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Economic significance of genetic diversity of Kyrgyz Mountain Merino sheep based on STR analysis of nuclear DNA

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Abstract. Preserving and assessing the genetic diversity of farm animals is one of the key tasks for sustainable development in the agricultural sector. This paper examined the economic significance of genetic diversity in Kyrgyz Mountain Merino (KMM) sheep based on an analysis of nuclear DNA variability using microsatellite markers (STR). The aim of the study was to determine the level of heterozygosity, inbreeding coefficients and allele richness in KMM compared to related fine-wool sheep breeds from Russia, Kazakhstan, Poland and Pakistan, as well as to determine their significance for breeding programmes and the economic sustainability of the industry. The methodological basis of the study included molecular genetic analysis of 12 STR markers, statistical evaluation of genetic parameters, and comparison of the results with international databases. It was found that the level of observed heterozygosity in KMM (Ho = 0.70) exceeds that of Russian (0.66), Polish (0.64) and Pakistani (0.65) fine-wool sheep. Kazakh breeds show similar values (0.68), but are characterised by a higher inbreeding coefficient

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(FIS = 0.06), which indicates a tendency towards a decrease in genetic diversity. In contrast, the inbreeding coefficient for KMM was only 0.03, indicating a balanced population structure. The results of the study confirmed that the preservation of the genetic diversity of the KMM breed is not only biologically but also economically important: higher genetic variability ensures adaptability to changing climatic conditions, increases productivity and reduces the costs of veterinary and breeding measures. Thus, the integration of genetic monitoring into the economic management of sheep breeding is a necessary condition for the sustainable development and competitiveness of KMM products in domestic and foreign markets

Keywords: sheep breeding in Kyrgyzstan; STR markers; molecular genetic analysis; population stability; genetic polymorphism; biotechnology in animal husbandry

Introduction

Sheep farming has traditionally occupied one of the leading places in the agricultural sector of the Kyrgyz Republic, providing the rural population with meat, dairy products and wool, as well as forming the country's export potential. According to the National Statistical Committee of the Kyrgyz Republic (n.d.), the share of sheep breeding in the overall structure of livestock production remains consistently high, despite the climatic and socio-economic challenges of recent decades. Of particular importance is the Kyrgyz Mountain Merino (KMM), a unique breed of fine-wool sheep characterised by high adaptability to high-altitude conditions, resistance to environmental stress factors and valuable productive characteristics of wool and meat. These qualities determine its strategic role in the development of sheep breeding and the formation of the country's food security. However, in recent years, threats related to the loss of KMM genetic diversity have been increasing. The intensive use of a limited number of producers, the reduction of grazing land, climate change and globalisation processes are leading to a narrowing of the gene pool and an increase in the risks of inbreeding. As noted by A. Kappes *et al.* (2023), G. Wanjala *et al.* (2023), the consequences of reduced genetic diversity are manifested in weakened reproductive qualities, increased susceptibility to disease, and reduced overall animal productivity, which in turn directly affects the economic efficiency of the industry.

Modern molecular genetic methods allow for a more detailed study of the structure of farm animal populations. Short Tandem Repeats (STR) analysis, or microsatellite analysis, occupies a special place among these methods. This method is considered a reliable tool for assessing intraspecific diversity, identifying degrees of kinship and population differentiation. STR markers are used in breeding programmes to control genetic variability and develop long-term strategies for sustainable sheep breeding (Teneva *et al.*, 2018). For example, studies by T. Odjakova *et al.* (2023) showed that the use of STR analyses allows for the objective determination of the degree of genetic homogeneity in sheep populations, while R. Pichler *et al.* (2017) confirmed the effectiveness of the method in a comparative analysis of the genetic diversity of 11 domestic sheep breeds from Asia, Africa, Europe and Latin America with wild Asian urials.

From an economic point of view, the preservation and maintenance of genetic diversity is one of the most important factors for the sustainability of the livestock industry. Genetic variability provides opportunities to increase productivity, improve wool and meat quality, resistance to infectious diseases and adaptation to changing climatic conditions. Molecular genetic studies show that the adaptation of sheep to different environmental conditions is ensured by a complex of mechanisms: the HIF-1α and EPAS1 genes contribute to high-altitude adaptation through the regulation of hypoxic stress, UCP1 provides cold resistance, and SLC4A4 and GPX3 increase drought resistance (Zhu *et al.*, 2025). These mechanisms are implemented through DNA methylation, transcriptional regulation, and metabolic pathways, which emphasises the importance of preserving genetic diversity to maintain the adaptive potential of breeds. In the long term, this is directly linked to increased profitability of agricultural enterprises and reduced risks associated with environmental fluctuations.

The issue of preserving genetic diversity is particularly important for the mountainous regions of Central Asia, where natural and environmental conditions are highly variable. In such regions, maintaining intraspecific diversity is a prerequisite for food security and the competitiveness of the industry. M. Nei's (1972) concept of genetic distance, based on the identity of genes between populations, laid the theoretical foundation for the quantitative assessment of genetic diversity and remains a key tool in population genetics. Its application to the analysis of farm animals shows that, under conditions of high pressure on ecosystems, it is genetic diversity that ensures the flexibility of adaptation and the stability of sheep productivity characteristics. Despite growing interest in this issue, research on the genetic resources of Kyrgyz sheep breeds is limited. The lack of systematic data reduces the effectiveness of breeding and selection work and limits strategic planning opportunities. K. Dossybayev *et al.* (2019) emphasised that the integration of molecular genetic methods with economic analysis of productivity can significantly improve the effectiveness of industry programmes. This approach is already being actively used in other countries: for example, R. Sharma *et al.* (2020) showed that taking genetic diversity into account increases the efficiency of fine-wool sheep breeding in India, and K. Dossybayev *et al.* (2019) described similar examples for Central Asia.

Thus, the relevance of this study is determined by the need for a comprehensive approach combining molecular genetic assessment of intraspecific diversity with economic analysis of its significance. The aim of the study was to assess the economic significance of the genetic diversity of the Kyrgyz Mountain Merino based on STR analysis of nuclear DNA, which can not only reveal the current state of the breed, but also form scientifically sound recommendations for breeding and selection work, as well as propose long-term measures to increase the sustainability and competitiveness of sheep breeding in Kyrgyzstan.

Materials and Methods

The work was carried out in 2022-2024 on Kyrgyz Mountain Merino sheep bred on farms in the Chüy, Naryn, Talas, Issyk-Kul and Osh regions of the Kyrgyz Republic. The study included 312 animals aged 2 to 5 years, of which 152 were females and 160 were males. The animals represented different intra-breed types bred on the breeding farms named after Lushchikhin (n = 85), Orgochor (n = 74), Katta-Taldyk (n = 68), as well as a number of private farms in the Chüy (n = 35), Naryn (n = 25), Issyk-Kul (n = 15) and Osh (n = 10) regions. Blood samples were collected from the jugular vein in a volume of 5 ml using vacuum tubes with EDTA (ethylenediaminetetraacetic acid). The tubes were transported in a cooled state (4°C) and stored for no more than 48 hours prior to analysis. All procedures were performed in accordance with the principles of bioethics CIOMS (1985) and Directive 2010/63/EU (2010).

DNA extraction was performed using a commercial Qiagen DNeasy Blood & Tissue Kit (Qiagen, Germany). DNA concentration and purity were determined using a NanoDrop 2000 spectrophotometer (Thermo Scientific, USA). Genotyping was performed using STR analysis with a panel of 12 microsatellite loci (OarFCB20, OarCP49, OarCP20, BM6506, ILSTS11, MAF214, MAF209, INRA63, INRA49, McM527, HSC, OarAE119) recommended by ISAG (2019). Amplification was performed by PCR (polymerase chain reaction) on a Bio-Rad T100 thermocycler (USA) according to the following protocol: initial denaturation at 95°C for 5 min; followed by 35 cycles: denaturation at 95°C for 30 seconds, primer annealing at 58-62°C (depending on the locus) for 30 seconds, elongation at 72°C for 45 seconds; final elongation at 72°C for 10 minutes. Fragment analysis was performed on an ABI 3130 Genetic Analyzer (Applied Biosystems, USA) using GeneMapper 5.0 software.

A total of 126 alleles were identified, of which 67 (53.2%) were classified as rare (criterion: frequency of occurrence <0.05). To assess genetic diversity, standard indicators were calculated: number of alleles per locus (Na); effective number of alleles (Ne); observed (Ho) and expected (He) heterozygosity. Calculations were performed using formulas (1) and (2):

$$Ho = \frac{number\ of\ heterozygous\ genotypes}{total\ number\ of\ genotypes}. \quad (1)$$

$$He = 1 - \sum p_i^2, \quad (2)$$

where p_i is the frequency of the i-th allele.

The inbreeding coefficient (FIS) was calculated using formula (3):

$$FIS = \frac{H_e - H_o}{H_e}. \quad (3)$$

The fixation coefficient (FST) was calculated using formula (4) (Wright, 1978):

$$FST = \frac{H_t - H_S}{H_t}, \quad (4)$$

where H_t is the total heterozygosity, H_s is the average across subpopulations.

Genetic distance was calculated using formula (5) (Nei, 1972):

$$D = -\ln(I), \quad (5)$$

where I is the genetic similarity index.

The economic significance of genetic diversity was determined through productive and financial indicators: wool productivity (clipping, fineness and fibre length); meat productivity (live weight, slaughter yield, meat-bone ratio); economic parameters (production cost, gross income, profit and profitability). The calculations were carried out in accordance with the methodological recommendations of the Kyrgyz National Agrarian University, which include analysis of direct and indirect costs, determination of gross income and profitability. Data from international and national studies were used to substantiate the assessment of the economic significance of sheep genetic diversity and to compare productivity indicators.

For the analytical part of the study, publications from the Scopus, Web of Science and Google Scholar databases were analysed. The search was conducted using the following keywords: “Kyrgyz Mountain Merino sheep”, “genetic diversity”, “nuclear DNA”, “STR markers”, “economic efficiency”. Articles with the results of genetic studies were included, as well as works with economic interpretation of data on sheep breeding. The FAO (2015) report was used as a general database of statistical information. To compare the wool and meat productivity of fine-wool breeds, studies from Kazakhstan (Iskakov *et al.*, 2017), Russia (Lavrentieva *et al.*, 2021), Poland (Kawęcka *et al.*, 2022) and Pakistan (Want *et al.*, 2020) were used. Data from similar surveys in Central Asia (Kerven, 2002) were used to compare regional trends. In addition, review publications demonstrating the link between genetic diversity and livestock productivity and sustainability (Wanjala *et al.*, 2023; 2025) were used.

To analyse the impact of genetic diversity on the economic sustainability of farms, scenario modelling was used, applying a modified partial budgeting model in combination with the cost-benefit method. The following data were used as input:

- the results of STR analysis (Na, Ne, Ho, He, FIS);
- indicators of wool yield, tonnage, live weight and slaughter yield;
- data on feed costs, veterinary services and breeding work, obtained on the basis of surveys of breeding farms in the Chüy, Naryn and Talas regions (2023-2024);
- official methodological recommendations for assessing the profitability of agricultural production.

The following conditions were set for the assessment of scenarios:

- baseline – maintaining current genetic diversity parameters (Na, Ne and Ho/He at the level of the present study);
- negative – a 20% reduction in diversity (modelled through a decrease in Na and an increase in FIS), which led to an increase in morbidity (according to FAO data, 2015) and a decrease in wool productivity;
- innovative – strengthening of selection work (improved control of inbreeding, maintaining FIS < 0.05), which ensured growth in wool and meat productivity.

The profitability level (R) was calculated using formula (6):

$$R = \frac{GR - \mathrm{C}}{\mathrm{C}} \times 100\%, \quad (6)$$

where GR is gross revenue from product sales (wool, meat), C is total costs (feed, veterinary expenses, labour, breeding work).

Statistical data processing in Stata 16.0 and @RISK 8.3 (Palisade Corp.) were used for modelling, allowing scenario forecasting with elements of Monte Carlo simulation (1000 iterations). The STRUCTURE 2.3.4 programme was used to identify intrapopulation clusters.

Results and Discussion

The results of STR analysis showed that the Kyrgyz Mountain Merino breed is characterised by a high level of genetic variability, reflecting its unique evolutionary formation and adaptation to the extreme conditions of the highlands. In the study of 12 microsatellite loci, 126 alleles were identified, of which 67 (53.2%) were rare, i.e., occurred with a frequency of less than 0.05. Such a number of rare alleles indicates a rich gene pool, providing a wide range of opportunities for selection. The average number of alleles per locus (Na) was 10.5, which is higher than the average for many fine-wool breeds (6-9) described in similar studies (Punuru *et al.*, 2025). The effective number of alleles (Ne) was 6.2, confirming the uniform distribution of variants and the absence of dominance of individual genes. High values of observed (Ho = 0.62-0.78) and expected (He = 0.65-0.80) heterozygosity indicate that the KMM population has a high level of genetic variability (Ceccobelli *et al.*, 2023). The low difference between Ho and He indicates that the population does not suffer from pronounced inbreeding. The calculated inbreeding coefficient (FIS = 0.03) also demonstrates minimal risks of accumulation of close kinship ties, while, according to S. Ceccobelli *et al.* (2023), this indicator reaches 0.10-0.15 in some local breeds. The Nei genetic distance when compared with breeds from Kazakhstan, Russia, Poland and Pakistan ranged from 0.12 to 0.18, indicating a moderate degree of differentiation characteristic of breeds formed in different environmental conditions.

The use of the STRUCTURE 2.3.4 programme made it possible to identify the presence of several intrapopulation clusters that coincide with regional breeding lines – Chüy, Naryn and Talas. Such clustering reflects the peculiarities of breeding practice and confirms that a rich diversity of lines is preserved within the breed. From an economic point of view, this is extremely important: the presence of several genetically differentiated lines allows for flexible selection work aimed at strengthening certain productive traits. For example, in the Chüy line, attention can be focused on increasing meat productivity, while the Naryn and Talas lines are more promising for the development of wool production. Thus, the richness of the genetic structure of the KMM confirms its strategic value in the development of sheep breeding in Kyrgyzstan.

Preserving the genetic diversity of KMM has direct economic implications. Firstly, allele diversity and high heterozygosity ensure the stability of productive traits even under climatic stress conditions. The data obtained show that the average wool yield for rams was 5.2-5.5 kg, for ewes – 3.8-4.2 kg, with a fibre fineness of 19.8-20.5 microns. These indicators testify to the stability of productivity and confirm that the presence of a broad genetic background allows for the maintenance of high wool quality. For Kyrgyzstan, where a significant part of the wool is exported, the preservation of these characteristics has a direct impact on foreign exchange earnings and the competitiveness of the industry in the international market. Secondly, rare alleles identified in the population have the potential to increase disease resistance and adaptation to new conditions, including climate change. Their presence increases the breeding value of KMM, as it is precisely these unique genetic variants that can become a source of new traits that will be in demand in the future. This is where the long-term economic benefit lies: by maintaining genetic diversity, farms are effectively investing in production sustainability and reducing future risks. Thirdly, low levels of inbreeding and moderate population differentiation create favourable conditions for effective breeding work without the need for large-scale imports of breeding material from abroad. This significantly reduces the cost of renewing livestock and minimises dependence on external supplies. At the same time, the internal structure of the KMM makes it possible to create economically advantageous crossbreeding programmes within the country, which contributes to the development of the national breeding system. It is also important to note that the economic significance of the KMM goes beyond direct productivity indicators and includes a broader context: ensuring food security, maintaining employment in rural areas and preserving the cultural heritage associated with traditional sheep breeding. Support for this breed has a multiplier effect: by increasing genetic stability and productivity, Kyrgyzstan is simultaneously strengthening its position in the agricultural market and developing its export potential.

The live weight of rams ranged from 80 to 85 kg, ewes from 55 to 60 kg, and the slaughter yield reached 46 to 48%. These indicators are comparable to international standards and confirm the competitiveness of the Kyrgyz Merino (FAO, 2015; Deniskova *et al.*, 2018). It is important to note that it is precisely the high level of genetic diversity that contributes to the stability of these parameters. For example, according to farmer surveys, farms with a limited genetic base in Central Asia experienced significant fluctuations in wool yield and a decline in wool quality due to the loss of genetic resources, which directly affected economic performance and production profitability (Kerven *et al.*, 2002).

Observed and expected heterozygosity, as well as inbreeding coefficients, showed population stability and no significant deficit in genetic diversity. To systematise the results, an analysis of the main indicators of STR markers was carried out, including the number of alleles, heterozygosity and inbreeding coefficient. The summary data are presented in Table 1.

Table 1. Genetic parameters of the Kyrgyz Mountain Merino based on STR analysis

Indicator	Value (average)	Range	Interpretation
Number of alleles per locus (Na)	10.5	8-13	High diversity
Effective number of alleles (Ne)	6.2	5-8	Balanced population
Ho (observed heterozygosity)	0.70	0.62-0.78	High variability
He (expected heterozygosity)	0.72	0.65-0.80	No heterozygote deficiency
FIS (inbreeding coefficient)	0.03	0.01-0.05	Moderate level of inbreeding

Source: compiled by the authors

Table 1 presents the main indicators of genetic diversity of the Kyrgyz Mountain Merino sheep obtained on the basis of STR analysis performed within the framework of this study. The number of alleles per locus (Na = 10.5) indicates a high level of variability, confirming the preservation of a broad gene pool for the breed (Wanjala *et al.*, 2025). The effective number of alleles (Ne = 6.2) indicates a balanced distribution of genes and the absence of dominance of individual alleles. The observed (Ho = 0.70) and expected (He = 0.72) heterozygosity indices demonstrate a high level of variability and indicate the population's resistance to inbreeding. The low inbreeding coefficient (FIS = 0.03) confirms that there is no tendency towards degeneration in the breed and that selection work is being carried out while preserving genetic diversity. The number of alleles per locus (Na = 10.5) indicates a high level of variability, which confirms the preservation of the breed's broad gene pool. The effective number of alleles (Ne = 6.2) indicates a balanced distribution of genes and the absence of dominance of individual alleles. The observed (Ho = 0.70) and expected (He = 0.72) heterozygosity indices demonstrate a high level of variability and indicate the population's resistance to inbreeding. The low inbreeding coefficient (FIS = 0.03) confirms that there is no tendency towards degeneration in the breed and that selection work is being carried out while preserving genetic diversity.

For an objective assessment of the genetic potential of the Kyrgyz Mountain Merino, it is important to compare its characteristics with other fine-wool breeds common in Central and Eastern Europe, as well as in South Asia. The analysis included sheep from Kazakhstan, Russia, Poland and Pakistan, where breeding work is actively carried out to improve the fine-wool direction (Dimitriou *et al.*, 2024). A comparative analysis of heterozygosity and inbreeding coefficients in Kyrgyz Mountain Merino and foreign sheep breeds revealed significant differences in the level of genetic diversity. The data obtained show that it is the Kyrgyz Mountain Merino that has the most stable parameters, combining a high level of heterozygosity and low inbreeding coefficients. This indicates the preservation of a rich gene pool and the effective use of breeding lines in breeding work.

Russian fine-wool breeds are characterised by lower heterozygosity rates, which indicates a gradual decline in genetic reserves (Lavrentieva *et al.*, 2021). This trend can be explained in large part by the history of the formation of these breeds, when the main focus was on increasing wool productivity through intensive selection, but less attention was paid to preserving intrapopulation variability. In the long term, this may lead to an increase in the frequency of hereditary diseases and a decrease in the adaptability of animals. Polish Merinos are also characterised by a relatively limited gene pool, which is reflected in low levels of both observed and expected heterozygosity (Kawęcka *et al*., 2022). This is due to the fact that breeding work in European countries has traditionally been focused on obtaining stable but highly specialised lines. As a result, there is a reduction in the number of rare alleles, which limits the possibilities for further genetic improvement of the breed. Pakistani sheep show an even higher level of differentiation compared to Kyrgyz Mountain Merinos, which is reflected in the Nei genetic distance values. This is due to both geographical isolation and the fact that in Pakistan, local adaptive lines with a limited gene pool are often used in sheep breeding (Want *et al*., 2020). Kazakh fine-wool sheep occupy an intermediate position: their heterozygosity indices are close to those of KMM, but a higher inbreeding coefficient indicates that breeding work here is more focused on the use of a limited number of breeding producers (Iskakov *et al*., 2017). This strategy allows for the temporary consolidation of economically useful traits, but in the long term, it carries the risk of reducing the overall stability of the population.

Thus, a comparison of the KMM with foreign breeds demonstrates its strategic advantage: it combines high genetic variability and a low degree of inbreeding, which creates a solid foundation for maintaining productivity and economic efficiency. For a more visual representation of these data, the summary results are presented in Table 2.

Table 2. Comparative indicators of genetic diversity of sheep in different countries

Breed/region	Ho	He	FIS	Nei (to KMM)	Interpretation
Kyrgyz Mountain Merino	0.70	0.72	0.03	–	High variability, low inbreeding
Kazakh fine-wool sheep	0.68	0.71	0.06	0.12	Moderate diversity, signs of inbreeding
Russian fine-wool	0.66	0.69	0.07	0.15	Decrease in heterozygosity
Polish Merinos	0.64	0.68	0.08	0.16	Limited gene pool
Pakistani sheep	0.65	0.67	0.09	0.18	High differentiation

Source: compiled by the authors

As can be seen from Table 2, the Kyrgyz Mountain Merino is characterised by the most favourable combination of indicators: the observed heterozygosity Ho = 0.70 and expected He = 0.72 confirm a high level of intrapopulation variability. The inbreeding coefficient FIS = 0.03 indicates a low degree of related mating. The genetic distance Nei in relation to other breeds has not been calculated (base breed), which emphasises its importance as a reference object for research. Kazakh fine-wool sheep have similar heterozygosity indices (Ho = 0.68, He = 0.71), but a higher inbreeding coefficient (FIS = 0.06) indicates a decrease in genetic diversity. The genetic distance of 0.12 in relation to KMM indicates that the breeds remain closely related, which is due to the geographical and historical similarity of breeding conditions. Russian fine-wool breeds are characterised by lower heterozygosity (Ho = 0.66, He = 0.69) and an inbreeding coefficient FIS = 0.07, which reflects the limited gene pool due to intensive selection. The genetic distance Nei (0.15) indicates a more pronounced differentiation compared to KMM. Polish Merinos show even lower values (Ho = 0.64, He = 0.68, FIS = 0.08), which is associated with long-term targeted selection and a limited base of producers. The genetic distance (0.16) confirms a significant difference from the Kyrgyz Mountain Merino. Pakistani sheep have values of Ho = 0.65, He = 0.67 and the highest inbreeding coefficient (FIS = 0.09). This is explained by traditional breeding methods based on the use of local lines. The genetic distance (0.18) indicates the greatest differentiation in relation to KMM.

Wool productivity. Wool quality remains the main criterion for the competitiveness of fine-wool breeds. At KMM, wool yield is 5.2-5.5 kg for rams and 3.8-4.2 kg for ewes, with a fineness of 19.8-20.5 microns. This meets international standards for high-quality fine-wool, for example, in studies with Merino sheep, where improved nutrition for ewes resulted in a clean wool weight of about 5 kg and a fibre diameter of about 18-20 μm (Thompson *et al*., 2011). For comparison, Russian Merinos have a fineness of 21-22 μm, Polish Merinos 20-21 μm, Kazakh Merinos 20-21 μm, and Pakistani Merinos over 22 μm. Thus, Kyrgyz Merino wool has competitive advantages in the international market. It is important to note that the protective properties of the fleece, which determine the degree of contamination and the content of mineral impurities, also affect the yield of clean wool and its technological characteristics. V. Tyrunskiy *et al*. (2023) showed, using the example of Tavrian-type ewes of the Askanian fine-wool breed, that individual variability in the degree of staple contamination is quite high (coefficient of variation 28.5-30.4%), and these indicators correlate with the rank of selection differentiation of animals. Similar patterns are relevant for KMM, since the high genetic diversity of the breed creates prerequisites for selection improvement not only of quantitative but also qualitative characteristics of wool, including its protective properties.

Meat productivity. The live weight of KMM rams is 80-85 kg, ewes – 55-60 kg, with a slaughter yield of 46-48%. In Kazakhstan, the indicators are similar, but the quality of wool is inferior. Russian and Polish breeds demonstrate slightly higher meat characteristics (slaughter yield 48-50%), but their wool is coarser.

Economic efficiency. Economic analysis has shown that the profitability of farms breeding KMM while preserving genetic diversity reaches 22-25%, while farms with a limited gene pool show indicators at the level of 15-18%. This is because high heterozygosity ensures the stability of productive traits, reducing the risk of losses in unfavourable climatic conditions.

The impact of genetic diversity on stress resistance. Stress factors – climatic fluctuations, diseases, fluctuations in the feed base – are a key factor affecting the economics of livestock farming. High genetic diversity ensures the adaptability and resilience of animals. For example, in the Chüy Valley, where droughts are common, the preservation of rare alleles associated with stress resistance allows sheep to maintain their productivity. In the Naryn region, where the climate is harsher, genetic diversity contributes to the development of resistance to low temperatures. At the same time, the molecular mechanisms of high-altitude adaptation in sheep are being actively studied in various breeds. X. Li *et al.* (2024) showed that in Tibetan sheep, adaptation to high altitudes is ensured by a complex of genomic changes, including genes for energy metabolism, response to hypoxia, and resistance to ultraviolet radiation. Similar adaptive mechanisms are likely to be present in KMM, which explains its successful breeding in the high-altitude pastures of Kyrgyzstan.

An analysis of productive characteristics has shown that the Kyrgyz Mountain Merino combines high wool quality with sufficient meat productivity and stable farm profitability. In terms of wool yield and fineness, the breed occupies a leading position among the region's fine-wool sheep, and its live weight and slaughter yield indicators confirm its versatility. At the same time, the level of profitability of farms breeding KMM is significantly higher than that of foreign counterparts. For a clear illustration of the differences between the Kyrgyz Mountain Merino and other fine-wool breeds, summary data are presented in Table 3.

Table 3. Productivity indicators of the Kyrgyz Mountain Merino compared to foreign breeds

Breed	Wool yield (rams), kg	Wool fineness, microns	Live weight of rams, kg	Slaughter yield, %	Profitability, %
Kyrgyz Mountain Merino	5.2-5.5	19.8-20.5	80	46	22
Kazakh fine-wool sheep	5.0-5.3	20	78-82	45-47	18-20
Russian fine-wool	5.5-6.0	21-22	85-90	48-50	15-18
Polish Merinos	4.8-5.2	20-21	82-86	47-49	16-18
Pakistani sheep	4.0-4.5	>22	75-80	45-46	12-15

Source: compiled by the authors

Table 3 reflects a comparative analysis of the productive characteristics of the Kyrgyz Mountain Merino and fine-wool sheep breeds bred in Kazakhstan, Russia, Poland and Pakistan. The Kyrgyz Mountain Merino has a wool yield of 5.2-5.5 kg for rams and 3.8-4.2 kg for ewes, which is comparable to or higher than that of Kazakh and Polish breeds, and only slightly lower than that of Russian Merinos. At the same time, the quality of KMM wool is higher: its fineness is 19.8-20.5 microns, which corresponds to the category of high-quality fine wool in demand on the international market. Most foreign breeds have higher wool fineness (less fine): Russian and Polish breeds have a fineness of 21-22 microns, and Pakistani breeds have a fineness of more than 22 microns. KMM also occupies a competitive position in terms of meat productivity. The live weight of rams is 80-85 kg, ewes are 55-60 kg, with a slaughter yield of 46-48%. These indicators are higher than those of Pakistani sheep and are close to those of Kazakh and Polish breeds. Russian Merinos have a slightly higher live weight (85-90 kg), but their wool is less fine.

The most interesting indicator is profitability, which reflects the economic significance of the breeds. For KMM, it is 22-25%, which is significantly higher than for Russian (15-18%), Polish (16-18%) and Pakistani (12-15%) breeds. Kazakh sheep occupy an intermediate position with a profitability level of 18-20%. The higher profitability of the Kyrgyz Merino is explained by a combination of stable productivity, high wool quality and adaptability to mountain conditions, which reduces the cost of keeping the animals. Thus, the data in Table 3 confirm that Kyrgyz Mountain Merino sheep have an optimal combination of wool and meat productivity, as well as high economic efficiency in breeding. This makes them a strategically important breed for the further development of sheep breeding in Kyrgyzstan and creates potential for the export of both wool and breeding stock.

Economic interpretation of genetic diversity. In a market economy, the genetic diversity of farm animals becomes an important asset that directly affects farm profitability. For sheep farmers in Kyrgyzstan, maintaining high heterozygosity and preserving rare alleles of the Kyrgyz Mountain Merino is not only a biological but also an economic priority. Gene diversity affects product quality (wool and meat), stability of performance in different climatic conditions, disease resistance, herd reproduction efficiency, and reduction of veterinary and breeding costs. Scenario modelling was carried out to assess the impact of genetic diversity on the economic sustainability of the industry. The analysis was based on three scenarios: a baseline scenario characterised by the preservation of the current level of genetic variability; a negative scenario assuming its decline; and an innovative scenario associated with intensified selection work and inbreeding control. Each scenario allowed for tracking changes in profitability and veterinary costs depending on the state of the gene pool. The results of the modelling are presented in Table 4.

Table 4. Scenario modelling of the impact of genetic diversity on farm profitability

Scenario	Genetic diversity	Profitability, %	Veterinary costs	Economic interpretation
Baseline	High (Na ≈ 10.5, Ho ≈ 0.70)	22	Low	Balanced development
Negative	20% decrease	15-17	+12-15%	Risks of productivity decline
Innovative	Increased (inbreeding control)	27	Decrease by 8-10%	Export potential

Source: compiled by the authors

As can be seen from Table 4, the results of the analysis indicate significant variation in the economic significance of genetic diversity in Kyrgyz Mountain Merino sheep. The indicators presented allow for tracing the relationship between the level of genetic heterozygosity, the inbreeding coefficient and key economic parameters such as productivity, disease resistance and profitability. In particular, it has been found that a high level of genetic diversity contributes to a reduction in economic risks associated with loss of productivity and also increases the adaptive potential of animals in the context of climate change. Thus, the data in Table 4 confirm the close link between genetic and economic aspects in sheep breeding and highlight the need for a comprehensive approach to the assessment and management of breed resources.

The impact of genetic diversity on export potential. Kyrgyzstan traditionally exports limited volumes of wool, but due to its high fineness (19.8-20.5 microns), KMM wool can become a competitive commodity on the world market. Preserving genetic diversity ensures that wool quality will not decline in the event of climate change or changes in the feed base. Based on calculations, if wool exports are increased by 15% through support for breeding farms, the industry's revenue could increase by 12-14 million soms per year.

Practical significance for selection and breeding work:

- preservation of rare alleles: their loss can lead to a decrease in disease resistance;
- control of inbreeding: even a moderate increase in FIS to 0.08 can reduce productivity by 5-7%;
- development of zonal types: Chüy, Naryn and Talas types of KMM can be used as a basis for regional specialisation (wool production in the Chüy region, meat and wool production in the Naryn region, and combined production in the Talas region).

International practices and lessons for Kyrgyzstan. The experience of Australia, New Zealand and Spain shows that preserving genetic diversity and controlling it through molecular markers (STR, SNP) leads to long-term sustainability of the industry. For example, a study of wild sheep in New Zealand demonstrated a significant level of polymorphism in genes associated with wool and productivity, indicating the potential to preserve productive and adaptive qualities through genetic monitoring (McKenzie *et al.*, 2010). Based on this, it is advisable for Kyrgyzstan to develop genetic banks (cryobanks); integrate into FAO programmes for biodiversity conservation; and stimulate the export of breeding stock, not just wool. An analysis of the economic significance of the genetic diversity of the Kyrgyz Mountain Merino also reveals the relationship between the level of genetic variability and the stability of productive traits. In particular, it is important to consider not only heterozygosity and inbreeding coefficient indicators, but also their impact on long-term breeding strategy and the economic profitability of the industry. For clarity, Table 5 presents summary data reflecting the key parameters of the economic assessment based on the results of STR analysis and their practical significance for the development of sheep breeding in Kyrgyzstan.

Table 5. Economic efficiency of farms with different levels of genetic diversity

Indicator	High diversity	Average diversity	Low diversity
Wool yield (rams), kg	5.5	5	4.5
Wool fineness, microns	19.8-20.5	21	22.5
Live weight of rams, kg	80-85	78-80	74-76
Slaughter yield, %	46-48	44-45	42-43
Profitability, %	25-27	18-20	12-15

Source: compiled by the authors

Table 5 shows the dependence of the economic efficiency of sheep farms on the level of genetic diversity of the Kyrgyz Mountain Merino sheep population. It can be seen that with high diversity, productive and financial indicators significantly exceed similar values in farms with medium and low diversity. Thus, the wool yield of rams reaches 5.5 kg compared to 4.5 kg at a low level of diversity, and its fineness remains at 19.8-20.5 microns, which corresponds to high-quality fine wool that is in demand on the international market. The live weight of rams with high diversity is 80-85 kg, while with low diversity it decreases to 74-76 kg. The meat yield in the first case reaches 46-48%, and in the latter it falls to 42-43%. The differences are most evident in the level of profitability: farms with a rich gene pool demonstrate 25-27% profitability, while with a decrease in genetic diversity, this figure falls almost twice – to 12-15%. Thus, the data confirm that maintaining high genetic variability not only strengthens the biological stability of the breed, but also has a direct economic impact in terms of increasing product competitiveness and reducing the risk of losses.

Particular attention should be paid to the comparison of data on the Kyrgyz Mountain Merino with Kazakh fine-wool breeds: despite similar heterozygosity indicators, the latter have been found to have an increased FIS level, which indicates a risk of losing part of the genetic diversity when using a limited number of lines in breeding. Thus, the results of the analysis confirm that the Kyrgyz Mountain Merino retains a unique gene pool, which has both scientific and practical value for further improvement of the breed and ensuring sustainability in a changing climate.

The study showed that the Kyrgyz Mountain Merino (KMM) has a high degree of genetic diversity, confirmed by STR analysis data. The level of observed heterozygosity (Ho = 0.70) in KMM significantly exceeds similar indicators in a number of foreign breeds of fine-wool sheep (Russian, Polish, Pakistani), which indicates the preservation of a broad genetic base in the population. A comparative analysis also revealed a low level of inbreeding, which is an important factor for sustainable reproduction and preservation of the productive qualities of the breed. The economic interpretation of the data obtained is of particular importance: high genetic variability is directly related to the animals' resistance to changes in the external environment, increased adaptability to climatic stresses and the preservation of high levels of wool and meat productivity. This creates the conditions for increasing farm profitability, reducing fiscal risks associated with livestock losses, and forming a long-term breeding strategy. A comparative analysis with other breeds has shown that the Kyrgyz Mountain Merino retains unique adaptive qualities that can be used in breeding programmes not only in Kyrgyzstan but also in other countries in the region. Thus, the results of the study confirm the strategic importance of the KMM as a national gene pool with both scientific and economic value.

Conclusions

The study showed that Kyrgyz Mountain Merino sheep are characterised by a high degree of genetic diversity, as confirmed by the level of observed heterozygosity (Ho = 0.70), which exceeds the indicators for most foreign sheep breeds. A comparative analysis revealed that the inbreeding coefficient in KMM is lower than in Kazakh and a number of other fine-wool sheep breeds, indicating a favourable population status and no significant risk of reduced genetic variability. It has been established that KMM has unique adaptive qualities that allow it to effectively use high-altitude pastures and remain resistant to climatic fluctuations, which is important for the strategic development of livestock farming in Kyrgyzstan. The economic significance of the research results lies in the fact that high genetic variability is directly related to productivity, herd stability and reduced economic risks, which confirms the need to preserve and rationally use this gene pool. The Kyrgyz Mountain Merino has a higher level of heterozygosity compared to Russian, Polish and Pakistani sheep breeds, which indicates the preservation of a broad genetic base. The inbreeding coefficient of the KMM is lower than that of Kazakh sheep, which indicates that there is no pronounced tendency towards a decline in genetic diversity. It has been established that the KMM retains unique adaptive qualities that ensure its suitability for high-altitude pastures and variable climatic conditions.

The results obtained are of significant economic importance: high genetic variability is associated with increased productivity, reduced risk of loss and effective breeding. KMM can be considered a strategic gene pool of considerable scientific and practical value, which should be preserved and used in breeding programmes. Thus, the results of the study confirm that the Kyrgyz Mountain Merino is an important genetic and economic resource with the potential to increase the sustainability of Kyrgyzstan's agricultural sector, and its conservation and rational use will contribute to strengthening the country's food and economic security. Prospects for further research include the integration of molecular genetic data with economic modelling and the development of recommendations for practical use in farms.

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Conflict of Interest

The authors declare that they have no conflict of interest.

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Кыргыз тоо мериносу тукумундагы ядролук ДНКнын STR-анализи боюнча генетикалык ар түрдүүлүктүн экономикалык мааниси

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Аннотация. Айыл чарба жаныбарларынын генетикалык ар түрдүүлүгүн сактоо жана аны баалоо агрардык тармактын туруктуу өнүгүүсүнүн негизги милдеттеринин бири болуп эсептелет. Бул изилдөөдө кыргыз тоо мериносу (КТМ) кой породасынын ядролук ДНКсынын микросателлиттик маркерлерин (STR) колдонуу менен вариабелдүүлүгүн талдоо аркылуу генетикалык ар түрдүүлүктүн экономикалык мааниси каралган. Изилдөөнүн максаты – КТМ породасынын гетерозиготтуулук деңгээлин, инбридинг коэффициентин жана аллелдик байлыгын Россия, Казакстан, Польша жана Пакистандагы жука жүндүү кой породалары менен салыштыруу жана аларды селекциялык программалардагы жана тармактын экономикалык туруктуулугундагы маанисин аныктоо болгон. Методологиялык негиз катары 12 STR-маркер боюнча молекулярдык-генетикалык анализ, генетикалык параметрлердин статистикалык баасы жана алынган натыйжаларды эл аралык маалымат базалары менен салыштыруу пайдаланылган. Жыйынтыгында, КТМ породасында байкалган гетерозиготтуулук деңгээли (Ho = 0,70) Россиялык (0,66), Польша (0,64) жана Пакистандык (0,65) жука жүндүү кой породаларына салыштырмалуу жогору экени аныкталды. Казакстандык породалардын көрсөткүчтөрү (0,68) жакын болгону менен, алардын инбридинг коэффициенти жогору (FIS = 0,06) болуп, генетикалык ар түрдүүлүктүн төмөндөөгө багыт алганын көрсөтөт. Ал эми КТМде бул көрсөткүч 0,03 гана болуп, популяциянын тең салмактуу түзүлүшүн билдирет. Изилдөөнүн жыйынтыктары КТМ породасындагы генетикалык ар түрдүүлүктү сактоонун биологиялык гана эмес, экономикалык мааниси да бар экенин тастыктады: жогору генетикалык вариабелдүүлүк өзгөрүп турган климаттык шарттарга ыңгайлашууну камсыз кылат, продуктивдүүлүктү жогорулатат жана ветеринардык жана селекциялык иш-чараларга кеткен чыгымдарды азайтат. Демек, генетикалык мониторингди кой чарбасын экономикалык башкарууга интеграциялоо – туруктуу өнүгүүнүн жана КТМ продукциясынын ички жана тышкы рыноктогу атаандаштыкка жөндөмдүүлүгүнүн маанилүү шарты болуп саналат

Негизги сөздөр: Кыргызстандын кой чарбасы; STR-маркерлер; молекулярдык-генетикалык анализ; популяциялардын туруктуулугу; генетикалык полиморфизм; мал чарбасындагы биотехнологиялар

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Аннотация. Сохранение и оценка генетического разнообразия сельскохозяйственных животных является одной из ключевых задач устойчивого развития аграрного сектора. В данной работе рассмотрена экономическая значимость генетического разнообразия овец породы кыргызский горный меринос (КГМ) на основе анализа вариабельности ядерной ДНК с использованием микросателлитных маркеров (STR). Цель исследования заключалась в выявлении уровня гетерозиготности, коэффициентов инбридинга и аллельного богатства у КГМ в сравнении с родственными тонкорунными породами овец из России, Казахстана, Польши и Пакистана, а также в определении их значения для селекционных программ и экономической устойчивости отрасли. Методологическая основа исследования включала молекулярно-генетический анализ по 12 STR-маркерам, статистическую оценку генетических параметров и сопоставление полученных результатов с международными базами данных. Установлено, что уровень наблюдаемой гетерозиготности у КГМ (Ho = 0,70) превышает показатели российских (0,66), польских (0,64) и пакистанских (0,65) тонкорунных овец. Казахстанские породы демонстрируют близкие значения (0,68), однако характеризуются более высоким коэффициентом инбридинга (FIS = 0,06), что свидетельствует о тенденции к снижению генетического разнообразия. В отличие от них, у КГМ коэффициент инбридинга составил лишь 0,03 что указывает на сбалансированную структуру популяции. Результаты исследования подтвердили, что сохранение генетического разнообразия породы КГМ имеет не только биологическое, но и экономическое значение: более высокая генетическая вариабельность обеспечивает адаптивность к изменяющимся климатическим условиям, повышает продуктивность и снижает затраты на ветеринарные и селекционные мероприятия. Таким образом, интеграция генетического мониторинга в экономическое управление овцеводством является необходимым условием устойчивого развития и конкурентоспособности продукции КГМ на внутреннем и внешнем рынках

Ключевые слова: овцеводство Кыргызстана; STR-маркеры; молекулярно-генетический анализ; устойчивость популяций; генетический полиморфизм; биотехнологии в животноводстве