

Phylogenetic position of the Caucasian wolves (*Canis lupus*) compared to the European and Siberian populations of the species

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Grey wolf (*Canis lupus*) evolved in central Asia and then expanded and colonized the whole Northern Hemisphere. We analysed a fragment of mitochondrial DNA (223 bp) of 119 wolf samples from Eastern Siberia (Yakutia, n=70) and the Caucasus Mts. (Armenia, n= 33, Georgia, n=16). Data were compared with over 80 wolf haplotypes from Europe, Asia, and North America available in GenBank. Among our samples, we found 17 mtDNA haplotypes (Yakutia – 9; Caucasus – 8); ten of them belonged to haplogroup 1, and seven to haplogroup 2. Both populations had high haplotype and nucleotide diversity (Yakutia: Hd = 0.817, π = 0.014; Caucasus: Hd = 0.794, π = 0.021). The Caucasian wolves shared mtDNA haplotypes with both the west Asian (Turkey, Iran, Saudi Arabia) and the European (mostly the Balkan region) wolves. Six out of 9 haplotypes found in Yakutia have not been previously described. Two were earlier reported from north-eastern Europe, and one from Alaska, Canada and Japan. This suggests that area of Eastern Siberia is an important place for our understanding of evolutionary history of wolves and the origin of American and European populations of the species. The studied wolf populations differed in frequencies of haplotypes belonging to haplogroups 1 and 2. Haplogroup 1 dominated in Georgia (100% of samples), and Yakutia (63%), whereas haplogroup 2 dominated among Armenian wolves (67%).