Studying the Genetic Diversity of the Taimyr Population of the Nenets Reindeer Breed

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Abstract. For the first time, the genetic diversity of farm populations of domesticated Nenets reindeer bred in Taimyr has been studied to form their DNA bank. A comparative analysis of the genetic characteristics of the Nenets reindeer populations bred in other regions (Nenets and Yamalo-Nenets Autonomous District, the Murmansk Region, and the Komi Republic) has been performed using DNA markers. The genetic diversity markers - microsatellites have been used as DNA markers in the study. As a result of the research, it has been revealed that this group of domesticated reindeer has a low level of genetic polymorphism and diversity. A comparative analysis of this population with the regional ones from the Nenets and Yamalo-Nenets Autonomous District, the Murmansk Region, and the Komi Republic has revealed genetic ties with reindeer bred in the Komi Republic and Yamalo-Nenets Autonomous District. A low level of both allelic and genetic diversity may further negatively affect the animals’ adaptation to environmental conditions.

1. Introduction

Great attention is globally paid to the preservation of biological diversity. Declining biodiversity threatens humanity with an irretrievable loss of many both already developed and potential resources, and the further degradation and destruction of the biosphere. Despite some similarities in the problems of preserving the genetic diversity of wild species and domesticated animals, there are distinctions associated, first of all, with the different nature of the variability of wild and domesticated animals. Populations of wild animals, as a rule, are outwardly similar to each other and morphologically homogeneous, but they are highly polymorphic in biochemical and physiological characteristics. This polymorphism not only ensures the possibility of further species evolution but also serves as a prerequisite for its ability to adapt to changing environmental conditions [10].

Currently, one of the Taimyr reindeer population research objectives is studying their genetic characteristics.
Until the middle of the 20th century, genetic changes have been registered by the number of gene mutations with visible morphological manifestations. Since the 50s of the last century, the antigenic blood properties have been widely detected in various farm animals. In the 60s of the 20th century, the use of gel electrophoresis in population genetics started. With the improvement of methods for studying the variability of characteristics, the use of more accurate molecular genetic techniques began [1].

The genetic variability of the Taimyr reindeer has been studied using techniques corresponding to the genetics development stages.

Genetic research of blood groups in reindeer breeding was associated with the development of scientifically justified reindeer stock breeding techniques. On Taimyr, the first studies have been performed by L.F. Savaderova and included introducing immunogenetic techniques into the reindeer stock breeding and studying the antigenic blood properties in domesticated reindeer. The study has been performed to establish the genetic status of breeds and offspring of domesticated reindeer. The goals and objectives set have comprised the differentiation of domesticated reindeer by genealogical lines, identifying the related groups, and control over recording young animals. In the study, isoimmune sera, antisera specific to pig blood groups and revealing antigenic factors Acp, Eb, Eg, Kas, Kb, Ca, and Fa, and monoreceptor sera specific to antigenic cattle blood factors A1, B2, Z, A2, R1, V, I1, Y2, Y', C1C1, and 1245/55/26 have been used. The frequency of occurrence of the domesticated Taimyr reindeer blood factors antigenic to reagents for determining the cattle and pig blood groups varied within 0.77 to 95.7%. As a result of the research, a high frequency of occurrence of factors antigenic to antibodies of A1, Z, and V sera specific to cattle blood has been determined.

The current stage of research allowed revealing the antigenic composition of the blood of reindeer from the Potapov domesticated herd [11]. Studying the immunogenetic reindeer characteristics supposed an increase in the breeding efficiency to identify the reindeer gene pool. But further research has not been performed due to the complexity of the work.

The use of new physicochemical genetic research techniques has allowed analyzing the genetic heterogeneity of the wild and domesticated reindeer’s blood, milk, and tissue proteins. It has been established that domesticated and wild reindeer have their gene pool and evolve as relatively independent units [15]. The esterases, which could be used as gene markers in the analysis of the population’s hereditary structure dynamics in space and time, have been studied from the genetic system standpoint. When studying the genetic characteristics of the Taimyr wild reindeer population, slight differences in the esterase locus alleles were found in the western (Pyasinsky) and eastern (Khatanga) groups.

At the next stage, the genetic variability was studied using the molecular genetic technique on DNA-containing samples, which included determining the mitochondrial DNA characteristics, finding microsatellite markers (RAPD) to identify genetic changes, etc. With the introduction of new techniques, the wild Taimyr reindeer’s genealogic lines have been determined [8] and the genetic variability of individual wild reindeer groups of the Taimyr population studied [9]. The study results have shown an intensive genetic exchange between the reindeer groups from different regions.

When studying domesticated reindeer breeding, the ISSR analysis technique has been used [7]. ISSR markers are highly reproducible and informative. Such ISSR markers have been used to map genomes and mark the economic traits of plants, as well as to study interspecific and intraspecific plant polymorphism [17, 19]. When studying the Western Taimyr wild reindeer samples using ISSR markers, it has been found that the Western Taimyr reindeer migration flow includes two genotypes of animals [2].

Population-genetic studies of domesticated reindeer have revealed a high level of inbreeding in herds of less than 500 heads. A series of polymorphic blood protein systems have been discovered and their genetic determination investigated [5].

When analyzing the polymorphism of the control region of mitochondrial DNA in the wild Taimyr reindeer samples, a high level of haplotype (H) and nucleotide (R) diversity (0.987 and 0.018,
respectively) has been revealed indicating a long-term existence of this population with a fairly stable growth [14].

Genetic studies of reindeer are being performed in different regions of Russia by A.A. Yuzhakov, 2017 [16], V.R. Kharzinova, 2017 [13], and others. Genetic monitoring of animals is performed to preserve biodiversity - Yu.A. Stolpovsky [12].

Federal State Budgetary Scientific Institution Federal Scientific Center for Livestock Breeding - Ernst All-Russia Research Institute for Animal Husbandry (VIZh) performed work on Taimyr to introduce the technique for artificial insemination of reindeer into practice, develop technology for cryopreservation of reindeer semen, and create a cryobank of sperm [6].

However, the genetic monitoring of reindeer and creating their genetic database have not yet been performed on Taimyr. This work should be done to study the genetic diversity of the farm populations of domesticated reindeer and the wild reindeer population.

Similar work on the domesticated Nenets reindeer herds was performed by the staff of the Naryan-Mar Agricultural Experimental Station under experimental conditions in 2016 (4).

Creating a genetic bank of the Taimyr reindeer population will allow preserving the material, ensuring its availability, and multi-purposely using it by experts in different scientific fields.

Earlier, an opinion was expressed on the need to preserve the island population of wild reindeer inhabiting the Severnaya Zemlya archipelago [3]. The extinction of this population will significantly impoverish the species gene pool since this is the only wild reindeer population in the Eurasian Arctic adapted to live in the Arctic desert. Studying the genetic characteristics of this group of animals has yet to be performed.

This research should fill the gap in the genetic study of Taimyr reindeer.

2. Material & techniques

In research, tissue samples of 14 Nenets reindeer bred by the brigade of the Tukhard settlement of the Taimyr Dolgano-Nenets District of the Krasnoyarsk Territory have been used as biological material. These samples were compared with those of domesticated Nenets breed animals from the Nenets (NAO, n = 31) and Yamalo-Nenets (YNAO, n = 56) Autonomous Districts, the Murmansk Region (MUR, n = 43), and the Komi Republic (n = 24). DNA isolation and PCR were performed according to the conventional procedure. To process the analysis results, a genotype matrix was built in Microsoft Excel format. To characterize allelic and genetic diversity in the GenAlEx 6.5 software [23], the average (NA) and effective number (NE) of alleles per locus, observed (HO) and expected (HE) heterozygosity, and inbreeding coefficient (FIS) were defined in R ‘diveRsity’ package with subsequent visualization in ‘pophelper’ package [18]. Principal Component Analysis (PCA) was performed using R ‘adeegen’ package [21] with visualization in R ‘ggplot2’ package [24]. The degree of genetic differentiation of the breeds studied was estimated based on pairwise DJost values [22]. The matrix of pairwise values Jost’s D was used to build a phylogenetic tree using the Neighbor-Net algorithm in the SplitsTree 4.14.5 software [20].

3. Results

The main allelic and genetic diversity parameters have been calculated; the calculation results are given in the below table 1.
Table 1. Allelic and genetic diversity parameters of the Taimyr domesticated reindeer population with other regional Nenets breed populations.

| Population | Indicator | NA     | NE      | PR   | HO    | HE     | FIS (FIS 95 % CI > 0) |
|------------|-----------|--------|---------|------|-------|--------|-----------------------|
| KOM        |           | 7.11   | ± 4.624 | ± 0.333 | ± 0.56 | ± 0.751 | ± 0.256 [0.14; 0.372] |
|            | 0.564     | 0.54   | 0.167   | 0.057 | 0.036 |         |                       |
| TUCH       | 4.444     | ± 2.660 | ± 0.222 | ± 0.468 | ± 0.609 | ± 0.195 |                       |
|            | 0.503     | 0.310  | 0.147   | 0.061 | 0.034 |         |                       |
| NAO        | 7.222     | ± 4.226 | ± 0.444 | ± 0.573 | ± 0.742 | ± 0.225 [0.106; 0.344] |                       |
|            | 0.521     | 0.447  | 0.242   | 0.052 | 0.027 |         |                       |
| YNAO       | 7.667     | ± 3.578 | ± 0.444 | ± 0.522 ± 0.1 | 0.623 | ± 0.135 [-0.082; 0.352] |                       |
|            | 0.782     | 0.650  | 0.242   | 0.08  |         |         |                       |
| MUR        | 8.000     | ± 4.381 | ± 1.667 | ± 0.556 | ± 0.556 | ± 0.681± 0.088 |                       |
|            | 1.155     | 0.644  | 0.577   | 0.079 | 0.079 |         |                       |

Note: NA is the average number of alleles per locus; NE is the average number of effective alleles per locus; PR is the number of private alleles per locus; HO is the heterozygosity observed; HE is the heterozygosity expected; FIS is the inbreeding coefficient with a 95 % confidence interval.

Principal Component Analysis (PCA) was performed. The results of the PCA analysis, which allows estimating the range of variability and trace the main patterns of population-genetic differentiation of the Taimyr reindeer population individuals from the comparison groups, are given in Figure 1.

![PCA Figure](image_url)

**Figure 1.** Projection of Taimyr Domesticated Reindeer Population Individuals with Other Regional Nenets Breed Populations on a Two-Dimensional Plane According to PCA Analysis.

The visualization of this numerical matrix using the NeighborNet algorithm is shown in Figure 2.
Figure 2. Phylogenetic Dendrogram of the Genetic Relationships of the Taimyr Domesticated Reindeer Population with Other Regional Nenets Breed Populations Built Based on the Jost’s D Pairwise Genetic Distance Matrix Using the NeighborNet Algorithm.

4. Discussion

According to the tabular data, the Taimyr Dolgano-Nenets District reindeer population is characterized by a minimum level of genetic polymorphism and diversity, as testified by the minimum values of almost all population-genetic indicators. However, when analyzing the distribution of private alleles per locus, i.e. those specific to each the group studied, the Taimyr population surpasses the Murmansk Region reindeer in this indicator. Also, all reindeer groups studied are characterized by the predominance of the heterozygosity expected over that observed, which indicates the inbreeding of populations. This conclusion is justified by the positive inbreeding coefficient FIS values varying within 0.135 for NAO and 0.256 for KOM. Herewith, the 95% confidence interval (CI) of the inbreeding coefficient included zero only in two reindeer groups, including TUCH, indicating the genetic equilibrium.

The Figures show the distribution of genetic variation by geographic location and ethnicity. When studying the population, this is an important source of information on historical events and processes a particular species has faced.

The results of the phylogenetic dendrogram (Fig. 2) of the genetic relationships of the Taimyr domesticated reindeer population are consistent with the projection of the individuals studied on a two-dimensional plane based on the PCA analysis (Fig. 1): this population stands out as an independent branch in the Komi Republic and Yamalo-Nenets Autonomous District cluster of animals.

The Taimyr reindeer population is genetically closer to the Komi Republic and Yamalo-Nenets Autonomous District animals and far from the Murmansk Region reindeer. Herewith, there is a slight overlap of massifs with the Nenets Autonomous District reindeer probably due to the breed formation factors. According to the results of both the PCA analysis and the phylogenetic dendrogram of genetic relationships built based on the pairwise genetic distance matrix Jost’s D according to the NeighborNet algorithm, the nature of the genetic relationships revealed is most likely determined by the geographical localization of the Taimyr population individuals, indicating a genetic structure more similar to the Komi Republic and Yamalo-Nenets Autonomous District animals. Analysis of the main population-genetic parameters has shown the minimum level of both allelic and genetic diversity of the population studied, a further decrease in which may destroy local adaptations and coadapted gene complexes that ultimately will affect the population’s resistance to unfavorable environmental conditions.
5. Conclusion

It is recommended to use the information obtained to implement programs for the improvement of the reindeer selection and breeding industry in the Tukhard settlement. Also, it should be considered when performing genetic monitoring and building a DNA bank of the Taimyr domesticated and wild reindeer population.

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