

MITOCHONDRIAL DNA ANALYSIS OF SNOW SHEEP (*Ovis nivicola*) POPULATIONS

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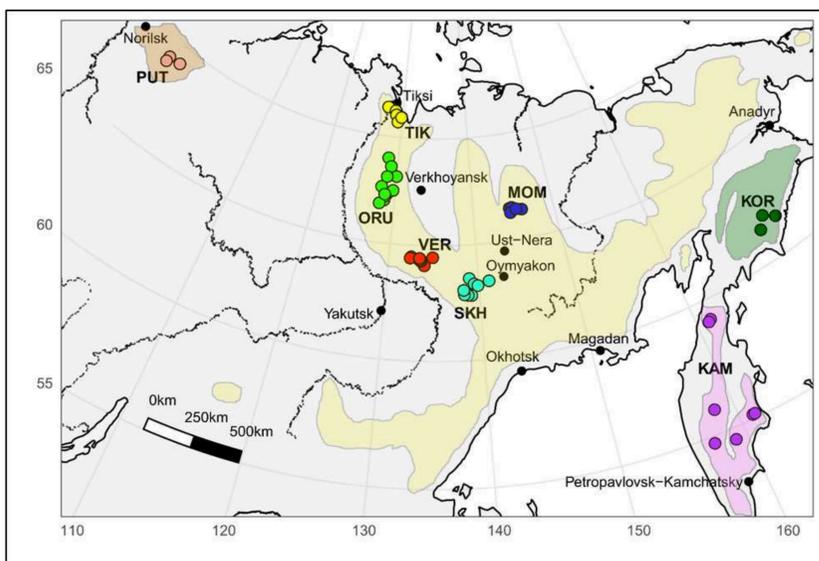
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INTRODUCTION. Currently, the intraspecific taxonomy of snow sheep (*Ovis nivicola*) is controversial and needs to be specified using DNA molecular genetic markers. In our previous work using whole genome SNP analysis, we found that the population inhabiting Kharaulakh Ridge was genetically different from the other populations of Yakut subspecies to which it was usually referred. Here, our study was aimed at the clarification of taxonomic status of Kharaulakh snow sheep using mitochondrial cytochrome b gene.

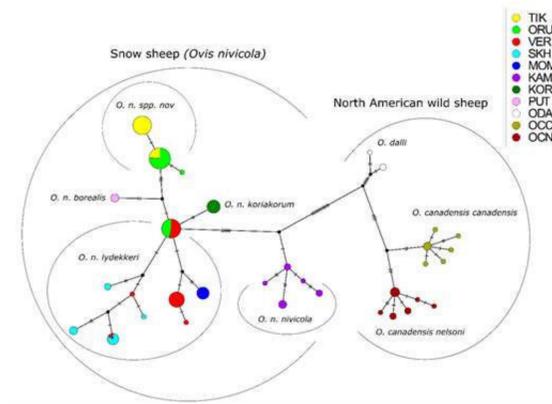


Two rams of snow sheep

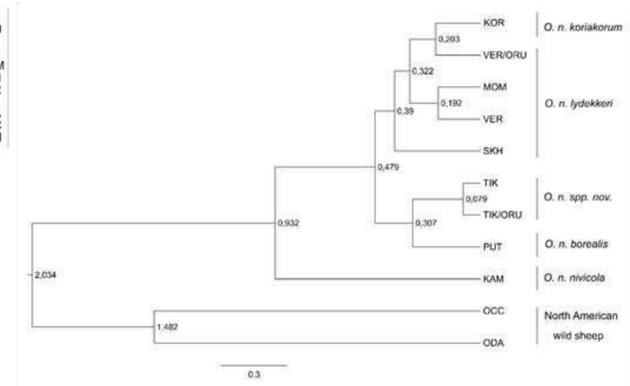
MATERIAL AND METHODS. A total of 87 specimens from five different geographic locations of Yakut snow sheep as well as 20 specimens of other recognized subspecies were included in this study. The whole sequences of cytb gene of Yakut snow sheep were determined by Sanger and NGS sequencing. The cytb gene sequences of North American wild sheep were downloaded from the GenBank NCBI database. The alignment was performed using the MUSCLE algorithm in the MEGA 7.0.26 software. To construct a median joining network, PopART 1.7 software was used. The construction of the Bayesian phylogenetic tree was carried out using the program BEAST 2.5 with subsequent visualization in FigTree 1.4.2. Calculations of pairwise F_{ST} as well as AMOVA analysis were carried out in the program Arlequin 3.5.2.2. Neighbor-Net phylogenetic tree was constructed in the SplitsTree 4.14.6



Map of the sampling sites of the snow sheep individuals included in the study

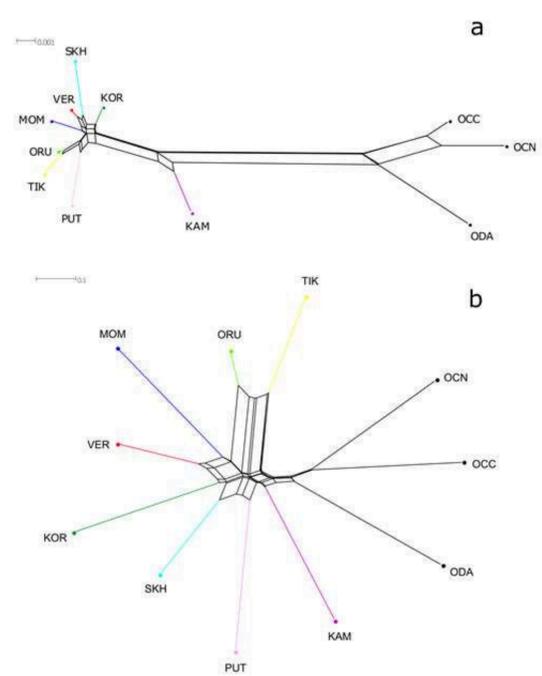


Median joining network

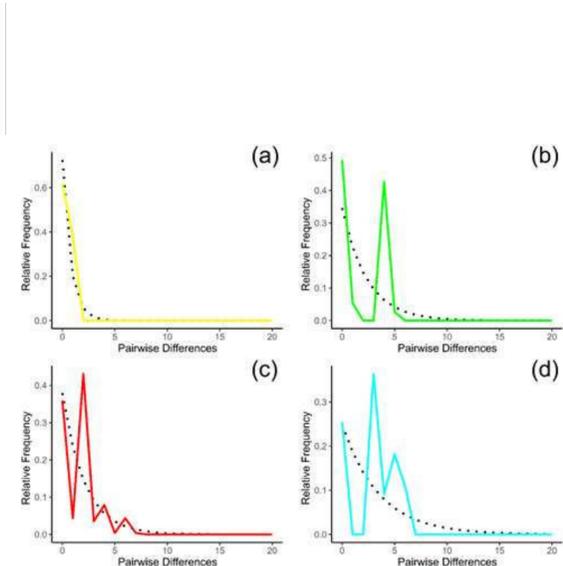


Bayesian phylogenetic tree

RESULTS. Our study of the whole cytb sequence in the four most recognized subspecies of Asian snow sheep (*Ovis nivicola*) showed the most genetic distance of the Kamchatka population (*O. n. nivicola*). The haplotypes of all other populations were originated from a single haplotype currently found in the central Verkhoyansk Range and the Orulgan Ridge. It was shown that, in terms of the number of nucleotide substitutions, the Kharaulakh population differs from this “main” Yakut haplotype even more than the officially recognized Putorana and Koryak subspecies. The Orulgan population has the admixture origin and is represented by two major haplotypes, differing from each other by four nucleotide substitutions.



Neighbor-Net tree based on genetic distances based on the Kimura-2-parameter model (a) and pairwise F_{ST} (b)



Mismatch distribution in four snow sheep populations. (a) TIK, (b) ORU, (c) VER and (d) SKH

CONCLUSION. Taking into account the high degree of divergence of Kharaulakh snow sheep from other groups, identified by both nuclear and mitochondrial DNA markers, we propose to classify the Kharaulakh population as a separate subspecies.

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