

## Mitochondrial DNA analysis of ancient Yakut skeletons

F.X. Ricaut<sup>a,b,\*</sup>, C. Keyser-Tracqui<sup>a</sup>, P. Blandin<sup>a</sup>,  
E. Crubézy<sup>b</sup>, B. Ludes<sup>a,b</sup>

<sup>a</sup>*Laboratoire d'Anthropologie Moléculaire, Institut de Médecine Légale, 11 rue Humann, 67085 Strasbourg, France*

<sup>b</sup>*Anthropobiologie, Université Paul Sabatier, CNRS, UMR 8555, Toulouse, France*

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**Abstract.** The excavation of 10 frozen graves in central Yakutia (dated to be 300–600 years old) revealed 11 human bodies belonging to the ancient Yakut population. To investigate the origin and evolution of the Yakut population, DNA was extracted from these skeletons and analysed by sequencing of the hypervariable region 1 (HV1) of the mitochondrial DNA (mtDNA). Comparison of haplotypes obtained with those of 8774 Eurasian individuals suggested a relative continuity of the ancient mitochondrial Yakut lineages during the three last centuries, as well as their putative central Asian origin. © 2003 Elsevier B.V. All rights reserved.

*Keywords:* Yakuts; Ancient DNA; Mitochondrial DNA

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### 1. Introduction

The Sakha (also known as Yakuts) are an enigmatic ethnic group living in northeastern Siberia in the Sakha republic, an autonomous republic within the Russian Federation. Their origin, in spite of numerous archaeological and recent genetic studies [1,2], is still fully debated.

The difficulties encountered by molecular biologists could arise from many historic and demographic events since the formation of the Sakha population, such as the Russian colonisation starting in the 17th century, as well as the high degree of isolation and genetic drift of the Siberian populations. These events could have obscured the ancestral Yakut gene pool. Consequently, a direct access to the gene

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\* Corresponding author. Laboratoire d'Anthropologie Moléculaire, Institut de Médecine Légale, 11 rue Humann, 67085 Strasbourg, France. Tel.: +33-390-243347; fax: +33-390-243362.

*E-mail address:* fx.ricaut@infonie.fr (F.X. Ricaut).

Table 1  
Modern Eurasian populations sharing ancient Yakut haplotypes

Population	<i>n</i>	References	Ancient Yakut samples					
			IM2, AD1, AD3s, AD3n	SS3	Yak 3	AD2	SS2	SS1, Yak2, IM1
Yakut	139	[1,5]	12%	1.4%	3.6%	0.7%	2.9%	–
Buryat	166	[1,6]	–	–	1.8%	0.6%	0.6%	–
Mongol	103	[7]	–	–	0.8%	–	–	–
Tuvan	36	[6]	–	–	13.6%	–	–	–
Kazakh	55	[8]	–	–	1.1%	–	–	–
Chinese	378	[9]	0.3%	–	–	–	–	–
Turks	218	[10]	–	–	–	–	1.4%	–
NW Europeans	456	[10]	–	–	–	–	1.3%	–
NE Europeans	510	[10,11]	–	–	–	–	2%	–

pool of ancient Sakha individuals could lead to a better understanding of the genetic history of this Siberian population.

## 2. Material and methods

During the summer 2002, a French-Yakut scientific expedition excavated 10 Yakut frozen graves dating back from the 15th to 18th century and located in central Yakutia. The human bodies were well-preserved, the frozen graves being in direct contact with permafrost.

DNA was extracted from bone fragments by the silica-based method according to Fily et al. [3]. Hypervariable region 1 (HV1) of the mtDNA control region was amplified using the L15989/H16239 and L16190/H16410 primers, and were sequenced by means of the ABI Prism BigDye® Terminator cycle sequencing Ready Reaction Kit (PE Applied Biosystems), as described previously by Ricaut et al. [2]. The sequence reaction products were analysed on an ABI Prism 3100 automatic sequencer (PE Applied Biosystems).

The nucleotide sequences obtained from the 11 ancient Yakut samples were compared with the mtDNA sequences of 8774 Eurasians individuals, using the Blast 2.0 program ([www.ncbi.nlm.nih.gov](http://www.ncbi.nlm.nih.gov)). The reference sequences used for comparative analysis are listed in the Table 1 previously published by Ricaut et al. [2].

## 3. Results

A 366-base pair fragment of the mtDNA HV1 region was obtained for each of the 11 samples, and compared to the Cambridge Reference Sequence [4]. The current frequency distribution of ancient Yakut haplotypes in the reference populations presenting these haplotypes is indicated in Table 1.

## 4. Discussion

The distribution of the ancient Yakut haplotypes in Eurasian populations is principally limited to Yakut and central Asian modern populations. This suggests (i) a relative continuity of the mitochondrial Yakut lineage since the 15th–18th centuries and (ii) a

putative central Asian origin of these ancient mitochondrial Yakut lineages, which is in accordance with the origin of Yakut population postulated by archaeological and recent genetic studies [1,2]. Moreover, the presence in a Yakut subject (SS2) buried in the 15th century of a haplotype affiliated to East European Caucasoid indicates that the Caucasoid part of the Yakut population was present two centuries before the Russian colonisation (starting in the 17th century).

Nevertheless, the absence of ancient Yakut haplotypes shared by Siberian populations is surprising because a part of these populations, and notably the Evenks, have contributed to the mitochondrial modern Yakut gene pool as reported by Pakendorf et al. [1]. A possible explanation could be that the smallness of our sample did not allow to detect the Siberian genetic contribution, but we cannot exclude a contribution of Siberian population to the mitochondrial Yakut gene pool subsequent to the 15th–18th centuries.

In conclusion, the molecular data obtained from the archaeological samples studied bring new elements to the understanding of origin and evolution of the mitochondrial Yakut gene pool. However, our results are inevitably constrained by the sample size, and the new archaeological samples could provide more comprehensive insights of the Yakut population history.

### Acknowledgements

This work has been supported by the program of the French/Sakha cooperation from the Action Cooperation Integred from the French Minister of the research “le complexe spatial Altaï-Baïkal. Plaque tournante des flux géniques en Haute Asie de la période protohistorique à l’époque moderne”.

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