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GENETIC CHARACTERISTICS OF AGRICULTURAL POPULATIONS OF DOMESTIC REINDEER OF THE CHUKCHI BREED OF THE CHUKCHI AUTONOMOUS OKRUG

Research article

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Abstract

The work was carried out in order to study the genetic structure of the populations of domestic reindeer of the Chukchi breed, occupying the distribution area in three districts of Chukotka. Using the ISSR method, eleven amplicons with a length of 180 to 1300 bp were identified. In the examined herds, fragments of medium length – 240-570 bp are most common. Genotypes with DNA fragments of length No. 3 (240-330 bp), No. 5 (350-430 bp), No. 6 (440-520 bp), No. 7 (520-570 bp) are more common than others. For the Chukchi breed, the spectrum of four fragments is typical. In the studied samples, all identified DNA fragments are polymorphic, presented with a different frequency of less than 1. Out of the 11 loci, 6-7 (54.5-66.7%) are informative with a frequency of more than 5%. The average number of alleles per locus is 8.4. The expected heterozygosity is from 0.847 to 0.858. The value of the genetic similarity index (0.964-0.994) between populations confirms the commonality of their origin. The genetic distance between all populations is insignificant ($D=0.006-0.036$). Allelofond exchange has had a significant impact on the genetic characteristics of agricultural deer populations. The differences in genetic indicators are probably related to the ecological and geographical features of the areas of the studied populations, which affect their genetic structure, thereby being the main factor of intraspecific differentiation. The practical significance of the data obtained is in their use in the formation of a genetic DNA bank for the control and management of genetic resources of Chukchi deer, as well as for the multipurpose use of information on genetic diversity, which allows to reveal the genetic potential of agricultural populations of reindeer.

Keywords: reindeer husbandry, Chukotka Autonomous Okrug, breeding work, genetic structure, ISSR method.

ГЕНЕТИЧЕСКАЯ ХАРАКТЕРИСТИКА СЕЛЬСКОХОЗЯЙСТВЕННЫХ ПОПУЛЯЦИЙ ДОМАШНИХ СЕВЕРНЫХ ОЛЕНЕЙ ЧУКОТСКОЙ ПОРОДЫ ЧУКОТСКОГО АВТОНОМНОГО ОКРУГА

Научная статья

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Аннотация

Работа выполнена с целью изучения генетической структуры популяций северных оленей чукотской породы в трёх различных пастбищно-географических районах Чукотского автономного округа. С использованием ISSR-метода получено 11 амплифицированных фрагментов ДНК длиной от 180 до 1300 п.н. В обследованных стадах наиболее встречаемы фрагменты средней длины – 240–570 п. н. Чаще других встречаются генотипы, имеющие в своем составе фрагменты ДНК длиной №3 (240-330 п.н.), №5 (350-430 п.н.), №6 (440-520 п.н.), №7 (520-570 п.н.). Можно предположить, что для чукотской породы спектр из четырёх фрагментов является типичным. В исследованных выборках все выявленные фрагменты ДНК полиморфные, представлены с разной частотой меньше 1. Из 11 локусов 6-7 (54.5-66.7%) являются информативными с частотой встречаемости более 5%. Среднее число аллелей на локус оказалось равным 8.4 с колебаниями от 7.7 до 8.5. Уровень ожидаемой гетерозиготности во всех исследованных группах оленей составил 0.847–0.858, что свидетельствует о генетическом разнообразии соответствующих локусов генома, обеспечивающих устойчивость популяций северных оленей. Значение индекса генетического сходства (0.964-0.994) между популяциями подтверждает общность их происхождения. Генетическое расстояние между всеми популяциями незначительно ($D=0.006-0.036$). Обмен аллелофондом оказал существенное влияние на генетические характеристики сельскохозяйственных популяций оленей. Различия по генетическим показателям, вероятно, связаны с эколого-географическими особенностями ареалов изученных популяций, которые влияют на их генетическую структуру, тем самым являясь основным фактором внутривидовой дифференциации. Практическое значение полученных данных состоит в использовании их при формировании генетического банка ДНК для контроля и управления генетическими ресурсами оленей чукотской породы, а также для многоцелевого использования информации о генетическом разнообразии, позволяющей раскрыть генетический потенциал сельскохозяйственных популяций северного оленя.

Ключевые слова: северное оленеводство, Чукотский автономный округ, селекционно-племенная работа, генетическая структура, ISSR-метод.

Introduction

In the Chukotka Autonomous Okrug (ChAO), reindeer husbandry is the primary sector of the agricultural sector of the economy and the main area of employment for indigenous peoples. The territory of the Chukotka Autonomous Okrug occupies a significant territory and agricultural enterprises engaged in reindeer breeding are located in different geographical, landscape and climatic conditions.

Reindeer (*Rangifer tarandus* L.) – as a unique species of farm animals, occupies a distribution area represented by the Arctic and subarctic tundras, unsuitable for grazing other domestic animals. The realization of the genetic potential and productivity of animals is directly dependent on the natural factors of their habitats [1], [2]. Selection and breeding work in reindeer husbandry is still based on mass selection based on phenotype, and the bulk of the activities are carried out using traditional techniques [3], [4]. The ineffectiveness of the methods used for a long time determined the relevance of the tasks of selection and breeding work with reindeer.

In modern conditions, molecular diagnostics is used in the selection of farm animals [5], [6], [7], [8], [9]. In this regard, there is a demand in reindeer husbandry for research aimed at developing more effective methods used in animal husbandry and based on the achievements of modern genetics [10]. DNA polymorphism makes it possible to study the genetic structure and differentiate breeds in reindeer herding. A special place, due to its high information content, speed of execution and low cost, is occupied by molecular multilocus analysis, or ISSR fingerprinting, which allows to use any tissues and organs, regardless of the stage of animal ontogenesis [11].

A significant genetic distance has been established between populations that are geographically more distant, between which there has been no exchange of allele pools. The identified differences in genetic indicators are probably associated with the environmental features of the reindeer grazing areas, which affect the genetic structure, thereby being a fundamental factor in intraspecific differences.

The purpose of this work is to study the genetic structure of populations of domestic reindeer of the Chukotka breed, occupying a distribution area in three regions of the Chukotka Autonomous Okrug (ChAO).

For the first time, an array of data has been obtained on the genetic characteristics of the populations of breeding enterprises of the Chukotka Autonomous Okrug, which has a certain scientific and practical significance for further improving the selection of the Chukotka breed.

Research methods and principles

The research was carried out in the herds of pedigree reindeer herding enterprises of the Chukotka Autonomous Okrug – municipal unitary enterprise "Ostrovnoye", "Khatyrsky" and "Kanchalansky", located in various pasture-geographical regions of the Chukotka Autonomous Okrug.

The pastures of the Anadyr region, located from the Chukotka Range to the Cross Bay in the north and to Cape Olyutorsky and the Koryak Range in the south, extend along the coast of the Anadyr Bay and the Bering Sea. The climate is subarctic, from temperate continental to maritime. The average annual temperature is $-7.7...-4.9$ °C. Pastures are represented mainly by sedge-cotton grass hummocky, hummocky-sedge-cotton grass lichen and hummock-furrow tundra. In winter, deer graze in mountainous areas due to the unavailability of food on the plains, and in summer – in coastal areas. The reindeer herding farms "Kanchalansky" and "Khatyrskoye" are located here.

The pastures of the North Anyui region are located in the north-west of the Chukotka Autonomous Okrug (Bilibinsky district) north of the Anyui Range. It is limited to the north by the East Siberian Sea. The climate zone is Arctic continental. The average temperature for the year is -12 °C. The coastal strip is used for summer grazing. In winter, the pastures are represented by larch forest. Pastures in mountainous areas are located on the slopes of the Anyui Range. Arctic hummocky tundras are suitable for transitional seasons: willow-sedge-cotton grass and sedge-cotton grass-moss. In this zone there are pastures of the Ostrovnoye farm.

The number of Chukchi deer (Pic. 1) in the farms under study at the beginning of 2020 was 25,300 individuals. The research used 374 deer tissue samples (ear plucks). Samples were taken randomly from clinically healthy animals of different sex and age groups: she-deer (uteruses over 2 years old), he-deer (stud bulls), young animals up to 1 year old. The samples were preserved by cold and ethyl alcohol.



Figure 1 - Chukotka breed of deer on the territory of pastures of the Chukotka Autonomous Okrug
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Analytical work was carried out in the DNA technology laboratory of the All-Russian Research Institute of Breeding in accordance with methodological recommendations for the use of the polymerase chain reaction method in animal husbandry [12], [13]. An analysis of statistically processed data was carried out using standard computer programs “Genepop” [14].

Main results

The research work was carried out in accordance with the topic: “Study of genotypic and economically significant traits of reindeer populations in order to create a database, rational conservation and effective use of the gene pool of the Chukotka breed in the breeding process”.

In the population of the Khatyrsky agricultural enterprise, 60 heads of deer were studied, according to 9 identified microsatellite loci, the frequency indicators of ISSR markers are statistically significant, all loci are polymorphic, DNA fragments of medium length are the most common (Pic. 1). In the studied animals, 362 amplicons were identified with a frequency distribution indicating their typicality for the Chukchi breed of deer. The most common six fragments are: 1, 3, 5, 6, 7 and 8, the occurrence of each of which exceeds 0.1. 100% of the animals studied had a DNA fragment 240-330 bp long. (locus №. 3); Locus №. 6 was detected in 98% of animals, locus №. 1 – in 85%, locus №. 5 – in 100% of the animals studied. Each individual has from one to nine DNA fragments (6.03 on average), which is fully confirmed by the analysis of their variability. For this population, 6 of 9 loci (66.7%) are informative, with a frequency of occurrence $\geq 5\%$. The most common genotype is 1/3/5/6/7/8. For all studied loci, the level of heterozygosity was 0.858 (Table 1).

In the population of the agricultural enterprise “Kanchalansky”, 150 heads of deer of various sex and age groups were studied. A total of 854 DNA fragments were found in all individuals; the frequency distribution is typical for reindeer. In adult animals, 8 marker DNA fragments were identified. In this population, 6 DNA fragments are most common: 1, 3, 5, 6, 7 and 8, the frequency of each of which exceeds 0.1 (Pic. 1). All studied individuals (100%) have a DNA fragment 240-330 bp long. (locus №. 3). Fragment №. 6 was detected in 91% of animals, locus №. 1 – in 95%, locus №. 5 – in 99% of the studied individuals. The analysis of the variability of DNA fragments showed that each individual has from 1 to 10 fragments, and their average number per animal is 5.69. Out of the 9 loci, 6 (66.7%) are informative, the occurrence of each of which is 5% or more. The most common genotypes are 1/3/5/6/7/8 (occurrence 37%) and 1/3/4/5/6/7 (23%). The level of expected heterozygosity in the population of the Kanchalansky agricultural enterprise was 0.847 (Table 1).

In the population of the Ostrovnoye reindeer herding farm, 150 heads of deer were studied. All loci in this sample are polymorphic, but fragments of medium length are most common. A total of 819 DNA fragments were identified in all deer. Eleven marker DNA fragments were identified in this population. Four DNA fragments are more common than others: 3, 5, 6 and 7, the frequency of each exceeds 0.1 (Pic. 1). In general, the distribution of fragments is similar to that of Chukchi deer. An intermicrosatellite DNA region of 240-330 bp in length was found in 100% of the animals studied. (locus №. 3). Loci №. 5 and №. 6 were identified in 100% of animals, locus №. 7 – in 95% of the studied individuals.

The analysis of the variability of DNA fragments showed that each individual has from 4 to 8 intermicrosatellite DNA fragments, the average number of fragments per animal is 5.46. Out of the 11 loci, 7 (63.6%) are informative for this herd, the frequency of occurrence of each is $\geq 5\%$. The most common genotype in the Ostrovnnoye farm herds is genotype 1/3/5/6/7 with a frequency of occurrence of 18%; the frequency of genotype 3/5/6/7 is 14%, genotype 1/3/5/6/7/8 occurs with a frequency of 12%. For all studied loci, the level of heterozygosity is 0.850 (Table 1).

The polymorphism of the discovered loci, presented with different frequencies less than 1, is the characteristic of the studied deer populations of different pasture-geographical regions.

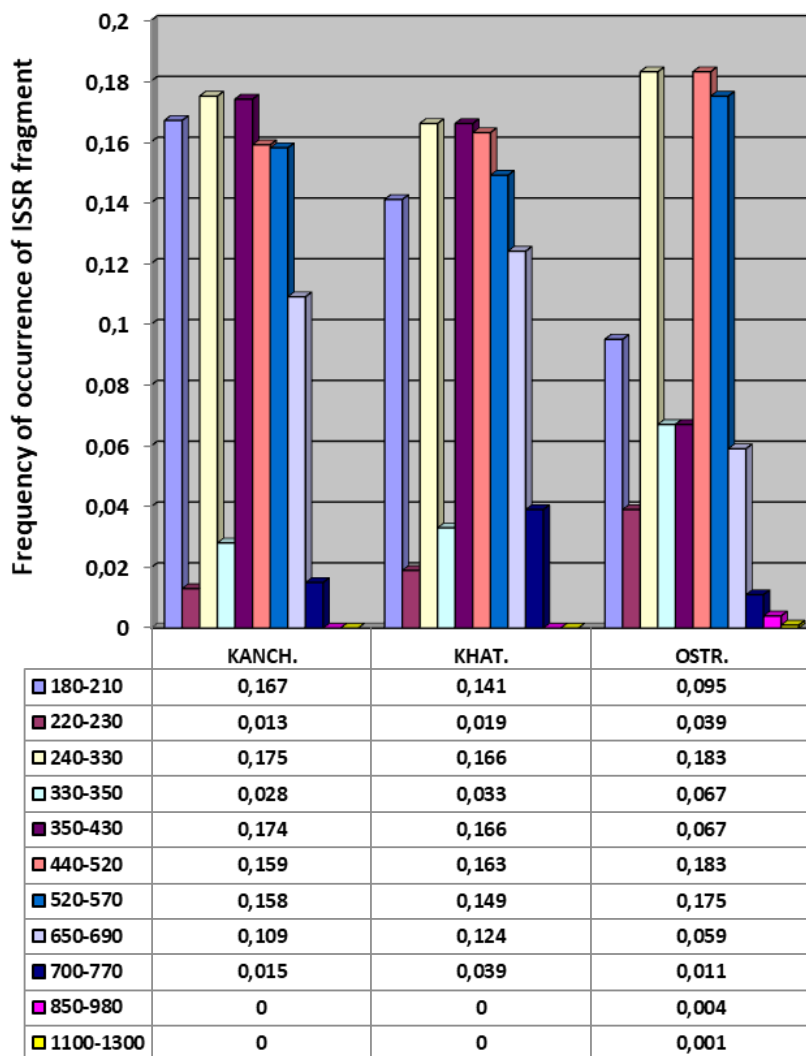


Figure 2 - Graphic representation of the frequency of ISSR markers in populations of the Chukchi breed
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In these samples, genotypes containing DNA fragments with a length of 240-330 bp, 350-430 bp, and 440-520 bp and 520-570 bp are more common than others. The number of effective alleles per locus is from 6.5 to 7.0 (54.5-66.7%).

The genetic variability of ISSR markers in the studied populations indicates a significant similarity between them in most allelic frequencies, which confirms the common origin, economic and breeding use of the Chukchi breed of deer.

One of the indicators reflecting intrapopulation diversity is the average number of alleles per microsatellite locus (μ), which in general for the studied populations of Chukchi deer is 8.4.

High values of this indicator were found in samples of the Ostrovnaya population: $\mu = 8.5$, the indicator of the Khatyrskaya population was equal to 8.1, and in the herds of the Kanchalanskaya population the average number of alleles per locus was 7.7 (Table 1).

Table 1 - Indicators of the genetic structure of Chukchi breed deer

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Index	Population			In the breed	
	Ostrovnaya	Kanchalanskaya	Khatyrskaya	Lim	Average
Average	8,5	7,7	8,1	7,3–10,4	8,4

number of alleles per locus (μ)					
Number of effective alleles per locus (N_e)	6,7	6,5	7,0	6,4–9,2	7,44
Homozygosity coefficient (C_a)	0,150	0,153	0,142	0,108–0,156	0,136
Heterozygosity expected (H_e)	0,850	0,847	0,858	0,844–0,891	0,863

The largest number of effective alleles (N_e) was found in the Khatyrskaya population – 7.0. In the Ostrovnoye agricultural enterprise $N_e = 6.7$. In the Kanchalanskaya population, the number of active effective alleles is 6.5. The homozygosity coefficient (C_a) characterizes the degree of genetic uniformity (homogeneity) of the animal population. An increase in the degree of homozygosity is accompanied by a decrease in the number of effective alleles and a decrease in genetic and phenotypic diversity, and leads to an increase in population homogeneity. In the reindeer herds of the Kanchalansky agricultural enterprise, this indicator is higher than in other farms – 0.153. In the Ostrovnoye population, the homozygosity coefficient is 0.150, which is lower than in the Kanchalansky agricultural enterprise. The Khatyrskaya population has the lowest homozygosity coefficient – 0.142.

Heterozygosity of intermicrosatellite DNA in the studied samples indicates the genetic diversity of the corresponding loci of the animal genome, ensuring the stability of populations of the Chukchi breed. The level of expected heterozygosity (H_e) serves as an indicator of the allelic diversity of populations. In the studied populations, this genetic parameter is quite high – 0.847–0.858, which is a consequence of the exchange of breeding material between herds and farms (Table 1).

To express the degree of genetic differences between populations numerically, an indicator of genetic similarity is used, the values of which vary from 1 (genetic identity of populations) to 0 (populations are monomorphic for different alleles).

The value of the genetic similarity index arranged the populations of breeding enterprises as follows: “Khatyrskoye” – “Kanchalansky”, “Ostrovnoye” – “Khatyrskoye”, “Ostrovnoye” – “Kanchalansky” (Table 2). The observed genetic similarity of populations is associated with interfarm exchange of the allele pool and the geographical location of reindeer herding farms.

Table 2 - Genetic similarity (I) and genetic distance (D) between Chukchi reindeer populations

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Population	Kanchalansky	Khatyrskoye	Ostrovnoye
Kanchalansky	0	0,006**	0,036
Khatyrskoye	0,994*	0	0,035
Ostrovnoye	0,964	0,965	0

Note: *Genetic similarity index (bottom left)

** Genetic distance (top right)

The genetic distance between all populations is insignificant: Ostrovnoye and Kanchalansky (0.036), Ostrovnoye and Khatyrskoye (0.035), Khatyrskoye and Kanchalansky (0.006) (Table 2).

During 2002–2018 the interfarm exchange of breeding animals according to the plan of selection and breeding work with the Chukchi breed exceeded 35,000 heads, that is, more than 2 thousand heads per year. This has had a significant impact on the genetic characteristics of agricultural deer populations.

ISSR-intermicrosatellite DNA identified during scientific research can be considered as promising markers for studying intra-breed genetic variability, identifying local populations in the Chukchi deer breed that are of interest for economically useful traits, and further use in selection and breeding work. Each deer population contains a unique set of genes, the product of mutation and genetic drift, adaptation with varying selection pressures combined with climate and other factors [15].

Conclusion

A difference was established between the Kanchalansky, Khatyrskaya and Ostrovnoye deer populations in the process of studying DNA fragments and their frequencies that are most subject to selection pressure from environmental factors and in the process of breeding work to improve them. Since individual DNA fragments were found in deer of all studied populations, it can be assumed that for the Chukchi breed a spectrum of 4 amplicons: 3, 5, 6 and 7 is typical. The frequency of occurrence of fragments varied significantly. Populations differed both in the number of polymorphic loci and in the level of polymorphism of amplified DNA fragments. The largest absolute number of alleles per locus was observed in the Khatyrskaya (7.0) and Ostrovnoye (6.7) deer populations. Based on this parameter of gene diversity, we can conclude that all studied populations have both intra- and inter-population diversity.

Differences in genetic indicators of the agricultural populations of Ostrovnoye, Khatyrskaya and Kanchalansky are probably associated with the ecological and geographical features of their distribution areas, which affect their genetic structure, thereby being the main factor of intraspecific differentiation.

Fundamental knowledge of the genetic specificity of the population is necessary to select a breeding strategy to improve the productive qualities of the Chukotka deer breed in the Chukotka Autonomous Okrug. The information obtained confirms the relevance of genetic monitoring.

Конфликт интересов

Не указан.

Рецензия

Все статьи проходят рецензирование. Но рецензент или автор статьи предпочли не публиковать рецензию к этой статье в открытом доступе. Рецензия может быть предоставлена компетентным органам по запросу.

Conflict of Interest

None declared.

Review

All articles are peer-reviewed. But the reviewer or the author of the article chose not to publish a review of this article in the public domain. The review can be provided to the competent authorities upon request.

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