

The Origins of the Yakut People: Evidence from Mitochondrial DNA Diversity

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ABSTRACT The Yakuts are a Turkic-speaking population of northeastern Siberia and based on archaeological and ethnohistorical evidence are believed to have originated from Turkic populations in south Siberia. To investigate this model, the HVS-I of the mitochondrial DNA control region was sequenced for 144 Yakut individuals representing seven communities from central Yakutia and compared to HVS-I data for other Asian populations. Haplogroups C and D comprise 75.7% of the Yakut sample, with only 9.7% assigned to west Eurasian lineages. The Ewens-Watterson homozygosity test revealed a significant deviation ($P = 0.045$) in the observed frequencies of common haplotypes relative to the expected values, indicating the genetic effects of a founder event. This is supported by a fragmented MJ network dominated by high-frequency haplotypes within haplogroups C and D. Nested cladistic analysis identified subhaplogroup D5a as the product of a long distance colonization event and potential founder lineage for the Yakuts, dating to approximately 1,630 years BP. SAMOVA analyses and MDS plot of genetic distances show close genetic affinities between the Yakuts and south Siberian populations, and thus affirming the south origin model.