

Monitoring of the genetic specifications of the reindeer of Chukotka

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Abstract. The aim of the work was to monitor the genetic characteristics of the Chukchi reindeer populations. The development of an effective breeding system, rational use and protection of genetic resources in the populations of the Chukchi reindeer determined the relevance of this work. During 2013-2020, 8 populations were studied - Vayegi, Chaunsky, Vozrozhdeniye, Amguema, Pioneer, Khatyrskaya, Kanchalansky, Ostrovnaya - of different pasture-geographic regions. The material for molecular genetic studies was 1002 samples of muscles and plucks of the deer auricle. Analytical work was carried out in the All-Russian Research Institute of Breeding DNA analysis laboratory. The most common fragments of medium length in the Chukchi breed are loci №. 3 (240-330 bp), 5 (350-430 bp), 6 (440-520 bp), 7 (520-570 bp) (15.38-13.17%). The indicator of the expected heterozygosity in all populations is at a high level: 0.844-0.891. For the first time, a significant amount of information has been obtained on the genetic characteristics of the populations of domestic reindeer in Chukotka - the most remote and vast peninsula of Russia, which is of current scientific and practical importance for the further improvement of selection and breeding work in reindeer breeding.

1 Introduction

Reindeer (*Rangifer tarandus* L.), being an object of breeding in Chukotka, retains economic and social importance for Russian agriculture (Fig. 1). The Chukchi reindeer breed is numerous and its distribution area covers a territory of 738 thousand km², stretching for 1400 km from west to east and 900 km from north to south.

Reindeer breeds consist of separate populations distributed in different areas of the range. Populations have not only common breed characteristics, varying in morphological features and adaptability to the conditions of their locality, but they differ from each other in genetic characteristics - the composition and frequency of alleles and genotypes [1-3]. The genetic population properties are formed under the influence of the environment, heredity, variability and selection, as a result of which its development occurs. In all populations, the process of microevolution is underway, due to feeding, maintenance, selection and natural differences. The breeding strategy choice to improve the productive properties of various deer populations is based on their genetic specificity [4-6].

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Fig. 1. Domestic reindeer (*Rangifer tarandus* L.) in Chukotka

Each reindeer population has a certain genetic structure and gene pool - a set of genes that all individuals of the population have. The genetic structure is determined by the concentration of each gene (or its alleles) in the population, the nature of the genotypes and the frequency of their distribution. In breeding practice, the identification of the genetic structure is essential. A population can change its genetic structure under the influence of external and internal factors. At the same time, it is able to maintain the structure in a number of generations, due to the adaptability of the individuals that form the population. Factors that can change the genetic structure of a population are diverse and each has a specific effect on the frequency of alleles and genotypes: natural and artificial selection, gene and chromosome mutation process, migration of individuals from and into the population, type of crossing, selectivity or free mating of individuals, environmental changes [7-11].

Currently, molecular methods of analysis are widely used to study the genetic structure of breeds, their origin, biodiversity, differentiation and identification of populations. Using DNA markers, it is possible to increase the accuracy of determining the breeding value of the young animals which replenish the herd, to increase the likelihood of early selection of genetically the best animals [12-15].

The development of an effective system of breeding, rational use and protection of genetic resources in the populations of the deer of the Chukchi breed determined the relevance of this work.

The aim of the work was to monitor the genetic characteristics of the Chukchi reindeer populations.

2 Materials and methods

During 2013-2020, 8 populations were studied - Vayegi, Chaunsky, Vozrozhdeniye, Amguema, Pioneer, Khatyrskaya, Kanchalansky, Ostrovnyaya - of different pasture-geographic regions. (Table 1)

Table 1. Time, place and conditions of research

Years of research /Populations	Total livestock	Number of samples	Pasture-geographic region
2013/ Vozrozhdeniye	10935	100	Arctic tundra southwest of Chukotka and the eastern coast of the Kresta Bay, Iultinsky district.
2014/ Amguema	11360	160	Arctic tundra in the north-west of Chukotka, Iultinsky district.
2014/ Pioneer	8376	150	Arctic tundra on the Arctic Ocean coast, adjacent to the Chukchi Sea, Iultinsky district.
2016/ Vayegi	3331	89	Forest-tundra pastures southwest of Chukotka, Anadyrsky region.
2016/ Chaunsky	9089	143	Arctic tundra of the East Siberian Sea coast, adjacent to the Chaunskaya Bay, Aion Island. Chaunsky district.
2020 / Khatyrskaya	5017	60	Tundra pastures of the southwestern part of Chukotka on the Bering Sea coast, Anadyr region.
2020/ Kanchalansky	14969	150	Arctic tundra adjacent to the Gulf of Anadyr and the western coast of the Kresta Bay, Anadyr region.
2020/ Ostrovnaya	5314	150	Arctic tundra in the northwest of Chukotka, adjacent to the East Siberian Sea.
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The material for molecular genetic studies was 1002 samples of tissue samples (muscles, ear plucks) of deer. Analytical work was carried out in the DNA analysis laboratory of the All-Russian Research Institute of Breeding. The studies were carried out in accordance with the Guidelines for the use of the polymerase chain reaction method in animal husbandry. We studied the genetic characteristics of deer populations using DNA analysis, which was carried out by ISSR fingerprinting with primer (AG)_nC on a «Tertsik» amplifier, «DNA Technology» (Russia) with a set of dry reagents (Isogen, Moscow) and standard computer programs " Genepop.

3 Results and discussion

In order to monitor the genetic structure of the Chukotka breed reindeer populations, the research covered 38.8% of the number of adult reindeer grazing in the territory of Chukotka. The result of the research in 2013 showed that in the deer genotype of the Vozrozhdeniye population, seven out of 10 loci (70%) are informative with a frequency of occurrence above 5%. The most common genotype, having in its composition loci №. 1, №. 3, №. 5, №. 6, №. 7, №. 8 (occurrence 30%) (Table 2). The frequency of the genotype 1/3/4/5/6/7/8 is 25% of the studied sample. About 6% of deer have unique genotypes. In 2014, the populations of Amguema and Pioneer were studied. In the Amguema population, 9 marker DNA fragments were found. The most common are 6 fragments: 1, 2, 3, 5, 6, and 7, the frequency of each of them is from 0.113 to 0.150 (Table 2). 99% of deer have a 240-330 bp long fragment. (locus №. 3). Loci №. 6 and №. 7 were found in 93% of individuals, locus №. 5 - in 95%. As a result of the analysis of the variability of DNA fragments, it was found that an individual has from 1 to 9 DNA fragments. The average number of fragments per animal was 6.61. The 8 (88.9%) out of 9 loci with a frequency of

occurrence exceeding 5% are informative. The most common are genotypes that include loci №. 1, №. 2, №. 3, №. 5, №. 6, №. 7 (19% of individuals). The genotypes are evenly distributed.

In the Pioneer population, 11 marker DNA fragments were identified. More often than others, 5 fragments are found: 3, 5, 6, 7 and 9, which are typical for reindeer. In 96% of the studied sample of deer, there is an intermicrosatellite DNA fragment 240-330 bp long. (locus №. 3). Loci №. 6 and №. 7 were found in 100% of animals, locus №. 5 - in 96% of the studied deer (Table 2). The analysis of the variability of DNA fragments showed that each individual has from 3 to 11 DNA fragments, and the average number of fragments in one animal is 7.33. The 9(81.8%) loci out of 11 are informative for this herd with a frequency of 5% or more. The most common in the Pioneer population are the genotypes which include loci №. 3, №. 5, №. 6, №. 7, №. 9 (7%). The genotypes are evenly distributed.

Table 2. Frequency of ISSR markers in populations of reindeer of the Chukchi breed

№	Frag ment lent h (base pairs)	Population							
		Vozrozh deniye	Amgue ma	Pioneer	Vayegi	Chauns ky	Khatyr skaya	Kanchal ansky	Ostrov naya
1	180- 210	0.147 ±0.025	0.118± 0.018	0.008± 0.005	0.033± 0.013	0.140± 0.021	0.052± 0.018	0.041±0 .011	0.095 ±0.017
2	220- 230	0.024 ±0.011	0.113± 0.018	0.083± 0.016	0.065± 0.018	0.033± 0.011	0.062± 0.020	0.101±0 .017	0.039 ±0.011
3	240- 330	0.142 ±0.025	0.150± 0.020	0.131± 0.019	0.150± 0.027	0.213± 0.024	0.150± 0.029	0.142±0 .020	0.183 ±0.022
4	330- 350	0.075 ±0.019	0.046± 0.012	0.055± 0.013	0.043± 0.015	0.125± 0.020	0.046± 0.017	0.031±0 .010	0.067 ±0.014
5	350- 430	0.150 ±0.025	0.144± 0.020	0.131± 0.019	0.129± 0.025	0.203± 0.024	0.150± 0.029	0.142±0 .020	0.183 ±0.111
6	440- 520	0.148 ±0.025	0.141± 0.019	0.136± 0.020	0.151± 0.027	0.148± 0.021	0.150± 0.029	0.142±0 .020	0.183 ±0.022
7	520- 570	0.141 ±0.025	0.141± 0.019	0.136± 0.020	0.121± 0.024	0.103± 0.018	0.142± 0.029	0.142±0 .020	0.175 ±0.022
8	650- 690	0.136 ±0.024	0.061± 0.013	0.079± 0.016	0.062± 0.018	0.024± 0.009	0.092± 0.024	0.058±0 .013	0.059 ±0.014
9	700- 770	0.036 ±0.013	0.085± 0.016	0.131± 0.019	0.097± 0.022	0.000± 0.000	0.054± 0.019	0.141±0 .019	0.011 ±0.006
10	850- 980	0.001 ±0.002	0.000± 0.000	0.088± 0.016	0.101± 0.023	0.007± 0.005	0.017± 0.011	0.062±0 .013	0.004 ±0.004
11	1100- 1300	0.000 ±0.000	0.000± 0.000	0.020± 0.008	0.052± 0.017	0.004± 0.004	0.085± 0.023	0.000±0 .00	0.001 ±0.002

In 2016, two populations were studied: Vayegi and Chaunsky. It has been established that in the Vayegi population, each individual has from 1 to 9 DNA fragments, the average number per animal is 6.02. In this sample, 11 marker DNA fragments were found and five fragments are more common: 3, 5, 6, 7, and 10 (Table 2). All identified fragments are polymorphic, presented with different frequencies, less than 1. Intermicrosatellite DNA segments of medium length are most common. In 90% of the studied animals, a fragment of 240-330 bp is present. (locus №. 3). Locus 6 was found in 91% of individuals, locus №5 in 77%. Out of 11 loci, 9 (81.8%) are informative. The most common in the Vayegi population are genotypes that include loci №. 3, 5, 6, 7, 9, 10. The genotypes are evenly distributed, the same genotypes are found in no more than 3-4 individuals. About 50% of animals have unique genotypes.

The analysis of the Chaunsky population showed that each individual has from 1 to 8 DNA fragments, and the average number in one animal is 4.69. In this sample, all detected DNA loci are polymorphic, presented with different frequencies, less than 1. Intermicrosatellite DNA sections of medium length are most common. In this population, 6 DNA fragments are more common than others - №. 1, 3, 4, 5, 6, 7 (Table 2). 100% of the studied animals have a DNA segment 240-330 bp long. (locus №. 3). Locus №. 5 was found in 95%, locus №. 6 in 69% of individuals. Out of the 11 loci, 6 (54.5%) are informative with a frequency exceeding 5%. About 10% of the animals in this sample are unique genotypes.

In 2020, 3 deer populations of Chukotka were studied: Khatyrskaya, Kanchalanskaya, Ostrovnaya. In the Khatyrskaya population, out of 11 marker DNA fragments 4 fragments are most common: 3, 5, 6, 7 with a frequency exceeding 0.1. In 97% of individuals, loci №. 3, 5, 6 are present, and in 92% - locus №. 7. For this population, 9 loci out of 11 (81.8%) are informative, as the frequency of occurrence of each locus exceeds 5%. The most common genotypes in the Khatyrskaya population include loci №№. 3, 5, 6, 7, 8; the genotypes are evenly distributed. About 50% of the deer in this sample have unique genotypes.

In the Kanchalanskaya population, each individual has from 1 to 10 fragments of intermicrosatellite DNA, and the average number per individual is 7.06. 8 (80%) out of the 10 loci are informative with a frequency of occurrence of 5% or more. The most common genotypes in the Kanchalanskaya population are those, which contain loci №. 2, 3, 5, 6, 7, 9 (14% of individuals). The genotypes are evenly distributed.

In the Ostrovnaya population 4 DNA fragments are more common than others: 3, 5, 6 and 7, the frequency of each exceeds 0.1 (Pic. 2). In general, the distribution of fragments is similar to that of the Chukchi breed deer. In 100% of the studied animals, the intermicrosatellite DNA segment 240-330 bp long was found. (locus №. 3). Loci №. 5 and №. 6 were found in 100% of the animals, locus №. 7 - in 95% of the studied individuals.

In general, for the Chukchi breed, long fragments are less common than others - loci №. 10 and №. 11 (2.3-3.94%). The frequency of fragments №. 1, №. 2, №. 4, as well as №. 8 and №. 9 is in the range of 6.01-7.77%. The most common fragments of medium length in the Chukchi breed are loci №. 3, 5, 6, 7 (15.38-13.17%).

Indicators of the genetic diversity of populations are presented in Table №. 3. The average number of alleles per microsatellite locus (μ_{cp}), reflecting intrapopulation diversity, was 9.31 for the Chukchi breed. The highest values of the indicator were found in deer populations: Vazhsкая (10.4±0.26) and Khatyrskaya (10.16±0.339), as well as in individuals of Pioneer (9.95±0.263) and Kanchalanskaya (9.41±0.186) ones, exceeding the populations of Chaunskaya (8.0±0.41) , Vozrozhdenie (8.56±0.351), Amguema (8.71±0.125) and Ostrovnaya (8.47±0.378) (Table 3).

Table 3. Indicators of the genetic diversity of the Chukchi breed deer populations

№	Index	Population							
		Vozrozh deniye	Amgue ma	Pionee r	Vayegi	Chaun sky	Khatyr skaya	Kancha lansky	Ostrov naya
1	Average number of alleles per locus, μ	8.56±0.3 51	8.71±0 .125	9.95±0 .263	10.4±0 .26	8.0±0. 41	10.16± 0.339	9.41±0. 186	8.47±0 .378
2	Number of effective alleles, N_e	7.57±0.4 28	8.13±0 .210	8.85±0 .356	9.25±0 .426	6.41±0 .453	8.68±0 .52	8.33±0. 294	6.68±0 .439
3	Proporti on of	0.143±0. 024	0.033± 0.009	0.095± 0.016	0.052± 0.016	0.199± 0.023	0.076± 0.021	0.058±0 .013	0.230± 0.024

	rare alleles, h_{μ}								
4	Homozygosity coefficient, Ca	0.132±0.033	0.123±0.026	0.113±0.025	0.108±0.033	0.156±0.030	0.115±0.037	0.120±0.025	0.150±0.021
5	Expected heterozygosity, H_0	0.868±0.033	0.877±0.026	0.887±0.025	0.891±0.033	0.844±0.030	0.885±0.037	0.880±0.025	0.850±0.021

A similar pattern was observed for the number of active effective alleles (N_e). This indicator gives a certain characteristic of the structure of the allelic diversity of the population in terms of the ratio of the frequencies of the rarest and most frequent alleles in the sample. With a uniform distribution of allele frequencies, $h_{\mu}=0$, that is, there are no rare alleles, with an uneven distribution, always $h_{\mu}>0$. In the populations of the Chukchi breed, a moderate diversity of alleles in the samples was noted for this indicator (Table 3).

Homozygosity coefficient (Ca) characterizes the degree of genetic uniformity (homogeneity) of the animal population. The reciprocal of the homozygosity degree is the number of active effective alleles in the population. An increase in the homozygosity degree is accompanied by a decrease in the number of effective alleles, a decrease in genetic and phenotypic diversity, and leads to an increase in the homogeneity of the population. In the Chaunskaya and Ostrovnyaya populations, these indicators $Ca = 0.156\pm0.030$ and $Ca = 0.150\pm0.021$ - turned out to be significantly higher in comparison with the other populations. This fact is obviously associated with the insular localization of the Chaunskaya population (Ayon Island) and the remote Ostrovnyaya population, a smaller number of migrants, and the introduction of new genes.

Homozygosity parameters in the Vazhskaya, Pioneer, Khatyrskaya populations are significantly lower – 0.108 ± 0.033 ; 0.113 ± 0.025 ; 0.115 ± 0.037 , respectively. Unlike the population of Ayon Island, the pastures of these farms are located in the mainland of Chukotka, and they exchange breeding material with other farms. The middle position is occupied by the Kanchalanskaya, Amguema, and Vozrozhdenie populations, whose homozygosity is 0.120 ± 0.025 ; 0.123 ± 0.026 and 0.132 ± 0.033 , respectively, who take part in programs of inter-farm purchase and sale of breeding animals.

The level of the theoretical or expected heterozygosity serves as an indicator of the allelic diversity of populations. From 2013 to 2020, in all deer populations of Chukotka, the indicator of expected heterozygosity was at a high level: $0.844-0.891$.

In the surveyed populations of Chukotka, this genetic parameter of intrapopulation diversity is quite high, which is a consequence of the exchange of breeding material between herds and farms. In 2002, in the Kamchatka Territory and Yakutia, 1325 heads of unrelated groups of the Chukchi breed were purchased and poured into the reindeer herds of Chukotka. A significant level of heterozygosity gives animals an advantage in adaptive traits and ensures population stability.

4 Conclusions

As a result of the genetic monitoring carried out, information on the genetic characteristics of various populations of the Chukchi breed and in different time periods was obtained. The frequency of ISSR markers made it possible to determine the parameters of the general population for the Chukchi breed, which is characterized by polymorphism of all detected

loci. The frequencies of occurrence of ISSR markers vary significantly from population to population and from marker to marker. As individual DNA fragments were presented in deer of all populations, it can be assumed that for the Chukchi breed the spectrum of 4 amplicons: №. 3, №. 5, №. 6, №. 7 is typical. More often than others, there are genotypes that have in their composition microsatellites 240-330 bp, 350-430, 440-520 and 520-570 bp long. From 6 to 9 loci (54.5-88.9%) are the most informative in populations with the frequency of 5% or more.

The genetic variability of ISSR markers in populations indicates a significant similarity between them in most allelic frequencies, which confirms the common origin, economic and breeding use of the Chukchi deer. The average number of alleles per locus fluctuates in populations from 8.0 to 10.4, with an average of 9.31. Theoretical (expected) heterozygosity varies from 0.844 to 0.891, with an average of 0.876. A high level of heterozygosity gives animals an advantage in adaptive traits and ensures the stability of populations.

For the first time, a significant amount of information has been obtained on the genetic characteristics of the populations of domestic reindeer in Chukotka, which the most remote and vast peninsula of Russia, which is of current scientific and practical importance for the further improvement of selection and breeding work in reindeer breeding.

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