

Analysis and Assessment of Farm Animal Genetic Resources In Kyrgyzstan

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Submitted: 2026, Aug 21; Accepted: 2026, Sep 28; Published: 2026, Oct 07

Citation: Amangeldi, S., Chynara, K., Murzakarim, B., Zharkynay, I. K. (2026). Analysis and Assessment of Farm Animal Genetic Resources In Kyrgyzstan Analysis and Evaluation of Genetic Resources of Farm Animals In Kyrgyzstan. *J Gene Engg Bio Res*, 8(3), 01-08.

Abstract

The article presents an overview and analytical assessment of the main genetic resources of farm animals in Kyrgyzstan with an emphasis on cattle, sheep, goats and horses. The analysis combines data from classical breeding studies, domestic scientific works and modern achievements in molecular genetics and conservation genomics.

Particular attention is paid to locally adapted breeds and populations formed in the conditions of mountainous and foothill areas and pasture production systems. Literature data indicate the presence of valuable genetic resources in Kyrgyzstan, represented by the Alatau and Aulieata breeds of cattle, specialized meat types, several sheep populations, including the Kyrgyz mountain Merino, Kyrgyz downy and woolly goats, as well as indigenous populations of Kyrgyz horses.

The studies of S.M. Derkenbaev, U.A. Shergaziev, O.D. Duishekeev, A.S. Azhibekov, T.J. Chortonbaev, T.Zh. Turdubaeva, A.A. Abdykerimov, I.A. Almeev, A.Kh. Abdurasulov, B.Zh. Jeenbekova, E. Satkankulov and Ch.T. Kadyrova form an important scientific basis for the selection and preservation of the gene pool.

Genomic studies of Kyrgyz sheep and horses demonstrate the value of microsatellite and SNP approaches for assessing population structure and genetic differentiation. The level of genetic study of different species is uneven: sheep and horses have a relatively more developed molecular base, while cattle and especially goats need to expand the genome-wide characteristic.

An integrated national system is proposed, combining breed inventory, phenotypic accounting, pedigree data, SNP genotyping, homozygosity site analysis, effective population size estimation and cryopreservation. Such a system will contribute to the sustainable use of national genetic resources, reduce the risk of genetic erosion and increase the adaptability of livestock production to climate variability.

Keywords: Genetic Resources of Farm Animals, Kyrgyzstan, Genetic Diversity, Cattle, Sheep, Goats, Horses, Conservation Genomics

1. Introduction

Farm animal genetic resources are a strategic component of agrobiodiversity and the basis for sustainable livestock production. Genetic variability within and between breeds provides the biological basis for adaptation to changing environmental conditions, diseases, feed resources and production systems. The

international recommendations consider the characterization, monitoring, sustainable use and conservation of genetic resources as interrelated components of management, rather than as separate areas [1,2]. The relevance of this problem for Kyrgyzstan is particularly high. The country's livestock production is largely determined by the mountainous terrain, altitudinal zonality,

extensive use of natural pastures, seasonal fluctuations in feed availability, and pronounced climatic variability. These conditions favor animals that combine productive value with adaptability and functional stability. Therefore, locally adapted populations can retain alleles and combinations of traits that are valuable for future breeding, even if their current commercial productivity is lower than that of highly specialized imported lines [3,4].

At the same time, livestock production systems are changing. Intensification of production, substitution of local animals with imported genetic material, uncontrolled crossing, fragmentation of breeding records and small numbers of individual populations can change the genetic structure of local breeds. It is important to note that an increase in the total number of animals does not necessarily mean an increase in genetic diversity: demographic recovery and the preservation of genetic variability can have different trajectories [5]. This difference is fundamental for the planning of conservation activities. The scientific literature of Kyrgyzstan contains a significant array of studies on breeding, productivity, conformation, heritability and genetic characteristics of cattle, sheep, goats and horses. The studies of S.M. Derkenbaev and U.A. Shergaziev are important for assessing the productive characteristics and breeding value of cattle, the works of O. Duishekeev contributed to the improvement of the Alatau breed, the studies of A.S. Azhibekov, T.J. Chortonbaev, T.J. Turdubaev, Ch.T. Kadyrova and A. Abdykerimov are devoted to sheep breeding and breeding, I.A. Almeev, A.Kh. Abdurasulov, Ch.T. Kadyrova, B.Zh. Jeenbekova and E. Satkankulov contributed to the study of goat breeding and genetic resources, the research of B. Toktosunov, J. Isakova and A. Abdurasulov provides molecular data on the genetic structure of Kyrgyz horses and sheep.

Recent advances in international science make a new synthesis of the accumulated data relevant. The 2023 FAO Practice Guide on Genomic Characterization explicitly considers whole-genome sequencing and genotyping of single nucleotide polymorphisms (SNPs) as tools for assessing genetic variability within and between farmed animal populations [2]. Genomic information can also improve the accuracy of ancestry, inbreeding and kinship assessment, breed determination, and genomic evaluation [6]. Therefore, the assessment of genetic resources in Kyrgyzstan should not be limited to the breed catalog, it is necessary to assess the degree of their genetic knowledge and prioritize conservation and sustainable use. The purpose of this review is to analyze the main genetic resources of cattle, sheep, goats and horses in Kyrgyzstan, to summarize the results of national and international studies, to identify gaps in their genetic characterization and to propose practical priorities for integrated conservation and sustainable conservation of cattle, sheep, goats and horses. use. The methodological basis is a structured review of the literature of peer-reviewed scientific articles, FAO technical guidelines and national scientific publications, with an emphasis on research directly related to the populations of farm animals in Kyrgyzstan, their breeding value, genetic diversity and conservation. The data were compared in four areas: breed and population identity, productive and adaptive characteristics, level of genetic characteristics and

conservation needs.

2. Genetic Resources of Cattle in Kyrgyzstan and Their Breeding Value

Cattle are one of the main components of animal husbandry and genetic resources in Kyrgyzstan. The national cattle population includes the Alatau and Aulieata breeds, specialized dairy and beef types, as well as local and crossbred populations. The genetic value of these populations is determined not only by milk yield or meat productivity, but also by reproductive qualities, feed use efficiency, duration of economic use, resistance to diseases and adaptation to local production conditions. The Alatau breed has a special historical significance. Its formation was associated with the improvement of local cattle using selected European and regional genetic material with subsequent long-term selection in the conditions of Central Asia. The works of O.D. Duishekeev are closely related to the improvement of the Alatau breed and the formation of desirable productive types. From the standpoint of genetic resources management, the importance of the Alatau population is determined by a combination of productivity and adaptability, which makes it promising both for purebred breeding and for controlled crossing.

Aulieata cattle represent another important component of the regional dairy gene pool. In addition, specialized meat populations and crossbred types have been created to increase beef production. The creation and evaluation of the Kyrgyz beef type demonstrate the possibility of combining local livestock with specialized meat genetic material while maintaining a significant proportion of the local genetic background. However, such breeding strategies must be accompanied by ancestry control and genetic monitoring so that desirable adaptive traits are not lost due to uncontrolled substitution. The work of S.M. Derkenbayev, A.K. Samykbaev, U.A. Shergaziev and K.S. Aidakeeva is of particular interest, since it investigates the heritability and variability of cow traits depending on the breed composition. The results obtained show the relationship between milk yield, milk fat content and live weight, as well as the influence of breed composition on the manifestation of economically useful traits [7]. These data confirm the need to use quantitative genetic parameters when making breeding decisions, and not only to rank animals by phenotype.

U.A. Shergaziev also participated in studies of early estimation of breeding value of breeding bulls and testing them by offspring "Proper research is dedicated" to "direction". This principle is of great importance for the management of genetic resources: a small number of intensively used sires can have a disproportionately large impact on the genetic structure of the population. Therefore, the selection of high-value bulls should be combined with kinship management and inbreeding. Modern genomic tools make it possible to strengthen this approach by supplementing the pedigree information with genome-wide estimates of relatedness and homozygosity [8]. Another contribution from the studied studies of Shergaziev and his co-authors is related to the assessment of Aberdeen-Angus bulls by the quality of offspring. Such studies are of practical importance for the development of beef cattle

breeding, since the test on offspring links the genetic value of producers with the measurable indicators of their offspring. In the conditions of Kyrgyzstan, it is advisable to integrate this approach with the assessment of adaptability and efficiency of resource use, especially in pasture management.

Thus, the scientific evidence on cattle justifies a broader understanding of the value of genetic resources. Priorities should be the conservation of representative nuclei of locally adapted breeds, the documentation of pedigrees and reproductive indicators, the monitoring of genetic diversity and the assessment of the contribution of imported genetic material, rather than automatically considering it as a substitute for local resources. Genomic characterization of cattle populations will be particularly useful for the detection of impurities, the assessment of genomic inbreeding and the identification of animals that retain a characteristic local origin.

3. Sheep Genetic Resources and Molecular Data for Kyrgyzstan

Sheep breeding is of deep, significant economic and cultural importance for Kyrgyzstan and is represented by a number of genetically and phenotypically differentiated populations. The local gene pool of sheep includes the Alay, Aikol, Hissar, Kyrgyz coarse-haired, Tien Shan and Kyrgyz ermine populations and other groups. Their value is determined by various combinations of meat, wool, reproductive and adaptive productivity. Domestic breeding studies have traditionally been focused on phenotype, productivity and selection. A.S. Azhibekov, T.J. Chortonbaev and T.Zh. Turdubaev contributed to the development and assessment of sheep populations in the conditions of Kyrgyzstan, and Ch.T. Kadyrova and A. Abdykerimov participated, conducted research on the breeding work and exterior of Kyrgyz sheep. Modern research continues to show that productive traits are determined by the interaction of genotype and production environment, which makes a zonal approach to breeding important.

An important step in genomic characterization was a study by, in which 129 sheep representing five Kyrgyz populations were analyzed using genome-wide SNP arrays. The authors evaluated population structure, genetic relationships, effective population size, and genomic inbreeding indicators. The results demonstrated the differentiation between populations and confirmed that Kyrgyz sheep do not represent a single genetically homogeneous population [9]. In recent years, the Kyrgyz Mountain Merino has received additional attention in molecular studies. studied the genetic diversity of the population using microsatellite loci and demonstrated the possibility of its molecular characterization [10]. Earlier studies by Kyrgyz scientists also looked at and investigated the genetic variability of sheep using blood group polymorphism and other genetic markers. Taken together, these studies provide a link between traditional breeding data and modern population genetics.

Modern domestic studies are especially valuable because they link genetic and phenotypic variability with practical breeding.

Jolborsov analyzed phenotypic correlations between selected traits of sheep of different genotypes in southern Kyrgyzstan, highlighting the importance of the production environment and adaptation. Another 2024 study focused on the biochemical polymorphism of blood groups in sheep breeds in the south of the country. These results suggest that genetic diversity is appropriate to assess at several complementary levels, rather than using a single marker system. At the same time, international studies confirm the need to preserve the diversity of sheep breeds. Genome-wide analyses show a complex history of mixing and selection in sheep breeds, while genomic methods can identify differences that are difficult to detect by phenotype alone [11] Homozygosity regions (ROHs) provide an additional indicator of recent and historical inbreeding and can be used to identify populations that require closer monitoring.

In our opinion, the main scientific priority for sheep in Kyrgyzstan is not just the identification of a large number of breeds, but the quantitative assessment of intra-breed diversity, effective population size, genomic inbreeding and impurities. Such information will make it possible to distinguish small populations from genetically unique ones and form more reasonable conservation priorities. A special place in the modern gene pool of sheep in Kyrgyzstan is occupied by the new Kyrgyz meat and fat breeds "Arashan" and "Ala-Too". Their inclusion in the assessment of genetic resources is important, since both breeds are formed with the participation of local genetic material and are focused on obtaining meat and fat, but have a different history of creation and a modern level of documentation. The Arashan breed was officially registered in the Kyrgyz Republic on April 15, 2021 by order No110 of the People's Commissariat of Agriculture of the Kyrgyz Republic. According to the published description, its creation was carried out in the farms of Kyrgyzstan in 1970-2021 on the basis of reproductive crossing of local coarse-haired ewes with rams of the Hissar breed with the subsequent breeding of animals of the desired type "in themselves".

The breed belongs to the meat-fat direction and is characterized by a large size, pronounced meat and fat productivity, high growth energy and adaptation to the high-mountain and valley-steppe zones. From the point of view of genetic resources management, Arashan is a modern national breeding resource, for which it is necessary to maintain intra-breed variability and control the structure of reproduction. The Ala-Too sheep breed of the meat-fat direction is a modern breeding achievement in the south of Kyrgyzstan. According to the published description of the breeding achievement, it was bred by reproductive crossing of the desired type of crosses obtained by transformative crossing of local coarse-wool sheep with sheep of the Hissar breed, in breeding and farm farms of Osh, Jalal-Abad and Batken regions. In the structure of the breed, Jalal-Abad and Osh zonal types and a number of breeding lines are distinguished. The described features - high live weight, early maturity and meat-fat productivity - determine the prospects of the breed for the southern regions of Kyrgyzstan. associated with economically useful traits in local goats [12].

Therefore, phenotypic and quantitative-genetic studies of goats in Kyrgyzstan need to be complemented by SNP or genome-wide characterization of representative populations.

A national goat gene pool conservation programme should include representative breeding nuclei, controlled mating, conservation of locally distinct populations and cryopreservation of genetic material. As goat populations can change rapidly under the influence of cross-breeding and substitution, it is particularly important to combine pedigrees with genomic ancestry assessments. The meat direction of goat breeding deserves special attention. In the available domestic literature, which was verified from primary sources, the issues of meat productivity of goats are more often considered in combination with breeding, reproduction and use of local genetic material, and not as an independent direction. Thus, the official characteristic of the Kyrgyz dairy type of goats indicates that young animals after fattening at the age of 18-20 months reach an average live weight of 40-45 kg, with an average daily gain of 100-110 g and a slaughter yield of about 49%. These indicators indicate the presence of meat potential in goat populations and the need to include meat productivity in a comprehensive assessment of goat genetic resources. At the same time, for the scientifically substantiated identification of meat goat breeding as an independent breeding direction, it is necessary to study the dynamics of growth, slaughter qualities, morphological composition of the carcass, feed conversion and heritability of the corresponding traits.

4. Genetic Resources of The Kyrgyz Horse and The Preservation of Genetic Material

The Kyrgyz aboriginal horse is a nationally significant genetic resource associated with mountain conditions and traditional grazing maintenance. Its genetic value includes endurance, the ability to use natural pastures, and functional adaptation to the mountain environment. These characteristics are of practical importance for Kyrgyzstan's low-cost production systems and cultural heritage. The studies of Toktosunov and Abdurasulov, as well as Isakova and Isaev co-authors, provide molecular data on the genetic structure of the Kyrgyz horse. A study using 17 microsatellite markers demonstrated the possibility of using molecular markers to characterize the Kyrgyz breed and study its phylogenetic relationships. Such data are important for the genetic differentiation of local populations and crossbred animals.

Sydykbekov, Toktosunov and Abdurasulov (2022) investigated the conservation of the genetic biomaterial of the Kyrgyz horse breed and the possibilities of sperm cryopreservation. Cryopreservation is an important ex situ conservation strategy because it separates the preservation of genetic material from short-term fluctuations in the size of the living population. The updated FAO recommendations emphasize that the gene bank should function as an integrated system that includes material collection, quality management, storage, sanitation, data management and subsequent use of samples [13]. Therefore, the conservation of equine genetic resources should combine the maintenance of representative breeding

populations in situ with ex situ storage of sperm and, where these, associated with economically useful traits in local goats [12]. Therefore, phenotypic and quantitative-genetic studies of goats in Kyrgyzstan need to be complemented by SNP or genome-wide characterization of representative populations. A national goat gene pool conservation programme should include representative breeding nuclei, controlled mating, conservation of locally distinct populations and cryopreservation of genetic material. As goat populations can change rapidly under the influence of cross-breeding and substitution, it is particularly important to combine pedigrees with genomic ancestry assessments.

The meat direction of goat breeding deserves special attention. In the available domestic literature, which was verified from primary sources, the issues of meat productivity of goats are more often considered in combination with breeding, reproduction and use of local genetic material, and not as an independent direction. Thus, the official characteristic of the Kyrgyz dairy type of goats indicates that young animals after fattening at the age of 18-20 months reach an average live weight of 40-45 kg, with an average daily gain of 100-110 g and a slaughter yield of about 49%. These indicators indicate the presence of meat potential in goat populations and the need to include meat productivity in a comprehensive assessment of goat genetic resources. At the same time, for the scientifically substantiated identification of meat goat breeding as an independent breeding direction, it is necessary to study the dynamics of growth, slaughter qualities, morphological composition of the carcass, feed conversion and heritability of the corresponding traits.

5. Comparative Assessment of The Level of Genetic Characteristics

The literature available data indicate a different level of genetic characteristics of the four main groups of farm animals considered in Kyrgyzstan. Sheep have the strongest genome-wide evidence base, as five populations have already been studied using SNP arrays. A significant molecular base has been formed for horses on the basis of microsatellite studies and cryopreservation work. Cattle have a significant amount of quantitative genetic and breeding data, but the genome-wide characteristics of the main Kyrgyz populations are less developed. Important phenotypic and quantitative genetic studies are available for goats, but genome-wide characterization remains a priority.

Such unevenness has methodological implications. A breed may be well described phenotypically, but not sufficiently characterized genetically. Conversely, a population may have genomic data without sufficient information on the production environment, housing system and economically useful traits. FAO recommends combining phenotypic characterization, production environment description and molecular characterization to obtain a practical picture of farm animal genetic resources [1,14]. A comparison of the main species by the level of genetic study, economically useful traits and priority of conservation is presented in Table 1.

View	Representative Genetic Resources	Main features	Genetic data	Priority
Sheep	Arashan	Meat, lard, growth, adaptation	Selection and productive characteristics, SNP data required	Very high
Sheep	Ala-Too	Meat, lard, early ripeness, Maternal qualities	Breeding and productive research, Molecular characterization is required	Very high
Cattle	Alatau Aulietin breeds, meat types, local/ crossbred populations	Milk, meat, reproduction, adaptation	Ancestry data quantitative genetics, SNP data enhancement required	High
Sheep	Alay, Aikol, Hissar, Kyrgyz coarse-haired, Tien Shan, mountain merino, Arashan, Ala-Too	Meat, wool, adaptation	SNP arrays, microsatellites, phenotypic correlations	High
goats	Kyrgyz downy and woolly goats, dairy type, local populations	Down, wool, milk, meat, reproduction, adaptations	Phenotypic and genetic-statistical studies, SNP/ genomic data required Phenotypic and genetic	Very high
Horses	Kyrgyz horse and local populations	Endurance, pasture and mountain adaptation	Microsatellites and cryopreservation studies	High

Table 1: Comparative Assessment of the Main Genetic Resources And The Current Level Of Their Characteristics

6. Modern Genomic Approaches for Kyrgyzstan

The transition from traditional genetic characterization to genomics is one of the most significant areas for the development of modern livestock production and the conservation of genetic resources [15-19]. Microsatellites remain useful for a number of tasks, especially when historical data sets are available, but SNP genotyping and whole genome sequencing provide denser and more reproducible information. The 2023 FAO guideline considers whole genome sequencing and SNP genotyping as the main approaches to genomic characterization of farm animal genetic resources [2]. SNP data allow the assessment of genetic diversity, population structure, admixture, genetic distances and genomic relatedness [20]. They can also be used for ancestry verification, breed determination and genomic selection. highlight the practical application of genomic information – from ancestry and traceability to inbreeding and genomic assessment [6].

For local breeds in Kyrgyzstan, characterization and conservation should be an immediate priority rather than accelerated implementation of genomic selection, as existing diversity and threatened components must be identified first. Regions of homozygosity (ROH) represent another important indicator. Long segments of ROH are often associated with recent kinship of parents, whereas shorter segments may reflect more ancient demographic events [21,22]. Therefore, genomic inbreeding assessment based on ROH can complement pedigree coefficients, especially when ancestry data are incomplete [23]. This method is already being applied to the study of aboriginal cattle and goat populations in international studies and can be adapted to Kyrgyz breeds once sufficient SNP or sequence data sets are available [24].

Whole genome sequencing is becoming increasingly important for conservation, as it can identify rare alleles, structural variants, and potential genomic regions associated with adaptation. Conservation genomics is particularly important for local breeds whose distinctive features may not be present in commercial populations [25-30]. However, the results of genomic analysis must be interpreted in conjunction with production environment and phenotype data,

genomic uniqueness alone does not prioritize conservation [31]. It should be noted that the practical program for Kyrgyzstan should start with standardized sampling. Representative animals should be selected from different geographical zones and breeding systems, documenting breed affiliation, sex, age, pedigree, if any, housing system, production environment and basic phenotypic traits. DNA samples should be linked to a national database, and common identifiers should be used for live herds under conservation and cryopreserved material [32].

7. Risks of Genetic Erosion and Conservation Priorities

Analysis of the data considered above allows us to identify several risks that require attention.

- First, uncontrolled interbreeding can reduce the genetic independence of local populations [33]. Interbreeding in itself is not a negative phenomenon, it becomes a problem when the proportion and direction of introgression are not controlled, and characteristic local genotypes are gradually supplanted.
- Second, heavy use of a small number of sires can increase relatedness and reduce effective population size. This risk is particularly relevant for cattle and sheep, where artificial reproduction or highly sought-after sires are able to rapidly propagate individual genomes. Therefore, genetic management must take into account not only the actual number of animals, but also the effective population size and genomic relatedness [34].
- Third, insufficient accounting makes it difficult to distinguish between breeds, breed types and crossbred populations. The lack of standardized records reduces the value of both conventional breeding and molecular data. Fourth, climate variability can alter the relative value of adaptive traits. Locally adapted animals can become increasingly important with changing heat loads, droughts, forage availability and disease pressure [35].
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Therefore, the priorities for the conservation of the gene pool of breeds and populations should be determined by the totality of population size, genetic identity, adaptive value, productive value, cultural significance and practical feasibility of conservation. Molecular data should serve as the basis for decision-making, but

should not replace expert assessment. International experience shows that conservation measures can improve demographic dynamics without necessarily preserving genetic variability, if genetic management is not specifically included in the program [5,36-39].

8. Integrated National System for Sustainable Management of Genetic Resources

The most important practical conclusion of this review is the need for an integrated national system for the management of farm animal genetic resources. Such a system should not be limited to a list of breeds [40-42]. It should combine information on breed, population size, geographical distribution, pedigrees, phenotypic indicators, molecular profiles, conservation status and samples stored in the gene bank. The first component should be a national inventory and a standardized breed registry. The second is a digital record of pedigrees and productive data. The third is a national molecular characterization program with a unified sampling protocol [43]. The fourth is a national gene bank or a network of cryobanks with quality management procedures. The fifth is periodic risk assessment and reporting. The sixth is a coordinated breeding policy that distinguishes between increasing productivity and preserving genetic diversity.

For cattle, priority should be given to genomic characterization of the Alatau and other locally significant populations, with particular attention to impurity and genomic inbreeding. For sheep, the available SNP data need to be extended to additional herds and production areas. For goats, the genome-wide characterization is particularly relevant, as the available data are predominantly represented by phenotypic and quantitative genetic studies. For horses, molecular identification should be linked to the systematic cryopreservation of representative genetic lines [44]. The proposed system will also contribute to the development of scientific and educational activities [45]. The Kyrgyz National Agrarian University and other scientific institutions can act as centers for standardized sampling, analysis of genomic data, training of specialists in breeding work and the development of conservation protocols. Cooperation with international programs and the use of FAO recommendations will increase the comparability of national data with global information systems of farm animal genetic resources. [46]

9. Conclusion

Kyrgyzstan has a valuable and heterogeneous complex of genetic resources of farm animals, represented by cattle, sheep, goats and horses. As part of the sheep gene pool, the meat and fat breeds "Arashan" and "Ala-Too" are of particular modern importance. The data reviewed demonstrate that these resources have both productive and adaptive value and therefore should be considered as strategic components of agrobiodiversity [42,47]. The scientific literature of Kyrgyzstan provides an essential basis for such management. The studies of Derkenbaev S.M. and Shergaziev U.A. support the quantitative assessment of the breeding value of cattle, Duishekeev contributed to the improvement of Alatau cattle, Azhibekov A.S., Chortonbaev T.Zh., Turdubaev T.Zh.,

Kadyrova Ch.T. and Abdykerimov A.A. – in the development of sheep breeding and the characterization of sheep populations, Almeev, Abdurasulov, Jeenbekova and Satkankulov – in research on goat breeding and genetic resources, Toktosunov, Isakova and Abdurasulov – in molecular studies of importance for the conservation of horses and sheep [48].

The level of genetic characterization remains uneven. Sheep currently have the strongest genome-wide evidence base, horses have useful molecular and cryopreservation studies, for cattle, genomic characterization expansion is required, and for goats, the transition from phenotypic and quantitative genetic studies to SNP and whole-genome approaches is especially relevant. A modern conservation strategy should integrate in situ population management with ex situ cryopreservation and genomic characterization. The proposed national system should include standardized inventory, digital pedigree and productivity records, SNP or genome-wide analysis, ROH-based monitoring, effective population size estimation, genetic databases, and gene banks. The scientific novelty of this review lies in the integration of data on four main groups of farm animals and the comparison of their productive, adaptive and genetic characteristics. The generalization shows that the next stage of genetic resources management in Kyrgyzstan should be the transition from isolated studies of individual breeds to a coordinated national system in which genomic information, traditional breeding records and conservation policies will be interlinked.

Acknowledgments

The author expresses his gratitude to the researchers and scientific institutions of Kyrgyzstan, whose scientific publications have formed the national evidence base of this review.

Funding

The study did not receive special external funding.

Conflict of Interest

The author declares that there is no conflict of interest.

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