

Animal Genetic Banking in Georgia: Conservation and DNA/RNA Sequencing of *Capra caucasica* and *Capra cylindrica*

Nadiradze Dr. Kakha^[1]

[1] Association for Farmers Rights Defense, AFRD

The main objective of this initiative is to establish a reliable scientific foundation for the long-term conservation of Georgia's unique wild goat species by creating a structured animal genetic bank. The project aims to secure and preserve the DNA and RNA of *Capra caucasica* and *Capra cylindrica*, ensuring that their genetic diversity is fully documented and safeguarded for future research and restoration programs. Another key objective is to strengthen international scientific cooperation through collaboration with China Agricultural University, enabling advanced genomic analysis that supports conservation, breeding strategies, and the development of future gene banking systems. Ultimately, the project seeks to provide Georgia with a modern framework for protecting its valuable genetic resources and contribute to national and regional biodiversity conservation efforts.

The experimental work for this initiative followed internationally recognized genetic conservation protocols to ensure the accuracy, purity, and long-term usefulness of the collected material. Field specialists conducted controlled sampling of biological materials from *Capra caucasica* and *Capra cylindrica* populations in their natural habitats. Tissue, hair follicle, and blood samples were collected using sterile procedures to prevent contamination and to maintain the integrity of the genetic material. Samples were immediately preserved under regulated cold-chain conditions and transported to the partnering laboratory at China Agricultural University. In the laboratory, DNA and RNA were extracted using standardized molecular biology methods, including automated purification systems and high-fidelity extraction kits suitable for wild species. The quality and concentration of nucleic acids were evaluated through spectrophotometric measurement and gel electrophoresis. High-throughput sequencing technologies were employed to obtain whole-genome and transcriptome data, providing a detailed overview of genetic variability, population structure, and unique adaptive traits. The sequencing workflow included library preparation, fragment selection, amplification, and sequencing on next-generation sequencing platforms. Statistical analyses were performed using bioinformatics pipelines designed for wildlife genomics. Raw data underwent quality control, trimming, and alignment to reference sequences. Population genetic analyses—including heterozygosity estimates, genetic distance measurements, and phylogenetic assessments—were conducted using software such as STRUCTURE, MEGA, and R-based statistical tools. These analyses allowed researchers to identify genetic patterns, assess variation within and between populations, and evaluate the overall health and resilience of the species' gene pools. The results form the scientific foundation for future conservation strategies and the establishment of a national gene bank with strong genetic integrity.

The preliminary results of the genetic banking initiative demonstrate that the collected samples of *Capra caucasica* and *Capra cylindrica* were of high quality and suitable for full DNA and RNA sequencing. Laboratory analyses confirmed strong nucleic acid integrity, allowing for successful extraction, purification, and preparation of genomic libraries. The sequencing process generated a comprehensive dataset that reveals the presence of distinct genetic markers, adaptive traits, and population-level variations within both species. These findings provide valuable insight into the evolutionary relationships, genetic resilience, and potential vulnerabilities of Georgia's wild goat populations. Genetic diversity assessments indicate that both species retain significant levels of variability, which is essential for long-term survival, adaptation, and resistance to environmental pressures. The results also suggest meaningful differences between regional populations, emphasizing the need for targeted conservation measures. The bioinformatic analyses have enabled the identification of unique gene regions that may be relevant for future breeding, restoration, or reintroduction programs, as well as for the establishment of a national and regional animal gene bank. In conclusion, the project successfully demonstrated that Georgia's wild goat species possess strong and distinctive genetic characteristics that merit priority conservation. The collaboration with China Agricultural University provided high-quality genomic data that will play a critical role in shaping future biodiversity strategies. The findings confirm that the creation of an animal genetic bank is both feasible and scientifically justified, offering a secure foundation for future research, conservation planning, and long-term protection of Georgia's genetic heritage.