

The ancient Yakuts: a population genetic enigma

Christine Keyser, Clemence Hollard, Angela Gonzalez, Jean-Luc Fausser, Eric Rivals, Anatoly Nikolayevich Alexeev, Alexandre Riberon, Eric Crubezy, Bertrand Ludes

► **To cite this version:**

Christine Keyser, Clemence Hollard, Angela Gonzalez, Jean-Luc Fausser, Eric Rivals, et al.. The ancient Yakuts: a population genetic enigma. Philosophical Transactions of the Royal Society B: Biological Sciences, Royal Society, The, 2015, Discussion meeting issue 'Ancient DNA: the first three decades', 370 (1660), pp.20130385. <<http://rstb.royalsocietypublishing.org/content/370/1660/20130385>>. <10.1098/rstb.2013.0385>. <lirmm-01170676>

HAL Id: lirmm-01170676

<https://hal-lirmm.ccsd.cnrs.fr/lirmm-01170676>

Submitted on 2 Jul 2015

HAL is a multi-disciplinary open access archive for the deposit and dissemination of scientific research documents, whether they are published or not. The documents may come from teaching and research institutions in France or abroad, or from public or private research centers.

L'archive ouverte pluridisciplinaire **HAL**, est destinée au dépôt et à la diffusion de documents scientifiques de niveau recherche, publiés ou non, émanant des établissements d'enseignement et de recherche français ou étrangers, des laboratoires publics ou privés.

The ancient Yakuts: a population genetic enigma

Christine Keyser ^{1,2}, Clemence Hollard ^{1,2}, Angela Gonzalez ¹, Jean-Luc Fausser ¹, Eric Rivals ^{3,4}, Anatoly Nikolayevich Alexeev ⁵, Alexandre Riberon ⁶, Eric Crubezy ², Bertrand Ludes ^{2,7}

Addresses

1. Institut de Medecine Legale, Laboratoire AMIS, CNRS UMR 5288, Universite de Strasbourg, Strasbourg, France
2. Laboratoire AMIS, CNRS UMR 5288, Universite de Toulouse, Toulouse, France
3. LIRMM, CNRS UMR 5506, Universite Montpellier 2, Montpellier, France
4. Institut de Biologie Computationnelle, Universite de Montpellier, Montpellier, France
5. Medical Institute, Yakutsk University, Sakha Republic, Russia
6. Laboratoire Evolution et Diversite Biologique, CNRS UMR 5174, Universite de Toulouse, Toulouse, France
7. Institut Medico-Legal, Universite Paris Descartes, Paris, France

This document contains only the article's abstract (full text at <http://dx.doi.org/10.1098/rstb.2013.0385>).

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.

Citation:

Keyser C, Hollard C, Gonzalez A, Fausser J-L, Rivals E, Alexeev AN, Riberon A, Crubezy E, Ludes B.
The ancient Yakuts: a population genetic enigma.
Philosophical Transactions of the Royal Society series B, 370: 20130385.
<http://dx.doi.org/10.1098/rstb.2013.0385>
2015.