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Article

Variability of the Nuclear and Mitochondrial Genome of *Saiga tatarica tatarica*

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Simple Summary

This study is dedicated to the study of the genetics of saiga antelope, a species of antelope whose populations have experienced repeated critical declines in the past. The aim of our work was to identify genetic differences between individual saigas, which is extremely important for the survival of the species and its ability to adapt. We found that, despite population declines, saigas retained a moderate level of genetic diversity in both their nuclear and mitochondrial genomes. This is supported by the presence of unique genetic markers in each individual and variations in mitochondrial DNA. These results are significant because they demonstrate the species' potential for recovery and highlight the need to develop targeted conservation strategies.

Abstract

This study employs a combined k-mer based comparative genomics and mitochondrial genome analysis to investigate genetic variation in *S.t. tatarica*. Whole genome sequencing data were used to assess genomic diversity, revealing significant variation between samples, with 25.55-28.49% of k-mers being sample-specific. Mitochondrial genome sequencing provided 100% coverage for all samples and identified 532 variants. These variants were predominantly variants of the ND4, ND5, ND6, and CYTB genes, with uneven distribution among samples and mitochondrial genes. The results indicate a noticeable level of genetic diversity in *S.t. tatarica* and provide insight into the population structure of the species.

Keywords: *Saiga tatarica tatarica*; whole genome sequencing; K-mer analysis; mitochondrial genome; genetic diversity; Ural population; Betpak-dala population

1. Introduction

Saiga is a migratory herbivore inhabiting central Asia. Currently, it is found in Kazakhstan, Russia, Mongolia, Turkmenistan, and Uzbekistan. It has been reintroduced into the Ukrainian reserve (Askania Nova).

The genus Saiga is a member of the Polyhoridae family and according to various sources belongs to the subfamilies *Antilopinae* and *Saiga (Saiginae)* [1]. The animal has an unusual appearance due to its characteristic feature of a pair of closely flared nostrils, which point downwards and form a mobile, meek proboscis [2,3]. Males also have thick, slightly twisted horns with pronounced rings and a light waxy colour. The saiga is one of the few extant relics of the Ice Age, well adapted to the

harsh, sharply continental climatic conditions of the steppes. Saigas were previously widespread on the Eurasian continent, with their range extending from Western Europe to the Chukotka Autonomous Area of the Russian Federation [4,5].

To a greater or lesser extent, each of these populations undertakes seasonal migrations, heading north to their summer ranges and south to their winter ranges in search of favorable climatic conditions and more fertile pastures. As of April 2025, the saiga population in Kazakhstan reached 4.1 million individuals, an increase of 45% compared to the previous year. The Ural saiga population, the largest in Kazakhstan, numbers 2,300,000 individuals. The second largest population is the Betpak-dala population, which has 1,600,000 individuals. The smallest population, the Ustyurt population, numbers only 92,200 individuals [6]. Saigas are generally a migratory species that are prone to mass mortality, but their high reproductive rate helps populations recover. Dzud and disease are the two main factors causing mass mortality [7,8]. Poaching also poses a constant threat, leading to a sharp decline in population numbers [9,10]. Given that female saigas mainly give birth to twins, this fact allows populations to quickly increase in number after a decline [11].

An analysis of the dynamics of saiga population numbers over the last hundred years clearly shows that the species has twice experienced the “bottleneck effect”. This effect refers to a sharp decline in population numbers due to various factors (disease, natural disasters, uncontrolled hunting, etc.). A significant decline in population size leads to a reduction in the genetic diversity of the species. If the population subsequently increases, the previous levels of genetic diversity are not restored, as the frequency of inbreeding increases, reducing the heterozygosity of the population and causing the loss of alleles [12,13].

The first such effect was observed in the 1940s and 1950s, when no more than ten herds of several hundred individuals and one herd of just over a thousand were recorded in Kazakhstan [14]. After that, measures were taken to ban saiga hunting, and the population quickly grew to 1 million individuals, at which point hunting was once again permitted. A second similar case occurred in the late 1990s, when the saiga population fell to 21,000 (just over 2% of the original population survived). The main cause at that time was poaching [9,10]. In addition, in 2015, there was a mass death of saigas caused by *Pasteurella multocida* bacteria [7].

The recovery of the saiga population after each reduction was most likely accompanied by a loss of genetic diversity. The depletion of the gene pool leads to an increased probability of extinction, reduces the adaptive potential of the species, and decreases the viability of animals. Without the necessary work to restore the gene pool, there will be further loss of alleles that may be responsible for the body's immunity to infectious diseases, i.e., outbreaks of infections will occur more frequently and with more massive animal deaths. Diseases caused by genetic abnormalities will also spread [15,16].

However, the internal structure of populations and their level of genetic diversity remain poorly understood, especially at the genomic and mitochondrial DNA levels. It is worth noting that research on saiga genetic material has been and continues to be conducted by the international scientific community. However, the number of such studies is extremely small, and most of them are conducted by Chinese scientists on the Mongolian subspecies of saigas (*Saiga t. mongolica*) or on archaeological remains found in the Middle Paleolithic and Neolithic periods [17–20]. Work is underway to find molecular genetic methods for identifying biomaterial and determining its origin from saigas [21,22].

The last major study of the Kazakh saiga population was conducted in 2013, when the genome of two individuals from the Ural saiga population was analyzed and markers for microsatellite analysis of *Saiga t. tatarica* were identified [23]. A significant problem is the lack of data on sequences and genetic polymorphism, which seriously hinders the application of genomic approaches to solving biological problems. A whole-genome analysis capable of identifying polymorphic markers is required to assess the population characteristics of saigas.

Thus, in Kazakhstan, where all three modern populations of *Saiga tatarica tatarica* are predominantly concentrated, no studies have yet been conducted to characterize the genetic structure of the populations.

Our study aimed to determine the characteristics of genetic differences between individuals of *Saiga tatarica tatarica* based on whole-genome DNA analysis.

The results of studies on genomic and mitochondrial variation are fundamental to our understanding of the biology of species and broader ecological and evolutionary studies.

A detailed analysis of the mitochondrial genome, including the identification of variants, provides valuable markers for population genetic studies. These data can be used to reconstruct phylogenetic relationships within a species, assess population dispersal history, and identify centres of origin or refugia.

The results of this study will inform future conservation efforts for this species. Understanding the genetic structure will enable effective management strategies and plans for conserving genetic resources to be developed.

2. Materials and Methods

2.1. Sampling

Ear plucks from dead wild animals of the Ural and Betpak-dala saiga populations were used as biomaterial for research.

Table 1. Characteristics of selected samples.

Sample number	Population	Gender	Date of selection	Place of collection
10u	Ural	Male	May 2023	West Kazakhstan Region, Zhanibek district, Talovka village
14u		Male		
18u		Female		
20u		Female		
20b	Betpak-dala	Male	November 2023	Akmola Region, Korgalzhyn district, Sabyndy village
28b		Female		
41b		Male		
42b		Male		

2.2. DNA Extraction and Genetic Analysis

DNA from saiga tissues was extracted using the commercial «PureLink Genomic DNA Mini Kit» (Invitrogen, USA).

For sequencing, we used a platform from BGI (Beijing Genomics Institute) based on DNBseq technology. DNA libraries were prepared according to the manufacturer's recommendations, after which the concentration and quality of the material were checked using a fluorimeter and gel electrophoresis. The DNA was then fragmented to the desired size, and adapters and primers were added to the fragments to bind to the sequencing platform. This was followed by PCR amplification of the target regions. The data were read in paired-end sequencing mode with a read length of 100-150 bp. After sequencing, low-quality data were filtered and adapters were removed using FastQC, MultiQC, and Trimmomatic software [24]. The data obtained were saved in FASTQ format for further processing.

2.3. Sequence Processing and Quality Control

Paired-end whole genome sequencing data were obtained for eight *S. t. tatarica* samples. Raw sequencing reads were processed using fastp v0.20.0 [25] to remove low-quality sequences and adapter contamination. Quality filtering was performed with the following parameters: 4 bp sliding window for quality trimming with a mean quality threshold of 20, minimum base quality score of 15,

maximum percentage of unqualified bases allowed of 40%, maximum number of N bases of 5, and minimum read length of 36 bp after trimming. Adapter sequences were automatically detected and removed. Both 5' and 3' ends of reads were trimmed based on quality thresholds. Quality control metrics and reports were generated for each sample.

2.4. K-mer Based Comparative Genomic Analysis

To analyze genomic variation without requiring a reference genome assembly, we employed a k-mer based comparative approach [26,27]. Raw FASTQ files were converted to FASTA format using BBMap (version 38.90) [28]. For the k-mer analysis, we selected a k-mer size of 17 nucleotides, which provides an optimal balance between specificity and sensitivity for comparative genomics [29,30]. A minimum count threshold of 2 was implemented to filter potential sequencing errors [31]. For computational efficiency, 50,000 sequences were randomly sampled from each individual [32]. K-mers were extracted, counted, and filtered using a custom-developed computational pipeline. Pairwise genomic similarities between samples were calculated using multiple metrics including the Jaccard index ($J = |A \cap B| / |A \cup B|$) [33], Szymkiewicz–Simpson coefficient ($|A \cap B| / \min(|A|, |B|)$) [34,35], and Sorenson-Dice coefficient ($2|A \cap B| / (|A| + |B|)$), where A and B represent the sets of k-mers from two samples. Sample-specific genomic elements were identified by systematically removing k-mers shared with any other sample [36].

2.5. Mitochondrial Genome Mapping and Variant Analysis

Filtered paired-end reads were aligned to the *S.t. tatarica* mitochondrial reference genome (NC_020746.1, 16,375 bp) using BWA-MEM v0.7.17 [37] with default parameters and 20 threads. Read groups were assigned during alignment with sample identifiers. Post-alignment processing was performed using SAMtools v1.19 [38] and included the following steps: name-based sorting, fixing mate pair information, position-based sorting, and marking (but not removing) duplicate reads. Alignment statistics, including mapping rates and coverage, were generated using samtools flagstat and samtools coverage commands. Variant calling was performed using BCFtools v1.19 mpileup and call functions [39,40]. The mpileup command was executed with a maximum depth of 1,000,000 and a minimum base quality of 0 to ensure capture of all potential variants. The call command used the multiallelic-caller model to identify variants. Variants were filtered based on quality and depth using BCFtools filter with the criteria $QUAL \geq 20$ and $DP \geq 10$. The resulting variants were normalized using BCFtools norm to ensure proper representation of indels and complex variants.

Filtered variants were annotated using SnpEff [41] with a custom database built for the *S.t. tatarica* mitochondrial genome (NC_020746.1). The annotation process classified variants into four impact categories: HIGH (variants with high impact on gene function), MODERATE (non-synonymous substitutions), LOW (synonymous variants), and MODIFIER (variants with minimal impact, typically in non-coding regions). Variant statistics were generated using BCFtools stats [42] to summarize the types and distributions of variants across samples. Additional analyses included quantification of variant impact by gene, variant distribution across samples, and identification of patterns in variant distribution. Genomic features were compared using BEDTools [43]. Figures and statistical analyses were created using R v4.2.0 [44] with packages including ggplot2 [45], dplyr [46], tidyverse [47], and ggpublisher [48].

3. Results

Genetic variance

K-mer analysis of eight *S. t. tatarica* whole genome sequences revealed substantial genomic variation, with each sample containing a significant proportion of unique genomic content (Table 2).

Table 2. Sample-specific genomic content in *S. t. tatarica* whole genome sequences.

Sample ID	Total k-mers	Unique k-mers	Percent unique (%)
10u	216,751	61,095	28.19
14u	198,414	50,700	25.55
18u	229,716	64,426	28.05
20u	221,489	61,019	27.55
20b	223,576	62,011	27.74
28b	207,013	54,384	26.27
41b	230,539	65,689	28.49
42b	222,589	59,762	26.85

Pairwise genomic comparisons demonstrated relatively uniform genomic distances across all sample pairs, with Jaccard similarities falling within a narrow range (0.2785-0.2890). Table 3 presents the three most and least similar sample pairs, along with average similarity metrics across all pairwise comparisons.

Table 3. Genomic similarity between *S. t. tatarica* samples.

Ranking	Sample pair	Jaccard index	Shared k-mers	Total unique k-mers
Most similar 1	20b-42b	0.2890	100,027	346,138
Most similar 2	42b-20u	0.2889	99,528	344,550
Most similar 3	42b-41b	0.2877	101,235	351,893
Least similar 1	10u-42b	0.2785	95,694	343,646
Least similar 2	10u-20b	0.2791	96,081	344,246
Least similar 3	10u-41b	0.2803	97,918	349,372
Average	All pairs	0.2844	-	-

The Szymkiewicz-Simpson coefficient and Sørensen-Dice coefficient values averaged 0.4567 and 0.4429 respectively across all sample pairs. The consistency of similarity values, coupled with the substantial proportion of sample-specific k-mers (25.55-28.49%), suggests a population with moderate genetic diversity but no evidence of distinct subpopulations or highly divergent individuals.

Mitochondrial Variance

The analysis of the *S. t. tatarica* mitochondrial genome sequencing data revealed complete coverage across all samples, with each sample achieving 100% coverage of the reference genome (NC_020746.1, 16,375 bp total length). Despite the uniformity in coverage breadth, there was considerable variation in sequencing depth among the samples. Sample 20b exhibited the highest mean depth at 1048.06x, followed by sample 14u (887.55x) and sample 10u (831.87x). Moderate depth was observed in samples 18u (597.42x), 42b (526.15x), and 28b (461.63x). The lowest sequencing depths were found in samples 41b (395.45x) and 20b (306.96x). The average sequencing depth across all samples was 631.89x (Table 4).

Table 4. Mapping statistics for *S. t. tatarica* mitochondrial genome analysis.

Sample	Mean coverage	Mean depth	Mean baseq	Mean mapq	Total reads	Mapped reads	Mapping rate
10u	100	831.871	34.8	59.5	244 707 792	98 095	98.79
14u	100	887.549	34.8	59.5	256 199 931	106 036	98.82
18u	100	597.415	34.8	59.4	226 731 405	70 796	98.5
20u	100	306.962	34.5	59.5	87 524 401	35 609	98.68

20b	100	1048.06	34.7	59.6	253 852 993	122 952	98.94
28b	100	461.625	34.7	59.7	97 374 897	53 302	98.94
41b	100	395.453	35	59.6	102 013 937	45 799	98.87
42b	100	526.15	34.6	59.5	181 278 666	61 213	98.74

The sequencing quality metrics were consistent across all samples, with mean base quality scores ranging from 34.5 (sample 20u) to 35.0 (sample 41b), and a mean of 34.74 across all samples. Similarly, the mapping quality was highly uniform across samples, with values ranging from 59.4 (sample 18u) to 59.7 (sample 28b), and an average of 59.54. The high and consistent coverage across all samples, coupled with the substantial sequencing depth, provides a robust foundation for the identification of mitochondrial variants. The uniformity in quality metrics further indicates that the sequencing data is of high quality across all samples, making it suitable for downstream analyses, including variant calling and phylogenetic investigations.

Eight mitochondrial genome samples were analyzed for genetic variants (Figure 1). Three samples (18u, 20u, and 41b) each contained the highest number of variants, with exactly 101 variants. Sample 14u followed by 89 variants. Samples 10u and 20b both had 43 variants, while 28b contained 36 variants. Sample 42b showed the fewest variants, with only 18. The average quality scores for these variants were consistently high across all samples, ranging from 221.83 to 228.14, with 42b showing the highest average quality score.

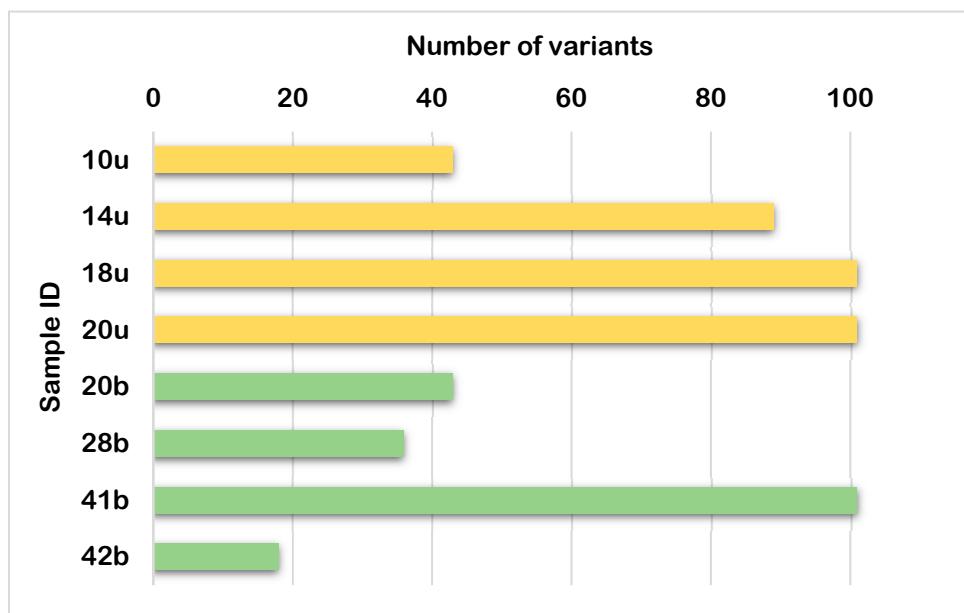


Figure 1. Distribution of mitochondrial genome variants across all samples.

The mitochondrial variants were classified into different types based on their predicted functional impact (Figure 2). Upstream gene variants were the most prevalent type, with 254 occurrences, followed closely by synonymous variants with 214 occurrences. Missense variants were the third most common type with 61 occurrences. Stop gained (2) and stop lost (1) variants were comparatively rare. This distribution indicates that while many variants occur in non-coding regions upstream of genes, a substantial proportion also occur within coding sequences, but most of these coding variants do not alter the amino acid sequence (synonymous variants). Comprehensive results of the annotation are available in supplementary table.

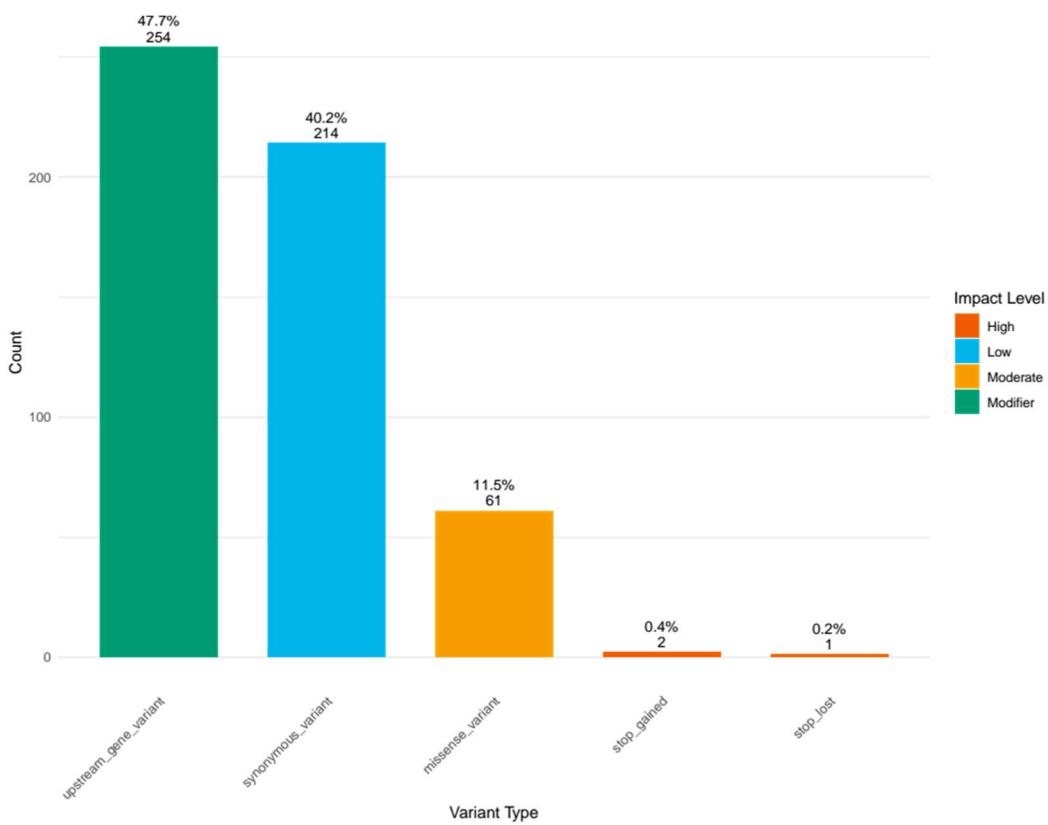


Figure 2. Distribution of functional impact of mitochondrial variants in *S. t. tatarica*.

The variants were mapped to specific genes within the mitochondrial genome to identify the most affected genes (Figure 3A). The analysis revealed that ND4 was the most affected gene with over 400 variants, followed closely by ND5 and ND6, each with approximately 350-380 variants. Other significantly affected genes included CYTB (~250 variants), ATP6 (~180 variants), and the COX family genes (COX1, COX2, and COX3), each with approximately 100-150 variants. The genes with fewer variants included ND3, ATP8, ND4L, ND2, and ND1, with variant counts ranging from approximately 50 to 100. The impact of these variants was classified into four categories: HIGH, MODERATE, LOW, and MODIFIER (Figure 3A). The majority of variants across all genes were classified as MODIFIER, indicating they likely have minimal impact on gene function. LOW-impact variants were the second most common category, followed by MODERATE-impact variants. HIGH-impact variants, which could potentially disrupt gene function, were rare across all genes. The distribution of variants across genes showed distinct patterns among the eight samples (Figure 3B). Samples 41b, 18u, and 20u had the highest number of variants across most genes, particularly in the ND4, ND5, ND6, and CYTB genes, where variant counts reached 60-80 per gene. In contrast, samples 42b and 28b showed fewer variants across all genes. The heatmap visualization (Figure 3B) revealed a clear pattern where samples 41b, 18u, 20u, and 14u formed a cluster with higher variant counts, while samples 10u, 20b, 28b, and 42b formed a separate cluster with lower variant counts. This pattern was consistent across all mitochondrial genes, suggesting potential population structure or evolutionary relationships between the samples.

The variant analysis revealed a total of 532 variants across all eight mitochondrial genome samples of *S. t. tatarica*. The variants were predominantly upstream gene variants (47.7%) and synonymous variants (40.2%), with a smaller proportion of missense variants (11.5%) and rare stop-gained/lost variants (0.6%). The variant distribution was not uniform across samples, with three samples showing significantly higher numbers of variants (101 each) compared to the sample with the lowest number (18). The variant distribution across genes and their functional impact

classifications provide a comprehensive overview of the genetic variation present in the mitochondrial genome of *S. t. tatarica*.

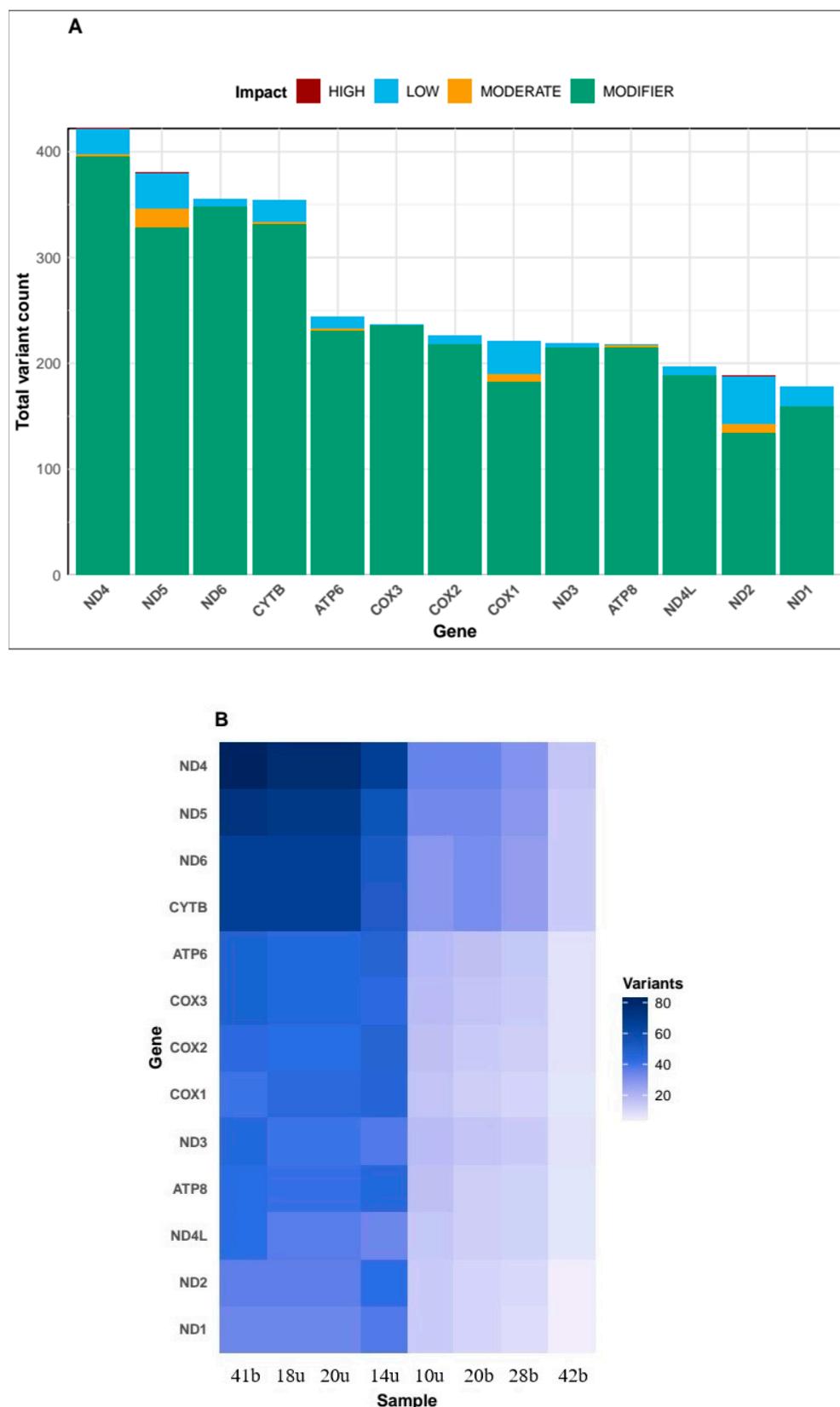


Figure 3. Distribution of variants across mitochondrial genes in *S. t. tatarica*. (A) Total number of variants detected in each mitochondrial gene, colored by predicted functional impact (HIGH, LOW, MODERATE, or

MODIFIER). (B) Heatmap showing the distribution of variants across all genes (y-axis) and samples (x-axis), with color intensity representing variant count as indicated in the legend.

4. Discussion

Authors should discuss the results and how they can be interpreted from the perspective of previous studies and of the working hypotheses. The findings and their implications should be discussed in the broadest context possible. Future research directions may also be highlighted.

This study represents the first attempt at a comprehensive analysis of the variability of the nuclear and mitochondrial genomes of the saiga antelope *S. t. tatarica* using whole-genome sequencing. The study of genomic variation within and between species is fundamental to understanding evolutionary processes, adaptation, and speciation. Advances in sequencing technologies have provided researchers with unprecedented access to genomic data, enabling detailed studies of the genetic architecture of diverse organisms.

K-mer analysis, a method that does not require a reference genome, allows the variability of the genome to be investigated by breaking down sequences into smaller units (k-mers) and comparing their presence and frequency of occurrence in different samples [26,27]. This approach is particularly useful for species where high-quality reference genomes are either unavailable or difficult to obtain [49] Jaccard index [33], Szymkiewicz–Simpson coefficient [34,35] and the Sorensen-Dice coefficient [50] are effective tools for quantitatively assessing the degree of genomic similarity and differences based on comparing a set of common and unique elements between two genomes.

Mitochondrial DNA (mtDNA) analysis is an additional, widely used approach in evolutionary and population genetics. The mitochondrial genome, due to maternal inheritance, the absence of recombination, and a relatively high mutation rate, is a powerful tool for reconstructing phylogeographic patterns and studying the demographic history of populations.

The combination of genomic and mitochondrial analysis provides a comprehensive picture of the genetic diversity of *S. t. tatarica*. This multifaceted approach contributes to a deeper understanding of the evolutionary processes that shape the genetic structure of this species.

Genetic analysis of *S. t. tatarica* individuals conducted as part of our work has provided new data on intraspecific variability and the potential structure of saiga populations. The results of our study showed that the population of *S. t. tatarica* maintains a moderate level of genetic diversity at the nuclear and mitochondrial levels, despite known cases of sharp declines in numbers in the past.

The use of a k-mer analysis approach without reference to a reference genome revealed moderate but stable divergence between samples, reflecting the overall picture of genetic diversity within the species. The proportion of unique k-mers, ranging from 25.5% to 28.5% in individual samples, indicates the presence of individual genetic characteristics.

While individual genomes showed unique features, pairwise comparisons indicated a relatively limited range of genomic distances, as reflected in the Jaccard index (0.2785–0.2890). The average values of the Jaccard index and Szymkiewicz–Simpson coefficient indicate a fairly high degree of genetic similarity between individuals, but the preservation of unique DNA fragments suggests that each individual contributes to the overall pool of genetic variability. These data are consistent with previous findings that, despite a sharp decline in population size, the saiga has been able to maintain a certain level of genetic heterogeneity [51,52]. A similar level of individual specificity was also observed in other studies on saigas and pointed to the important role of local adaptive processes and historical migrations in shaping genetic structure [51,52].

Analyzing the data in Table 3, it is necessary to note the high genomic similarity at the k-mer level between two samples belonging to different populations (42b – Betpak-dala and 20u - Ural populations). The most obvious explanation for the similarity found is the ongoing gene flow (migration and interbreeding) between the Betpak-dala and Ural populations. To confirm this theory, we randomly selected several genes for alignment (16S rRNA, cytochrome b, and RAG2-Recombination activating gene 2). Alignment was performed using the widely used ClustalW program. As a result, each alignment led to the formation of two fairly close clusters that separate the

populations according to the sampling locations (Figure 4). In each of the trees presented, sample 42b was closer to individuals from the Ural population. This fact may serve as further confirmation of migration between the indicated populations, although it was previously believed that the Ural population was more isolated from the other two due to the large distances between them and that the main migration occurs between the Betpak-dala and Ustyurt populations [51].

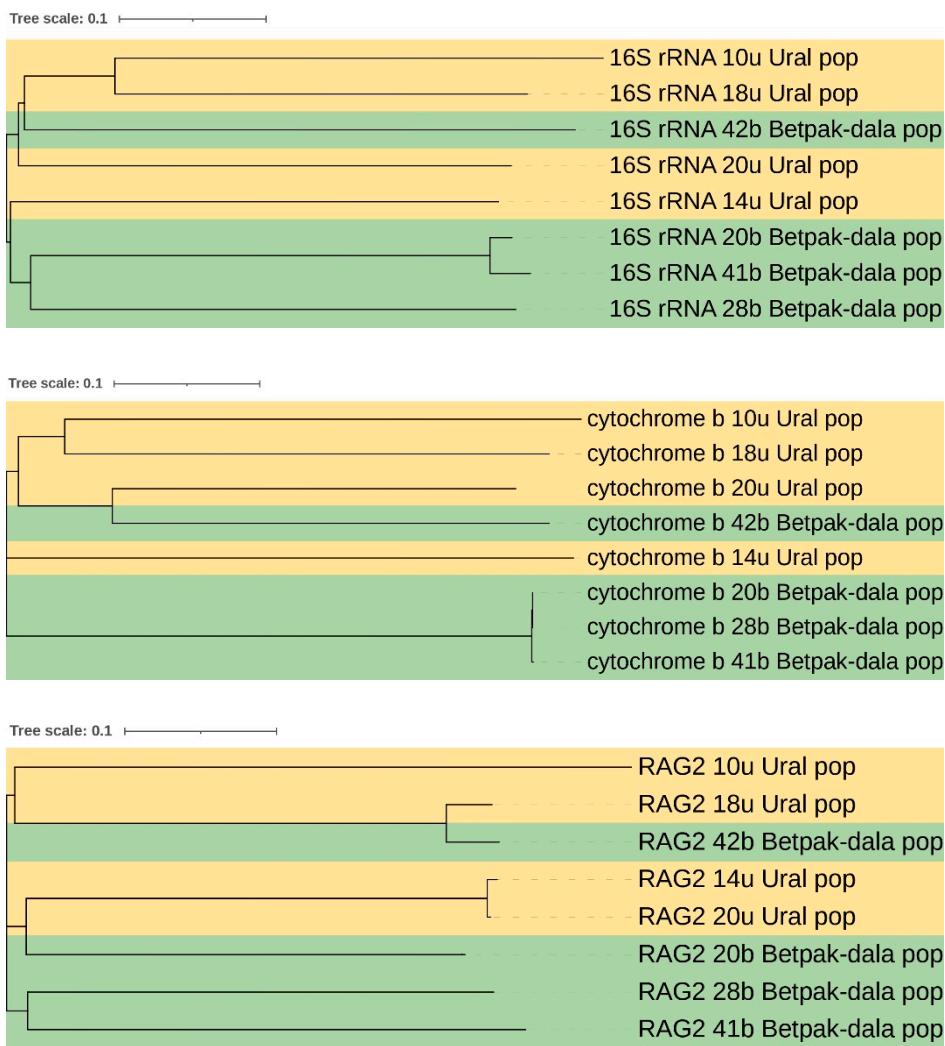


Figure 4. Phylogenetic trees based on gene alignment of 16S rRNA, Cytb, and RAG2.

Mitochondrial genome analysis has further contributed to our understanding of the genetic structure of *S. t. tatarica*. While all samples showed complete coverage of the mitochondrial reference genome, there was significant variation in sequencing depth. However, this variation in depth did not affect data quality, as sequencing quality metrics were consistent across samples.

Particular attention is drawn to the division of samples into two main groups based on the distribution of mitochondrial variants. One group, including samples 18u, 20u, 14u, and 41b, showed significantly more variants in key mitochondrial genes (ND4, ND5, ND6, CYTB) than the second group. Such differences may be the result of historical substructuring of the population, possibly due to geographical barriers or asynchronous waves of migration in the past, which has previously been noted for saigas in genetic studies [53,54]. Previously, a similar substructure was observed in saigas from Kalmykia and Kazakhstan based on mtDNA data [51], which suggests the presence of stable phylogenetic lines within the species.

In the mitochondrial genome of *S. t. tatarica*, 532 genetic variants were found, most of which were located in non-coding regions or represented synonymous substitutions, indicating the predominance of evolutionary pressure of stabilizing selection on mitochondrial genes [55] and

suggesting a potentially limited impact on protein function. The high proportion of upstream variants in mitochondrial genes is also consistent with data from other ungulates, where regulatory elements have been subject to more frequent mutations than coding regions [56]. This mutation profile is typical for the mitochondrial genomes of most mammals, where there is strong stabilizing pressure aimed at preserving the basic functions of cellular respiration [55,56]. However, the presence of missense variants and variants that alter the stop codon suggests the possibility of functional consequences, and these deserve closer attention in future work.

The distribution of polymorphic variants across mitochondrial genes was also uneven, with the ND4, ND5, and ND6 genes showing the greatest number of variants. This observation is consistent with data obtained for other ungulate species [57,58], as well as birds [59,60], rodents [61] and even amphibians [62], where these genes showed the greatest variability and potential role in adaptation to environmental conditions: in ungulates, to hypoxic conditions or high levels of physical activity; in birds, to hot climates; and in amphibians, to cold stress.

The ND4, ND5, and ND6 genes encode subunits of the NADH dehydrogenase complex (ubiquinone dehydrogenase complex, NADH-ubiquinone dehydrogenase (Complex I)), which plays a central role in cellular respiration and oxidative phosphorylation in mammals. Mutations in ND4 and ND6 prevent the assembly of complex I, leading to a deficiency of complex I [63–65], while mutations in ND5 disrupt the activity of complex I, causing a mild defect in the assembly of complex I [66,67]. Although the proteins encoded by these genes are involved in key cellular processes, mtDNA evolution has long been considered almost neutral, and many studies have ignored the direct influence of positive and/or negative selection on the formation of mitochondrial genome diversity. However, an increasing number of studies support the view that variations in the mitochondrial genome are not selectively neutral [59,68,69]. Negative (cleansing) selection is considered to be the predominant force shaping the evolution of the mitogenome, limiting the accumulation of harmful mutations in such evolutionarily constrained regions as NADH dehydrogenase (ND) subunits (Bazin et al., 2006). The identification of specific genes, such as ND4, ND5, and ND6, as hotspots of variation raises questions about the evolutionary pressure acting on these components of the mitochondrial respiratory chain.

5. Conclusions

In conclusion, this study provides a comprehensive analysis of genomic and mitochondrial variation in *S. t. tatarica*. The data obtained contribute to our understanding of the genetic diversity and population structure of this species and lay the foundation for future studies of the evolutionary and ecological factors shaping its genetic landscape.

The observed patterns of genomic and mitochondrial variation in *S. tatarica* raise several interesting questions. Moderate but uniform genomic diversity may indicate a recent population bottleneck or expansion event. Differences in the number of mitochondrial variants between samples may reflect population structure or historical demographic processes. The functional impact of the identified variants, especially in coding regions, requires further study to fully understand their potential adaptive significance.

From a practical point of view, the data obtained emphasize the need to take into account the identified genetic differences when developing strategies for the conservation and management of Saiga tatarica populations. Genetically enriched groups with higher levels of mitochondrial and nuclear variability may represent priority targets for biodiversity conservation measures.

Thus, the results confirm that, despite demographic shocks, the population of *S. t. tatarica* retains significant genetic potential for further recovery. High intrapopulation variability and signs of substructure confirm the need for a differentiated approach to the conservation of different population groups. An important direction for further research will be to include more samples from various regions of the range and expand the set of genetic markers through whole-genome sequencing and metagenomic approaches.

Supplementary Materials: The following supporting information can be downloaded at the website of this paper posted on Preprints.org.

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