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The ancient Yakuts: a population genetic enigma

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Abstract

This study is part of an ongoing project aiming at determining the ethnogenesis of an eastern Siberian ethnic group, the Yakuts, on the basis of archaeological excavations carried out over a period of 10 years in three regions of Yakutia: Central Yakutia, the Vilyuy River basin and the Verkhoyansk area. In this study, genetic analyses were carried out on skeletal remains from 130 individuals of unknown ancestry dated mainly from the fifteenth to the nineteenth century AD. Kinship studies were conducted using sets of commercially available autosomal and Y-chromosomal short tandem repeats (STRs) along with hypervariable region I sequences of the mitochondrial DNA. An unexpected and intriguing finding of this work was that the uniparental marker systems did not always corroborate results from autosomal DNA analyses; in some cases, false-positive relationships were observed. These discrepancies revealed that 15 autosomal STR loci are not sufficient to discriminate between first degree relatives and more distantly related individuals in our ancient Yakut sample. The Y-STR analyses led to similar conclusions, because the current Y-STR panels provided the limited resolution of the paternal lineages.

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