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Insights into the nuclear and mitochondrial genetic diversity of local Tuva population of domestic reindeer

Kharzinova V.R^{1*}, Dotsev A.V¹, Upadhyay M.², Kunz E.², Solovieva A.D¹, Krebs S.², Bardukov N.V¹, Medugorac I.², Zinovieva N.A¹.

¹ L.K. Ernst Federal Research Center for Animal Husbandry, Dubrovitsy, Podolsk Municipal District, Moscow Region, Podolsk 142132, Russia;

² Ludwig Maximilian University of Munich, Munich, 80539 Germany.

* Corresponding author: veronika0784@mail.ru



Federal Research Center for Animal Husbandry named after Academy Member L.K. Ernst

L.K. Ernst Federal Research Center for Animal Husbandry

Abstract: The reindeer of the Tuva population inhabiting the south of Eastern Siberia and belong to one of the southernmost populations of domestic reindeer. The population census size of those reindeer was declined dramatically from 15,000 in 1990 to 1,400 individuals in 2019. A genetic study of this population is mandatory for assessing the risk of loss of its genetic diversity in order to develop the proper management strategies for preserving this unique genetic resource. In our study, we examined genetic diversity of Tuva reindeer based on both a high-density SNP genotypes analysis (n=12) and a complete cytochrome b (cytb) sequences (1,140 bp) (n=6). To find out a possible genetic contribution toward the Tuva reindeer population structure, SNP genotypes and cytb sequences of all officially recognized breeds in Russia were added to our datasets. All genetic diversity indices calculated based on both nuclear and mitochondrial genomic data were lowest in Tuva population. Median-joining network, a principal component analysis and Fst-based Neighbor-Net tree showed that Tuva population was most distant, while other breeds formed well-separated clusters according to their geographic locations. The low level of genetic diversity of the Tuva population observed in our study, based on studies involving a genome-wide approach, as well as a complete cytochrome b sequences, indicated the need to take appropriate measures to avoid negative consequences for this domestic reindeer.

Keywords: *Rangifer tarandus*, Tuva population, SNP, cytochrome b, genetic diversity





The reindeer of the Tuva population belong to one of the southernmost groups of domestic reindeer inhabiting the autonomous republic of Tyva (Tuva) in south-central Russia. Despite the fact that this group of reindeer does not have an official breed status, unlike the other four breeds, Tuvan reindeer are of great importance to the socio-cultural activities of the indigenous peoples. The South Siberian and North Mongolian groups of reindeer herders breed small herds of reindeer in the taiga and al-pine tundra and use the reindeer mainly as beasts of burden and riding animals for hunting and for obtaining dairy products.

Recently, attention has been drawn to the dramatic rate of Tuva reindeer population decline from **15,000** in 1990 to **1,400** individuals in 2019.

- AIM:**
- to examine genetic diversity,
 - to characterize population structure,
 - to establish population relationships of Tuva reindeer population with all officially recognized reindeer breeds in Russia.

using both: a high-density SNP genotypes analysis
and
a complete cytochrome b (cytb) sequences



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Results

The genetic diversity parameters estimated based on the SNP genotypes and cytb gene sequences of all studied groups of reindeer

Table 1. Parameters of genetic diversity of the studied groups of reindeer calculated from SNP genotypes.

Breed/ Population ¹	n ²	A _R ³	H _O ⁴	_U H _E ⁵	_U F _{IS} ⁶
CHU	12	1.597±0.006	0.181±0.002	0.184±0.002	0.011[0.004;0.018]
EVN	13	1.676±0.005	0.195±0.002	0.201±0.002	0.028[0.021;0.035]
EVK	12	1.69±0.005	0.2±0.002	0.203±0.002	0.013[0.006;0.02]
NEN	21	1.63±0.005	0.189±0.002	0.193±0.002	0.017[0.011;0.023]
TUVA	12	1.547±0.006	0.169±0.002	0.173±0.002	0.019[0.011;0.027]
WLD	10	1.678±0.006	0.193±0.002	0.199±0.002	0.022[0.014;0.03]

¹ CHU, Chukotka; EVN, Even; EVK, Evenk; NEN, Nenets; TUVA, Tuva population; WLD, wild population; ²n, sample size; ³A_R, allelic richness; ⁴H_O, observed heterozygosity; ⁵_UH_E, unbiased expected heterozygosity; ⁶F_{IS}, inbreeding coefficient based on the difference between _UH_E and H_O with a 95% confidence interval (CI; in square brackets).

Table 2. Parameters of genetic diversity of the studied groups of reindeer calculated from sequence of mitochondrial cytb gene.

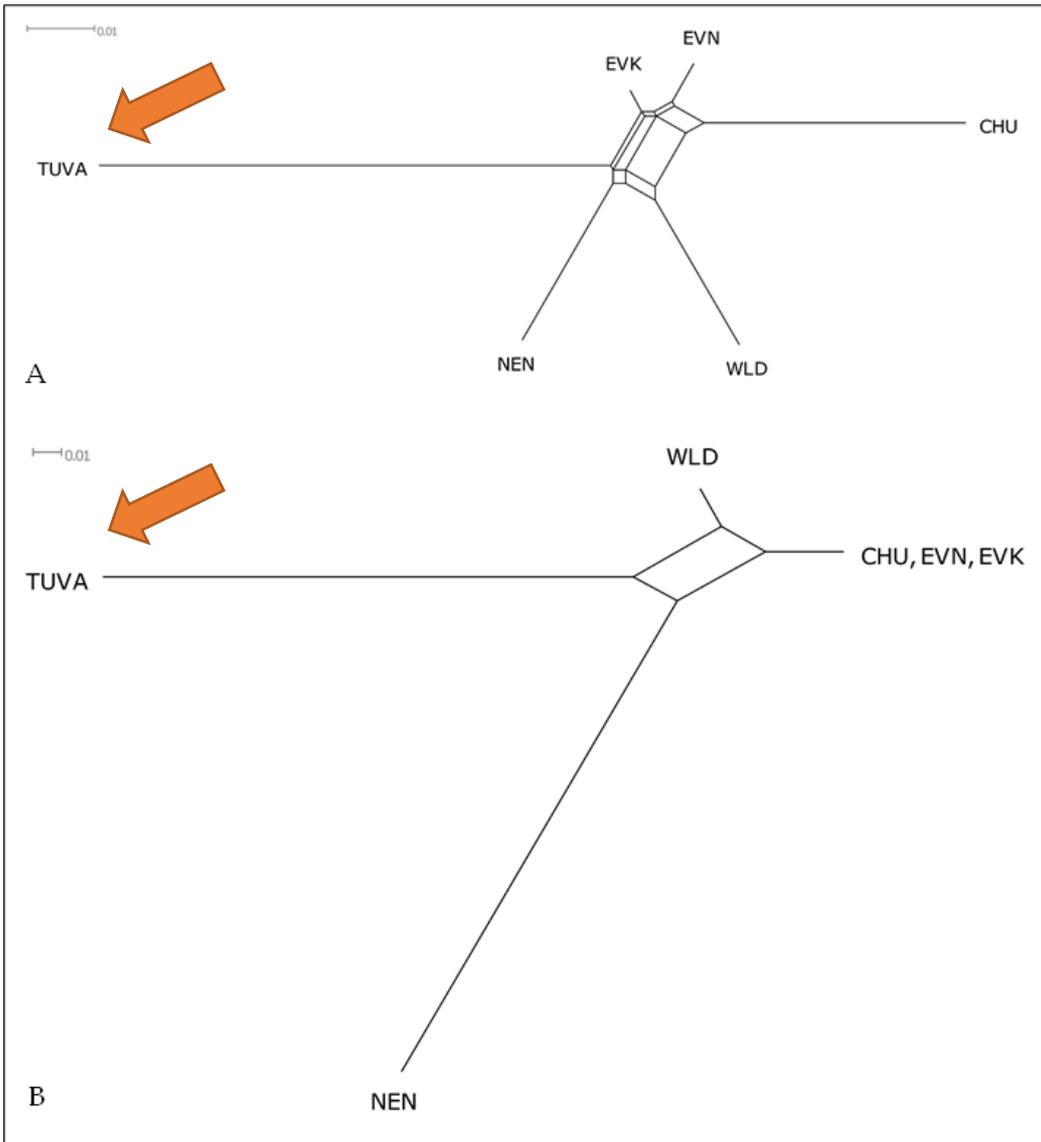
Breed/ Population ¹	n ²	S ³	H ⁴	K ⁵	HD ⁶	π ⁷
CHU	5	15	4	6.8	0.900±0.161	0.00596±0.00129
EVN	8	11	6	4.286	0.893±0.111	0.00476±0.00059
EVK	6	13	5	5.4	0.933±0.122	0.00474±0.00091
NEN	12	11	5	5.758	0.530±0.136	0.00542±0.00057
TUVA	6	10	5	4.533	0.933±0.122	0.00398±0.00110
WLD	10	26	9	7.511	0.978±0.054	0.00659±0.00079

¹ CHU, Chukotka; EVN, Even; EVK, Evenk; NEN, Nenets; TUVA, Tuva population; WLD, wild population; ²n, sample number; ³S, number of variable sites; ⁴H, number of haplotypes; ⁵K, average number of nucleotide differences; ⁶HD, haplotype diversity; ⁷π, nucleotide diversity.



Results

The results of the neighbor-net analysis conducted based on pairwise F_{st} values calculated from SNP genotypes (Figure 1A) and *cytb* gene sequences (Figure 1B).



A revealed consistency of the Neighbor-Net trees constructed based on genotypes of the nuclear and the mtDNA genomes, reflected a clear distancing of the Tuva population from the domestic reindeer, which are belong to officially recognized breeds and from the wild reindeer.



Conclusions

In our study, we succeed in a better understanding of the current genetic diversity and population structure of domestic Tuva reindeer inhabiting the south of Eastern Siberia using modern molecular genetic approaches such as a high-density SNP genotypes analysis and a complete cytochrome b (cytb) sequences.

We believe that our findings will be useful in solving problems of conservation and increase in the number of this important species for the normal functioning of ecosystems and for the life and culture of indigenous peoples.



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Thank you for your
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