calculated using the method of M. Nei (1972) in the Arlequin v.3.5 programme according to formula (6):

$$D = -\ln(I), \quad (6)$$

where  $I$  is the coefficient of genetic similarity. All calculations were performed automatically using the GenAlEx and Arlequin programmes, followed by manual verification of the frequencies.

For cluster analysis, the UPGMA (Unweighted Pair Group Method with Arithmetic Mean) method was used based on the genetic distance matrix of M. Nei (1972), calculated between all pairs of the studied groups. The dendrogram was constructed using the MEGA X programme, which allowed for visualisation the proximity of genetic profiles and identify clusters within the sample. Principal component analysis (PCA) was used to reduce the dimensionality of the data and identify the main axes of genetic variation. Allele frequencies at each locus were used as input variables. The analysis was performed using GenALEX v.6.5 (Peakall & Smouse, 2012), and the results were visualised as the dispersion of individuals on the first two principal components (Megdiche *et al.*, 2019). This approach allowed for assessing the degree of overlap between groups and identify potential subpopulations without making assumptions about the model.

The STRUCTURE v.2.3.4 programme was used to identify hidden subpopulations. As part of the analysis, an admixture model with independent allele frequencies was used; the number of clusters (K) ranged from 1 to 10 with 10 repetitions for each K; 100,000 MCMC (Markov Chain Monte Carlo) steps were used for “warming up” and 500,000 steps for parameter estimation. The optimal number of subpopulations was determined using the  $\Delta K$  criterion (Gurgul *et al.*, 2021), after which each individual was assigned a probability of belonging to each cluster. Geographical and tribal differences were assessed using AMOVA (Analysis of

Molecular Variance) and  $F_{ST}$  coefficient calculations in Arlequin v.3.5. The reliability of differences between groups was tested using permutation tests (10,000 permutations). All methods allowed for a comprehensive assessment of population structure, the degree of genetic differentiation, and the possible presence of hidden genetic subgroups.

## Results and Discussion

Analysis of nuclear loci in Kyrgyz Mountain Merino sheep allowed for obtaining a comprehensive characterisation of the genetic diversity of the breed and to identify patterns in its population structure. Genotyping using a panel of highly polymorphic microsatellite markers revealed significant allelic diversity, distributed unevenly among the studied groups of animals. The data obtained indicate the preservation of the basic level of genetic variability, despite the relatively narrow gene pool and geographical isolation of some breeding herds. According to the results of the analysis, the number of alleles per locus varied from 6 to 14. These indicators correspond to a high level of polymorphism, according to data from A. Grasso *et al.* (2014). The greatest allelic diversity was observed at the OarFCB20 and MAF214 loci, indicating the possible influence of historical breeding lines and the preservation of rare alleles in individual herds (Table 2). High values of effective allele number (from 3.41 to 6.21, averaging  $4.72 \pm 0.91$  across 15 loci) confirm the presence of moderately expressed genetic heterogeneity within the breed.

**Table 2.** Allele diversity at the studied nuclear loci

Locus	Number of alleles (Na)	Effective number of alleles (Ne)	PIC
OarFCB20	14	6.21	0.83
MAF214	12	5.78	0.81
OarFCB304	9	4.32	0.74
INRA63	7	3.89	0.71
MAF65	6	3.41	0.69

**Source:** compiled by the authors

The PIC polymorphic information coefficient for most loci exceeds 0.70, which classifies them as highly polymorphic markers. According to B. Moiola *et al.* (1998), such loci ensure high genotyping accuracy and allow for correct assessment of genetic distances, population structure, and the degree of genetic differentiation. The indicators presented in Table 2 confirm that the panel of nuclear markers used is highly

informative and adequately reflects the genetic diversity of the Kyrgyz Mountain Merino, as indicated by S. Ceccobelli *et al.* (2023). The parameters of expected and observed heterozygosity indicate a balanced genetic structure of the populations. In all studied groups, the  $H_o$  values were close to  $H_e$ , and the fixation coefficient  $F_{IS}$  did not exceed 0.05, which indicates the absence of pronounced inbreeding processes (Table 3).

**Table 3.** Indicators of heterozygosity and fixation coefficients

Group	$H_o$	$H_e$	$F_{IS}$
Group 1	0.71	0.72	0.014
Group 2	0.68	0.70	0.028
Group 3	0.73	0.74	0.012
Total sample	0.71	0.72	0.017

**Source:** compiled by the authors

The observed heterozygosity practically corresponds to the expected value, with a minimal difference between them, reflecting a balanced distribution of alleles and the absence of a significant deficit of heterozygotes.  $H_o$  values range from 0.68 to 0.73, which is typical for sheep breeds with moderate levels of intrapopulation variability. Low values of the fixation coefficient  $F_{IS}$  (0.012-0.028) indicate the absence of pronounced inbreeding. Positive but close to zero  $F_{IS}$  values may be associated with the natural structure of the population, breeding characteristics, or random genetic drift processes that do not significantly affect the breed's gene pool. The preservation of this level of heterozygosity may be due to the existence of several breeding lines; controlled use of producers; geographical distribution of herds,

minimising genetic isolation. A comparison of data between groups demonstrates the overall genetic stability of the breed, with no signs of fragmentation or local reduction in heterozygosity. These indicators point to the existence of a stable gene pool, supported by moderate genetic exchange between herds and possible control of breeding work.

The assessment of differentiation between groups by  $F_{ST}$  showed a low level of differences (0.018-0.032), indicating the preservation of common genetic lines and the absence of significant divergence between herds. Genetic distances according to Nei also demonstrated the proximity of the studied populations, varying between 0.038 and 0.051 (Table 4). This indicates a stable population structure and active exchange of genetic material between herds.

**Table 4.** Matrix of genetic distances between the studied groups

Group	1	2	3
Group 1	–	0.042	0.038
Group 2	0.042	–	0.051
Group 3	0.038	0.051	–

**Source:** compiled by the authors

The smallest genetic distance is observed between groups 1 and 3, which may indicate their closer historical connection or exchange of producers between the respective herds. A slightly higher distance value is noted between groups 2 and 3, but even this difference remains at a level characteristic of weakly differentiated populations. Such values indicate that the genetic structure of the breed remains intact and the degree of divergence between herds is minimal. Low genetic distance values confirm the results of the  $F_{ST}$  analysis, indicating weak differentiation and no significant

fragmentation of the breed. Such a genetic profile is characteristic of breeds with a moderately developed selection system and sustained exchange of genetic material between groups. Modelling using the STRUCTURE method revealed two conditional genetic clusters distributed among flocks without a clear geographical reference (Table 5). This structure corresponds to the conclusions of A. Abdelmanova *et al.* (2021) and S. Cecobelli *et al.* (2023) on high-altitude Merinos, where historical breeding lines form several overlapping genetic components without pronounced fragmentation.

**Table 5.** Share of genetic clusters in the studied groups (K = 2)

Group	Cluster 1	Cluster 2
Group 1	0.57	0.43
Group 2	0.61	0.39
Group 3	0.54	0.46

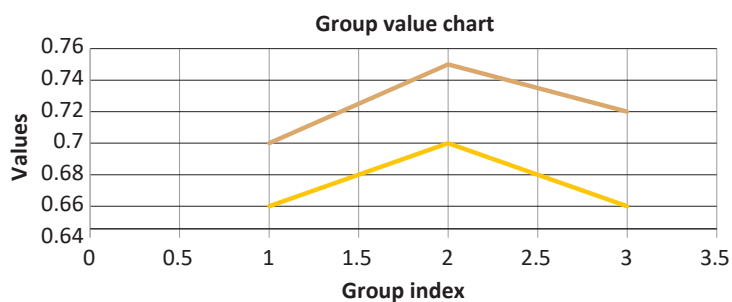
**Source:** compiled by the authors

The distribution of the shares of the two genetic clusters in each of the three groups studied shows insignificant differences. For example, Cluster 1 predominates in Group 1 with a share of 0.57, while the share of Cluster 2 is 0.43. A similar trend is observed in other groups. The absence of a sharp division between clusters confirms the integrity of the breed and the stability of its gene pool, reflecting historical breeding lines and the formation of separate brood flocks while maintaining overall genetic diversity. Principal component analysis confirmed the picture of weak differentiation, which is consistent with the data of A. Abdelmanova *et al.* (2021) on other highland breeds. Figure 1 shows the distribution of observed heterozygosity across the

studied groups.  $H_o$  values range from 0.68 to 0.73, indicating a relatively stable genetic background of the studied populations. The highest heterozygosity was observed in Group 3, while Groups 1 and 2 showed slightly lower but comparable values. Overall, the distribution of  $H_o$  reflects moderate genetic diversity among the groups. The results show that the Kyrgyz Mountain Merino breed has a moderately high level of genetic diversity. The heterozygosity indices of the studied population are comparable or even higher than those of similar local breeds, such as the Tajik Mountain Merino and Kazakh Arkharomerino, according to L. Colli *et al.* (2015). This indicates that the breed's gene pool retains sufficient variability to adapt to different natural

conditions and resist potential negative factors. Low values of genetic differentiation coefficients  $F_{ST}$  and genetic distances according to Nei indicate the absence of significant population fragmentation, as pointed out by T. Schillhorn van Veen (1995). This means that there is a regular exchange of genetic material between the main herds, which helps to maintain a uniform gene pool for the breed and reduces the risk of isolated lines

with limited genetic variability. Thus, it can be concluded that the Kyrgyz Mountain Merino breed currently maintains a sufficient level of genetic diversity. Nevertheless, in order to prevent a possible narrowing of the gene pool in the future, especially in the event of a decline in population size or an increase in inbreeding, regular monitoring of the genetic status and continued controlled selection work are necessary.



**Figure 1.** Distribution of observed heterozygosity ( $H_o$ ) across groups

**Source:** developed by the authors

## Conclusions

The Kyrgyz Mountain Merino breed maintains a moderately high level of genetic diversity. For 15 microsatellite loci, the number of alleles per locus ranged from 6 to 14, the effective number of alleles  $N_e$  was 3.41-6.21, and the polymorphism index PIC exceeded 0.69. The observed heterozygosity  $H_o$  was in the range of 0.68-0.73, the expected heterozygosity  $H_e$  was 0.70-0.74, while the fixation coefficients  $F_{IS}$  remained low (0.012-0.028), indicating the absence of pronounced inbreeding and a deficit of heterozygotes in the population. The indicators of genetic differentiation between the studied groups were minimal:  $F_{ST}$  = 0.018-0.032, genetic distances according to Nei – 0.038-0.051. Analysis of the population structure using the STRUCTURE model revealed two conditional genetic clusters. The absence of a sharp division between clusters confirms the integrity of the breed and the stability of its gene pool, reflecting historical breeding lines and the formation of separate ewe flocks while maintaining overall genetic diversity. Thus, the Kyrgyz Mountain Merino breed has a stable gene pool and a sufficient level of genetic diversity. To prevent

a possible narrowing of the gene pool in the future, it is recommended to conduct regular monitoring of the genetic status of the population, systematic registration of maternal lines, controlled selection work to preserve unique alleles and maintain a balance between breeding groups. Prospects for further research include: expanding the panel of microsatellite markers and including SNP typing for a more detailed analysis of genetic diversity; studying the associations of genetic markers with productive and adaptive traits of the breed; long-term monitoring of population structure dynamics and the impact of breeding measures on genetic potential.

## Acknowledgements

None.

## Funding

None.

## Conflict of Interest

The authors declare that they have no conflict of interest.

## References

- [1] Abdelmanova, A.S., *et al.* (2021). Comparative study of the genetic diversity of local steppe cattle breeds from Russia, Kazakhstan and Kyrgyzstan by microsatellite analysis of museum and modern samples. *Diversity*, 13(8), article number 351. [doi: 10.3390/d13080351](https://doi.org/10.3390/d13080351).
- [2] Bekturov, A.B., Isakova, Z., Kipen, V.N., Chortonbaev, T., Mukeeva, S.B., Osmonaliev, S.K., & Aitbaev, K.A. (2023). A genogeographic study of the Kyrgyz Mountain Merino via microsatellite markers. *Vavilov Journal of Genetics and Breeding*, 27(2), 162-168. [doi: 10.18699/VJGB-23-22](https://doi.org/10.18699/VJGB-23-22).
- [3] Botstein, D., White, R.L., Skolnick, M., & Davis, R.W. (1980). [Construction of a genetic linkage map in man using restriction fragment length polymorphisms](https://doi.org/10.1093/ajhg/32.3.314). *American Journal of Human Genetics*, 32(3), 314-331.
- [4] Ceccobelli, S., *et al.* (2023). A comprehensive analysis of the genetic diversity and environmental adaptability in worldwide Merino and Merino-derived sheep breeds. *Genetics Selection Evolution*, 55(1), article number 24. [doi: 10.1186/s12711-023-00797-z](https://doi.org/10.1186/s12711-023-00797-z).

- [5] Colli, L., et al. (2015). Whole mitochondrial genomes unveil the impact of domestication on goat matrilineal variability. *BMC Genomics*, 16, article number 1115. doi: [10.1186/s12864-015-2342-2](https://doi.org/10.1186/s12864-015-2342-2).
- [6] Directive 2010/63/EU of the European Parliament and of the Council of 22 "On the Protection of Animals Used for Scientific Purposes". (2010, September). Retrieved from <https://eur-lex.europa.eu/legal-content/EN/TXT/?uri=CELEX:32010L0063>.
- [7] Duncanson, G.R. (2025). *Veterinary treatment of sheep and goats (2<sup>nd</sup> ed.)*. Oxfordshire: Cabi.
- [8] FAO. (2011). *Molecular genetic characterization of animal genetic resources. FAO animal production and health guidelines. No. 9*. Rome: FAO.
- [9] Gáspárdy, A. (2021). Reality of mitogenome investigation in preservation of native domestic sheep breeds. In A. Elkelish (Ed.), *Landraces-traditional variety and natural breed* (Chapter 10). London: IntechOpen. doi: [10.5772/intechopen.95768](https://doi.org/10.5772/intechopen.95768).
- [10] Gootwine, E. (2020). Genetics and breeding of sheep and goats. In F.W. Bazer, G.C. Lamb & G. Wu (Eds.), *Animal agriculture* (pp. 183-198). Amsterdam: Academic Press. doi: [10.1016/B978-0-12-817052-6.00010-0](https://doi.org/10.1016/B978-0-12-817052-6.00010-0).
- [11] Granero, A., Anaya, G., Demyda-Peyrás, S., Alcalde, M.J., Arrebola, F., & Molina, A. (2022). Genomic population structure of the main historical genetic lines of Spanish Merino sheep. *Animals*, 12(10), article number 1327. doi: [10.3390/ani12101327](https://doi.org/10.3390/ani12101327).
- [12] Grasso, A.N., Goldberg, V., Navajas, E.A., Iriarte, W., Gimeno, D., Aguilar, I., Medrano, J.F., Rincón, G., & Ciappesoni, G. (2014). Genomic variation and population structure detected by single nucleotide polymorphism arrays in Corriedale, Merino and Creole sheep. *Genetics and Molecular Biology*, 37(2), 389-395. doi: [10.1590/s1415-47572014000300011](https://doi.org/10.1590/s1415-47572014000300011).
- [13] Gurgul, A., Jasielczuk, I., Miksza-Cybulska, A., Kawęcka, A., Szmatoła, T., & Krupiński, J. (2021). Evaluation of genetic differentiation and genome-wide selection signatures in Polish local sheep breeds. *Livestock Science*, 251, article number 104635. doi: [10.1016/j.livsci.2021.104635](https://doi.org/10.1016/j.livsci.2021.104635).
- [14] Iskakov, K.A., Kulatayev, B.T., Zhumagaliyeva, G.M., & Casanova, P.M.P. (2017). Productive and biological features of Kazakh fine-wool sheep in the conditions of the Almaty region. *OnLine Journal of Biological Sciences*, 17(3), 219-225. doi: [10.3844/ojbsci.2017.219.225](https://doi.org/10.3844/ojbsci.2017.219.225).
- [15] Kawęcka, A., Pasternak, M., Miksza-Cybulska, A., & Puchała, M. (2022). Native sheep breeds in Poland – importance and outcomes of genetic resources protection programmes. *Animals*, 12(12), article number 1510. doi: [10.3390/ani12121510](https://doi.org/10.3390/ani12121510).
- [16] Kulibaba, R., Sakhatskyi, M., & Liashenko, Y. (2023). Analysis of genotyping features of bovine cattle individuals at the CSN2 locus using ACRS-PCR methods. *Animal Science and Food Technology*, 14(2), 44-56. doi: [10.31548/animal.2.2023.44](https://doi.org/10.31548/animal.2.2023.44).
- [17] Li, X., et al. (2024). Whole-genome resequencing to investigate the genetic diversity and mechanisms of plateau adaptation in Tibetan sheep. *Journal of Animal Science and Biotechnology*, 15, article number 164. doi: [10.1186/s40104-024-01125-1](https://doi.org/10.1186/s40104-024-01125-1).
- [18] McKenzie, G.W., Abbott, J., Zhou, H., Fang, Q., Merrick, N., Forrest, R.H., Sedcole, J.R., & Hickford, J.G. (2010). Genetic diversity of selected genes that are potentially economically important in feral sheep of New Zealand. *Genetics Selection Evolution*, 42, article number 43. doi: [10.1186/1297-9686-42-43](https://doi.org/10.1186/1297-9686-42-43).
- [19] Megdiche, S., Mastrangelo, S., Ben Hamouda, M., Lenstra, J.A., & Ciani, E. (2019). A combined multi-cohort approach reveals novel and known genome-wide selection signatures for wool traits in Merino and Merino-derived sheep breeds. *Frontiers in Genetics*, 10, article number 1025. doi: [10.3389/fgene.2019.01025](https://doi.org/10.3389/fgene.2019.01025).
- [20] Muioli, B., Pilla, F., & Tripaldi, C. (1998). Detection of milk protein genetic polymorphisms in order to improve dairy traits in sheep and goats: A review. *Small Ruminant Research*, 27(3), 185-195. doi: [10.1016/S0921-4488\(97\)00053-9](https://doi.org/10.1016/S0921-4488(97)00053-9).
- [21] Nei, M. (1972). Genetic distance between populations. *American Naturalist*, 106, 283-292. doi: [10.1086/282771](https://doi.org/10.1086/282771).
- [22] Nei, M. (1978). Estimation of average heterozygosity and genetic distance from a small number of individuals. *Genetics*, 89(3), 583-590. doi: [10.1093/genetics/89.3.583](https://doi.org/10.1093/genetics/89.3.583).
- [23] Odjakova, T., Todorov, P., Kalaydzhiyev, G., Salkova, D., Dundarova, H., Radoslavov, G., & Hristov, P. (2023). A study on the genetic diversity and subpopulation structure of three Bulgarian mountainous sheep breeds, based WWon genotyping of microsatellite markers. *Small Ruminant Research*, 226, article number 107034. doi: [10.1016/j.smallrumres.2023.107034](https://doi.org/10.1016/j.smallrumres.2023.107034).
- [24] Peakall, R., & Smouse, P.E. (2012). GenAlEx 6.5: Genetic analysis in Excel. Population genetic software for teaching and research – an update. *Bioinformatics*, 28(19), 2537-2539. doi: [10.1093/bioinformatics/bts460](https://doi.org/10.1093/bioinformatics/bts460).
- [25] Punuru, P.R., Regula, V., Metta, M., Krovvidi, S., Bhumireddy, J.M., Baratam, P., Sunkara, V., & Poonooru, R.R. (2025). Genetic characterization of semi-arid sheep populations in India using microsatellite markers. *Frontiers in Animal Science*, 6, article number 1553610. doi: [10.3389/fanim.2025.1553610](https://doi.org/10.3389/fanim.2025.1553610).
- [26] Romanov, M.N. (2021). *British sheep breed diversity*. Kent: Kent Academic Repository.

- [27] Sambrook, J., & Russell, D.W. (2001). *Molecular cloning: A laboratory manual (3<sup>rd</sup> ed.)*. New York: Cold Spring Harbor Laboratory Press.
- [28] Schillhorn van Veen, T.W. (1995). *The Kyrgyz sheep herders at a crossroads*. London: Overseas Development Institute.
- [29] Weir, B.S., & Cockerham, C.C. (1984). Estimating F-statistics for the analysis of population structure. *Evolution*, 38(6), 1358-1370. doi: 10.2307/2408641.
- [30] Zholborsov, U., Chortonbaev, T., Azhibekov, A., & Bekturov, A. (2024). Biological and productive features of Kyrgyz Mountain Merino breed types in different climatic zones. *BIO Web of Conferences*, 83, article number 01005. doi: 10.1051/bioconf/20248301005.

## Кыргыз тоо мериносунун популяциялык түзүлүшү: ядролук локустардын өзгөрмөлүүлүгүн талдоо

### Тыргоот Чортонбаев

Айыл чарба илимдеринин доктору, профессор  
К.И. Скрябин атындагы Кыргыз улуттук агрардык университети  
720005, Медеров көч., 68, Бишкек ш., Кыргыз Республикасы  
<https://orcid.org/0000-0001-9820-2337>

### Жайнагүл Исакова

Медицина илимдеринин доктору, профессор  
Кыргыз молекулярдык биология жана медицина илим-изилдөө институту  
720040, Тоголок Молдо көч., 3, Бишкек ш., Кыргыз Республикасы  
<https://orcid.org/0000-0002-3681-6939>

### Эсенбек Белек уулу

Издөнүүчү  
К.И. Скрябин атындагы Кыргыз улуттук агрардык университети  
720005, Медеров көч., 68, Бишкек ш., Кыргыз Республикасы  
<https://orcid.org/0000-0002-5590-1354>

**Аннотация.** Бул изилдөөнүн актуалдуулугу глобалдык климаттын өзгөрүшүнө жана асыл тукум малдын азайышына карабастан, жергиликтүү, уникалдуу жана жогорку деңгээлде ыңгайлашкан мал тукумдарын сактоо зарылдыгынан келип чыгат. Кыргыз тоо мериносу тоо шарттарына жогорку деңгээлде ыңгайлашкан, жогорку сапаттагы жүн өндүргөн жана тартыш тоютту натыйжалуу колдонгон баалуу генетикалык ресурс болуп саналат. Бирок, генофонддун чектелүү болушу жана тукумсуздуктун көбөйүшү өндүрүмдүүлүктүн жана ыңгайлашуунун төмөндөшүнө алып келүүчү коркунучтарды жаратат. Бул изилдөөнүн максаты ядролук локустардын өзгөрмөлүүлүгүн баалоо менен кыргыз тоо меринос койлорунун популяциялык түзүмүн талдоо болгон. Бул максатка жетүү үчүн койлордун генотиптеширүүсү Эл аралык жаныбарлар генетикасы коому (ISAG) тарабынан сунушталган жогорку полиморфтук микросателлиттик маркерлердин (SSR) панелин колдонуу менен жүргүзүлдү. Аллельдик ар түрдүүлүк индекстери, байкалган жана күтүлгөн гетерозиготалуулук,  $F_{IS}$  фиксация коэффициенттери жана  $Ne_i$  генетикалык аралыктары эсептелген, ал эми популяциянын түзүмү кластердик анализ, PCA жана STRUCTURE моделин колдонуу менен талданган. Жыйынтыктар көпчүлүк локустарда аллельдик ар түрдүүлүктүн жогорку деңгээлин көрсөттү (локустагы аллелдер саны 6-14, аллелдеринин эффективдүү саны  $Ne$  3,41-6,21, маалыматтык мазмундун индекси  $PI_C > 0,69$ ). Байкалган гетерозиготалуулук ( $Ho = 0,68-0,73$ ) күтүлгөн гетерозиготалуулукка дээрлик окшош болгон ( $He = 0,70-0,74$ ), ал эми  $F_{IS}$  коэффициенттери төмөн бойдон калган (0,012-0,028), бул олуттуу инбридингдин жоктугун көрсөтүп турат. Топтордун ортосундагы генетикалык дифференциация алсыз болгон ( $F_{ST} = 0,018-0,032$ ),  $Ne_i$  боюнча генетикалык аралыктар минималдуу болгон (0,038-0,051) жана СТРУКТУРА анализи топтор боюнча бирдей бөлүштүрүлгөн эки шарттуу генетикалык кластерди аныктады, бул популяциянын бүтүндүгүн тастыктады. Бул изилдөөнүн практикалык баалуулугу кыргыз тоо мериносунун генофондунун азыркы абалын аныктоодо жатат, бул көзөмөлдөнгөн асылдандыруу боюнча сунуштарды иштеп чыгууга, уникалдуу аллелдерди сактоого жана тукумдун генетикалык ар түрдүүлүгүн сактоого мүмкүндүк берет, анын жагымсыз экологиялык шарттарга туруктуулугун камсыз кылат

**Негизги сөздөр:** генетикалык ар түрдүүлүк; микросателлиттик маркерлер; популяциянын түзүлүшү; гетерозиготалуулук; фиксация коэффициенти; аллельдик ар түрдүүлүк; кыргыз койлору

## Структура популяции кыргызского горного меринуса: анализ variability ядерных локусов

### Тыргоот Чортонбаев

Доктор сельскохозяйственных наук, профессор  
Кыргызский национальный аграрный университет им. К.И. Скрябина  
720005, ул. Медерова, 68, г. Бишкек, Кыргызская Республика  
<https://orcid.org/0000-0001-9820-2337>

### Жайнагуль Исакова

Доктор медицинских наук, профессор  
Кыргызский научно-исследовательский институт молекулярной биологии и медицины  
720040, ул. Тоголок Молдо, 3, г. Бишкек, Кыргызская Республика  
<https://orcid.org/0000-0002-3681-6939>

### Эсенбек Белек уулу

Соискатель  
Кыргызский национальный аграрный университет им. К.И. Скрябина  
720005, ул. Медерова, 68, г. Бишкек, Кыргызская Республика  
<https://orcid.org/0000-0002-5590-1354>

**Аннотация.** Актуальность исследования обусловлена необходимостью сохранения локальных, уникальных и высокоадаптированных пород сельскохозяйственных животных в условиях глобальных климатических изменений и сокращения численности маточного поголовья. Кыргызский горный меринус является ценным генетическим ресурсом, обладающим высокой адаптивностью к горным условиям, качественной шерстью и эффективным использованием скудных кормов. Однако ограниченный генофонд и рост инбридинга создают риски снижения продуктивности и адаптивности породы. Цель работы заключалась в анализе структуры популяции кыргызского горного меринуса на основе оценки variability ядерных локусов. Для достижения цели проведено генотипирование овец с использованием панели высокополиморфных микросателлитных маркеров (SSR), рекомендованных Международным обществом по генетике животных (ISAG). Были рассчитаны показатели аллельного разнообразия, наблюдаемая и ожидаемая гетерозиготность, коэффициенты фиксации  $F_{IS}$ , генетические расстояния по  $Ne_i$ , а также проведен анализ популяционной структуры с применением методов кластерного анализа, PCA и модели STRUCTURE. Результаты исследования показали высокий уровень аллельного разнообразия по большинству локусов (число аллелей на локус 6-14, эффективное число аллелей  $Ne$  3,41-6,21, индекс информативности  $PI_C > 0,69$ ). Наблюдаемая гетерозиготность ( $H_o = 0,68-0,73$ ) практически соответствовала ожидаемой ( $H_e = 0,70-0,74$ ), а коэффициенты  $F_{IS}$  оставались низкими (0,012-0,028), что свидетельствует об отсутствии выраженного инбридинга. Генетическая дифференциация между группами была слабой ( $F_{ST} = 0,018-0,032$ ), генетические расстояния по  $Ne_i$  – минимальными (0,038-0,051), а анализ STRUCTURE выявил два условных генетических кластера с равномерным распределением по группам, подтверждая целостность популяции. Практическая ценность исследования заключается в выявлении современного состояния генофонда кыргызского горного меринуса, что позволяет разрабатывать рекомендации по контролируемой селекционной работе, сохранению уникальных аллелей и поддержанию генетического разнообразия породы, обеспечивая ее устойчивость к неблагоприятным условиям окружающей среды

**Ключевые слова:** генетическое разнообразие; микросателлитные маркеры; популяционная структура; гетерозиготность; коэффициент фиксации; аллельное разнообразие; кыргызские овцы