

MITOCHONDRIAL DNA DIVERSITY WITHIN DOMESTIC REINDEER IN RUSSIA

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Introduction. The domestic reindeer in Russia constitute a value resource of vital importance to the physical and cultural survival of Northern indigenous minority.

Domestic reindeer in those regions are presented by Nenets, Evenk, Even, Chukotka breeds and Tuva subbreed



Aim. The assessing the mtDNA diversity of the domestic reindeer inhabiting the area from the Kola Peninsula in the west to the Chukotka region in the east.

Table 1. Genetic diversity indices of reindeer populations calculated from nucleotide sequence of mitochondrial cytb gene

Group	n	H	S	K	Hd (±SD)	π (±SD)
CHU	6	5	39	14.600	0.933±0.122	0.01281± 0.00464
CHUKH	6	4	56	28.333	0.800± 0.172	0.02485± 0.00744
EVK	6	5	13	5.400	0.933 ± 0.122	0.00474± 0.00091
EVN	12	10	62	27.409	0.955±0.057	0.02404±0.00453
NEN	16	5	60	14.108	0.600±0.127	0.01238±0.00559
TUVA	6	5	10	4.533	0.933±0.122	0.00398±0.00110

Materials and Methods. A complete cytochrome b (cytb) sequences (1,140 bp) from representatives of six populations, including Nenets (NEN, n=16), Evenk (EVK, n=12), Even (EVN, n=6), Chukotka (CHU, n=6), Chukotka-Khargin (CHUKH, n=6) and Tuva (TUVA, n=6) were obtained. Sequences' alignment was conducted using MUSCLE algorithm in R package msa. Median-joining network was constructed in PopART 1.7. AMOVA was calculated in Arlequin 3.5.2.2. Genetic diversity parameters was calculated in DnaSP 6.12.03.

Results. Genetic diversity indices of reindeer populations calculated from nucleotide sequence of mitochondrial cytb gene are presented in **Table 1**. In total, 34 haplotypes were identified. The average number of nucleotide differences was highest in CHUKH (28.333) and EVN (27.409) and lowest in TUVA (4.533) and EVK (5.400). Nucleotide diversity followed the same pattern. The median-joining network (**Fig.1.**) revealed that the identified haplotypes formed three major groups. The first group included samples from all the populations, the second one was represented by NEN, EVN and CHUKH, and the third group consisted of a single sample – CHU. No specific genetic structure was observed between the studied groups. These results were confirmed by AMOVA (**Table 2**). It was shown that 90.42% of variation was attributed to differentiation within populations and only remaining 9.58% corresponded to differences between populations.

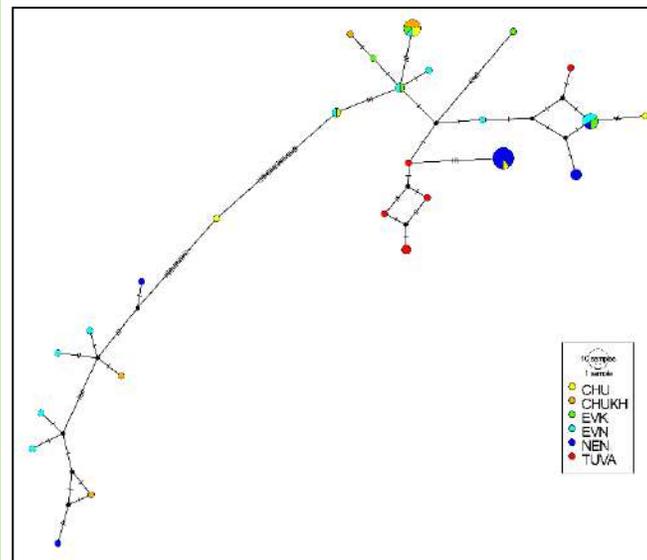


Fig. 1. Median joining network of reindeer populations

Table 2. The results of AMOVA for the studied reindeer.

Source of variation	d.f	Sum of squares	Variance components	Percentage of variation
Among populations	5	79.444	0.89533	9.58
Within populations	46	388.729	8.45063	90.42
Total	51	468.173	9.34597	

Conclusions. Our study demonstrated the lack of clear genetic structure of the studied reindeer populations in relation to cytb sequence. The level of genetic diversity was associated with census size and was lowest in the smallest Tuva population

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