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# Mitochondrial DNA analysis of ancient Yakut skeletons

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## INTRODUCTION

The Sakha (also known as Yakuts) of northeastern Siberia are an enigmatic ethnic group differing completely in their traditional way of live and language from their neighbours. Their origin, in spite of numerous archaeological and recent genetic studies, is still fully debated.

During the summer 2002, several Yakut frozen graves dating back from the 15<sup>th</sup> to 18<sup>th</sup> centuries and located in central Yakutia have been excavated, and bone samples from eleven ancient Yakut skeletons or natural mummies have been taken. The human bodies buried in wooden sarcophagus were well preserved (Figure 1). To investigate the ancestor-descendant relationships between ancient Yakuts and modern ones, and to clarify the still obscure origins of the Yakut population, mitochondrial DNA analysis of ancient bone samples was undertaken in our laboratory.

## MATERIAL AND METHODS

Several independent DNA extraction were performed from bone samples for each of the eleven ancient subjects by the silica-based method according to Fily et al. [1]. To minimise the risk of contamination by modern human DNA during each step of sample preparation (excavation, extraction procedure, etc.) all standard precautions were taken. Hypervariable region 1 (HV1) of the mitochondrial DNA was amplified using the L15989/H16239 and L16190/H16410 primers, and were sequenced with the BigDye Terminator Cycle Sequencing Ready Reaction Kit (PE Applied Biosystems). The haplotypes were determined on an ABI Prism 3100 automated DNA sequencer (PE Applied Biosystems) and compared with the HV1 sequence of 8774 Eurasian individuals.



Figure 1. Typical grave of ancient Yakuts. The frozen body is contained in a wooden sarcophagus.

## RESULTS

Table 1. HV1 sequences (np 16018-16383) of eleven ancient Yakut samples

Samples	Age	Polymorphic Positions <sup>a</sup>															
		1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
		6	6	6	6	6	6	6	6	6	6	6	6	6	6	6	6
		0	0	0	1	1	1	1	1	2	2	2	2	2	3	3	3
		6	6	9	2	7	7	8	8	8	2	4	5	6	9	9	1
		6	9	2	6	1	2	2	3	9	3	2	6	6	0	8	9
		7	2	6	1	2	2	3	9	3	2	6	6	0	8	9	7
		2	6	9	2	6	1	2	2	3	9	3	2	6	6	0	8
CRS		A	C	T	T	A	T	A	A	T	C	C	C	C	T	G	
Yak 1	17 <sup>st</sup>	-	-	C	-	-	C	C	C	T	-	-	T	-	-	-	
Yak 2	18 <sup>st</sup>	-	-	C	-	-	C	C	C	T	-	-	T	-	-	-	
Yak 3	18 <sup>st</sup>	-	-	C	-	-	C	C	C	T	-	-	T	-	-	-	
Yak 4	18 <sup>st</sup>	-	-	C	-	-	C	C	C	T	-	-	T	-	-	-	
Yak 5	15 <sup>st</sup>	-	-	C	-	-	C	C	C	T	-	-	T	-	-	-	
Yak 6	15 <sup>st</sup>	-	-	C	-	-	C	C	C	T	-	-	T	-	-	-	
Yak 7	15 <sup>st</sup>	-	-	-	-	G	-	-	-	T	-	T	-	-	C	-	
Yak 8	17 <sup>st</sup>	-	-	-	-	G	-	-	-	T	-	-	-	-	C	-	
Yak 9	17 <sup>st</sup>	-	-	-	-	G	-	-	-	T	-	-	-	-	T	-	
Yak 10	18 <sup>st</sup>	G	-	-	-	-	-	-	-	T	T	-	-	-	A	-	
Yak 11	15 <sup>st</sup>	-	T	-	C	-	-	-	-	-	-	-	-	-	-	-	

<sup>a</sup> Numbered according to Cambridge reference sequence [2].

Table 2. Modern Eurasian populations sharing ancient Yakut haplotypes

Population	n	Ref.	Ancient Yakut samples					
			Yak 1,2,3,4	Yak 7	Yak 8	Yak 10	Yak 11	Yak 5,6,9
Yakut	139	[3,4]	12%	1.4%	3.6%	0.7%	2.9%	-
Buryat	166	[3,5]	-	-	1.8%	0.6%	0.6%	-
Mongol	103	[5]	-	-	0.8%	-	-	-
Tuvan	36	[6]	-	-	13.6%	-	-	-
Kazakh	55	[7]	-	-	1.1%	-	-	-
Chinese	378	[8]	0.3%	-	-	-	-	-
Turks	218	[9]	-	-	-	-	1.4%	-
N.W. Europeans	456	[9]	-	-	-	-	1.3%	-
N.E. Europeans	510	[9,10]	-	-	-	-	2%	-

## 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 gene pool since the 15<sup>st</sup> -18<sup>st</sup> centuries and (ii) a putative central Asian origin of these ancient mitochondrial Yakut lineages. The presence in a Yakut subject buried in the 15<sup>st</sup> 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 colonization.

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. [3]. A possible explanation could be that the smallness of our sample did not allow to detect the Siberian genetic contribution, but we can not exclude a contribution of Siberian population to the mitochondrial Yakut gene pool subsequent to the 15<sup>st</sup> -18<sup>st</sup> century.

## 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. Nevertheless, our results are inevitably constrained by the sample size, and the new archaeological samples could provide more comprehensive insights of the Yakut population history.

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