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## Analysis of Mitochondrial DNA Lineages in Yakuts

**S. A. Fedorova<sup>1</sup>, M. A. Bermisheva<sup>2</sup>, R. Villems<sup>3</sup>,  
N. R. Maksimova<sup>1</sup>, and E. K. Khusnutdinova<sup>2</sup>**

<sup>1</sup>*Yakut Research Center, Russian Academy of Medical Sciences and Government of the Sakha Republic (Yakutia), Yakutsk, 677019 Russia; E-mail: sardaanafedorova@mail.ru*

<sup>2</sup>*Institute of Biochemistry and Genetics, Ufa Research Center, Russian Academy of Sciences, Ufa, 540054 Russia*

<sup>3</sup>*Estonian Biocentre, Tartu, 51010 Estonia*

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**Abstract**—To study the mitochondrial gene pool structure in Yakuts, polymorphism of mtDNA hypervariable segment I (16,024–16,390) was analyzed in 191 people sampled from the indigenous population of the Sakha Republic. In total, 67 haplotypes of 14 haplogroups were detected. Most (91.6%) haplotypes belonged to haplogroups A, B, C, D, F, G, M\*, and Y, which are specific for East Eurasian ethnic groups; 8.4% haplotypes represented Caucasian haplogroups H, HV1, J, T, U, and W. A high frequency of mtDNA types belonging to Asian supercluster M was peculiar for Yakuts: mtDNA types belonging to haplogroup C, D, or G and undifferentiated mtDNA types of haplogroup M (M\*) accounted for 81% of all haplotypes. The highest diversity was observed for haplogroups C and D, which comprised respectively 22 (44%) and 18 (30%) haplotypes. Yakuts showed the lowest genetic diversity ( $H = 0.964$ ) among all Turkic ethnic groups. Phylogenetic analysis testified to common genetic substrate of Yakuts, Mongols, and Central Asian (Kazakh, Kyrgyz, Uighur) populations. Yakuts proved to share 21 (55.5%) mtDNA haplotypes with the Central Asian ethnic groups and Mongols. Comparisons with modern Paleoasian populations (Chukcha, Itelmen, Koryaks) revealed three (8.9%) haplotypes common for Yakuts and Koryaks. The results of mtDNA analysis disagree with the hypothesis of an appreciable Paleoasian contribution to the modern Yakut gene pool.

*Key words:* mitochondrial DNA, Yakut gene pool, haplotypes, median networks, phylogenetic analysis

### INTRODUCTION

The molecular genetic approach is of importance for studying the evolutionary history of human populations and for estimating the contribution of individual ethnic components to the gene pools of modern ethnic groups. Mitochondrial DNA is among the most informative genetic systems suitable for characterizing the structure of a gene pool. Owing to the maternal inheritance, absence of recombination, and mutation rate higher than in nuclear DNA, mtDNA may be used as a major subject to study the origin of modern ethnic groups [1]. In the 1990s, extensive population-genetic studies have made it possible to identify and to classify the mtDNA types specific for individual races or populations [1–3], as well as to trace the major human migrations leading to colonization of Europe and America. Yet the origin of most individual ethnic groups, including Yakuts, is still poorly understood. Only two publications on Yakuts are available: Derenko and Shields [4, 5] have analyzed the mtDNA nucleotide diversity with a small sample of 22 individuals.

In this work, we for the first time used a vast material to characterize the Yakut mitochondrial gene pool. The mtDNA haplotypes were phylogenetically analyzed in order to elucidate the genetic relationships of

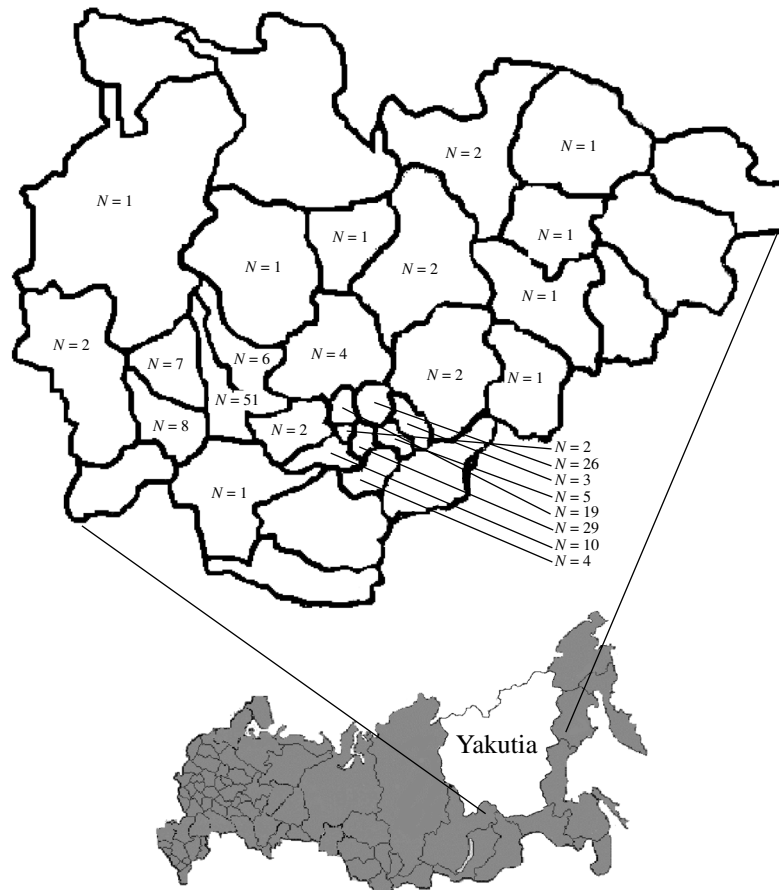
Yakuts with Central Asian ethnic groups, Mongols, and Paleoasian indigenous populations.

### EXPERIMENTAL

**Subjects.** We tested DNA specimens of 191 Yakuts from the indigenous population of the Sakha Republic (Yakutia). The specimens were obtained from the DNA bank (Department of Molecular Genetics, Yakut Research Center), which contained the material collected from 2001 to 2002 in the course of routine medical examination or sampled at the Blood Transfusion Department, National Medical Center of the Sakha Republic. Blood was obtained from adults who filled a questionnaire and gave their informed consent to participation in the study. The sample included unrelated subjects; the ethnicity was recorded for three generations of maternal lineage.

**Genomic DNA** was isolated from peripheral blood lymphocytes by proteinase K treatment and subsequent phenol–chloroform extraction [6].

**A fragment of the mtDNA control region** containing the hypervariable segment I (HVSI) was amplified and purified with an ExoSAP-IT kit (Applied Biosystems). HVSI (16,024–16,390) was



**Fig. 1.** Administrative map of the Sakha Republic (Yakutia). The number of specimens collected is indicated for each corresponding district (ulus).

sequenced with a DYEnamic ET terminator cycle sequencing premix kit (Amersham Pharmacia Biotech) in an ABI 377 DNA Sequencer. Nucleotide sequence alignment and analysis employed the Wisconsin software package.

**Haplogroups** were identified against the Cambridge reference sequence [7, 8] and verified by RFLP analysis of 13 restriction sites in the mtDNA coding region.

**Median networks** were constructed from the data on RFLPs and HVSI polymorphisms according to the median-joining algorithm [9]. An advantage of this method is that several equally possible phylogenetic trees are simultaneously present in one scheme.

Genetic diversity of mtDNA types was obtained as

$$H = (1 - \sum x_i^2)N(N-1),$$

where  $x_i$  is the population frequency of a particular mtDNA haplotype and  $N$  is the sample size [10].

## RESULTS AND DISCUSSION

Our sample included 191 Yakuts from various districts (uluses) of the Sakha Republic (Fig. 1). Analysis of the 367-bp HVSI (16,024–16,390) revealed 67 haplotypes with 65 variable nucleotide positions (Table 1).

The mtDNA haplotypes were classified; the assignment to a particular haplogroup was verified by RFLP analysis of 13 polymorphic sites of the mtDNA coding region and analysis of deletion of region V located between the *COII* and *tRNA<sup>Lys</sup>* genes. The mtDNA haplotypes of Yakuts proved to belong to 14 haplogroups. A median network of mtDNA haplotypes is shown in Fig. 2.

The vast majority (91.6%) of the Yakut mtDNA haplotypes belonged to haplogroups specific for East Eurasian ethnic groups. Asian mtDNA haplotypes represented haplogroups A, B, C, D, F, G, M\*, and Y. Peculiar of Yakuts, a high frequency was observed for mtDNA haplotypes representing Asian supercluster M: in total, mtDNA types belonging to haplogroup C, D, or G and nondifferentiated mtDNA types of haplogroup M (M\*) accounted for 81% of all haplotypes. The greatest diversity was characteristic of haplo-

**Table 1.** Diversity of mtDNA HVSI haplotypes in Yakuts ( $n = 191$ )

Haplogroup	RFLP site	no.	Haplotype*	<i>n</i>	Haplotype frequency	Haplogroup frequency			
A	<i>Hae</i> III663+	1	223, 242, 290, 319	1	0.0052	0.0209			
		2	39, 189, 223, 290, 319, 356, 362	1	0.0052				
		3	179, 223, 290, 311, 319, 362	1	0.0052				
		4	179, 223, 260, 290, 311, 319, 362	1	0.0052				
B	9-bp deletion	5	86, 136, 189, 217	1	0.0052	0.0052			
C	<i>Alu</i> I13262+	6	129, 223, 235, 298, 327	1	0.0052	0.4398			
		7	129, 150, 223, 298, 327	2	0.0105				
		8	129, 223, 298, 327	6	0.0314				
		9	129, 223, 327	1	0.0052				
		10	148, 164, 223, 288, 298, 327	9	0.0471				
		11	148, 223, 288, 298, 327	2	0.0105				
		12	167, 171, 223, 298, 327, 344, 357	1	0.0052				
		13	171, 223, 256, 298, 327, 344, 357	1	0.0052				
		14	171, 223, 295, 298, 327, 344, 357	1	0.0052				
		15	171, 223, 298, 327, 344, 357	12	0.0628				
		16	189, 223, 298, 327	1	0.0052				
		17	223, 260.1A**, 294, 298, 327	1	0.0052				
		18	223, 260.1A**, 298, 327	3	0.0157				
		19	223, 298, 311, 327	8	0.0419				
		20	223, 298, 327	10	0.0524				
		21	223, 298, 327, 344, 357	1	0.0052				
		22	223, 291, 298, 327	1	0.0052				
		23	93, 129, 223, 298, 327	6	0.0314				
		24	93, 129, 223, 327	13	0.0681				
		25	93, 129, 223, 327, 335	1	0.0052				
		26	93, 214, 223, 261, 288, 298	1	0.0052				
		27	93, 223, 261, 288, 298	2	0.0105				
		D	<i>Alu</i> I5176-	28	129, 189, 223, 362		1	0.0052	0.3037
				29	129, 223, 294, 362		1	0.0052	
				30	172, 189, 223, 266, 362		2	0.0105	
				31	180, 223, 294, 362		1	0.0052	
				32	223, 245, 362		2	0.0105	
				33	223, 291, 362		12	0.0628	
				34	223, 319, 320, 362		1	0.0052	
				35	223, 319, 362		4	0.0209	
				36	223, 362, 368		1	0.0052	
				37	42, 93, 214, 223, 362		1	0.0052	
				38	92, 129, 223, 271, 362		2	0.0105	
				39	92, 172, 189, 223, 266, 362		23	0.1204	
				40	92, 172, 189, 223, 362		2	0.0105	
				41	92, 172, 189, 223, 266, 305, 362		1	0.0052	
				42	93, 192, 223, 232, 362		1	0.0052	
43	93, 223, 232, 261, 290, 362			1	0.0052				
44	93, 223, 232, 290, 362			1	0.0052				
45	93, 223, 232, 362			1	0.0052				

**Table 1.** (Contd.)

Haplogroup	RFLP site	no.	Haplotype	<i>n</i>	Haplotype frequency	Haplogroup frequency
F	<i>HincII</i> 12406–	46	189, 232ëA, 249, 304, 311	4	0.0209	0.0628
		47	189, 232ëA, 304, 311	1	0.0052	
		48	92íA, 291, 304	3	0.0157	
		49	172, 189, 232ëA, 249, 304, 311	4	0.0209	
G	<i>HaeII</i> 4830+	50	223, 227, 278, 362	3	0.0157	0.0419
		51	189, 223, 227, 234, 278, 362	2	0.0105	
		52	223, 227, 274, 278, 362	2	0.0105	
		53	223, 227, 234, 278, 362	1	0.0052	
H	<i>AluI</i> 7025–	54	CRS	3	0.0157	0.0262
		55	291	2	0.0105	
HV1	<i>TruI</i> 114766–	56	67, 260, 355	2	0.0105	0.0105
J	<i>MvaI</i> 13704–	57	69, 126	2	0.0105	0.0105
M	<i>AluI</i> 10397+	58	145, 148, 188, 189, 223, 381	2	0.0105	0.0262
		59	145, 148, 162, 188, 189, 223, 381	1	0.0052	
		60	93, 129, 223, 311	1	0.0052	
		61	145, 223, 295, 304	1	0.0052	
T	<i>BamHI</i> 13366+	62	126, 294, 296, 362	2	0.0105	0.0105
U	<i>HinfI</i> 12308+	63	144, 189, 270	1	0.0052	0.0105
		64	189, 356	1	0.0052	
W	<i>HaeIII</i> 8994–	65	223, 292	3	0.0157	0.0157
Y	<i>MboI</i> 7933+	66	126, 231, 266, 342	1	0.0052	0.0157
		67	126, 231, 266	2	0.0105	

Notes: \* Haplotypes are described as HVSI nucleotides differing from those in the Cambridge reference sequence [7, 8]. Only the position is indicated in the case of transition; transversions are fully described.

\*\* Single-nucleotide insertion is indicated.

groups C and D, which comprised 22 (44%) and 18 (30%) haplotypes, respectively.

In addition to Mongoloid mtDNA haplotypes, the Yakut gene pool included haplotypes of groups H, HV1, J, T, U, and W, which are widespread in European and Middle Eastern populations. In total, Caucasian mtDNA haplotypes accounted for 8.4% of all haplotypes.

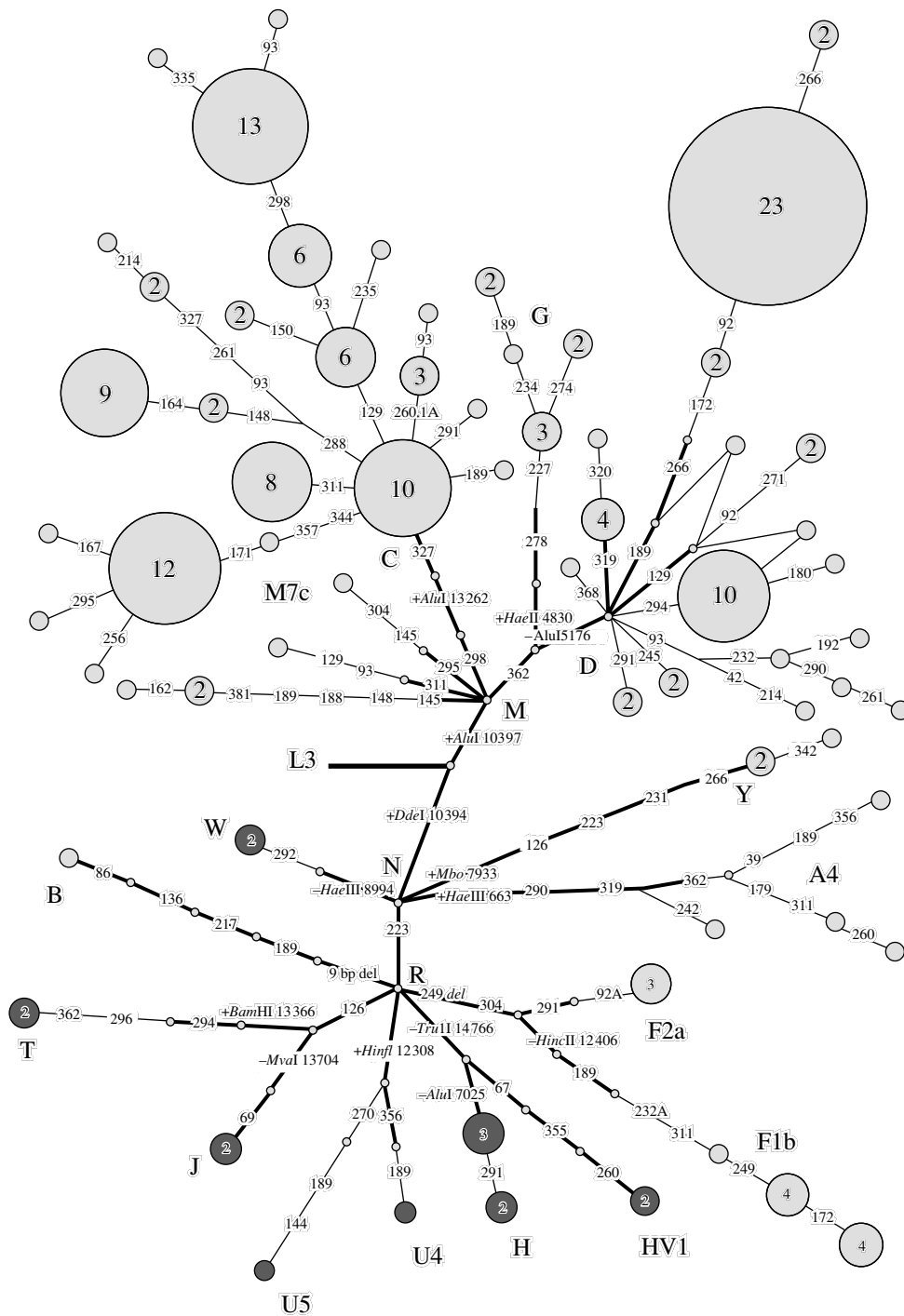
For comparison, we used the published data on genetic diversity and frequencies of Caucasian and Mongoloid mtDNA haplotypes in Turkic ethnic groups, Mongols, and North-East Asian populations (Table 2). Generally, there is certainly a west-east cline in frequencies of race-specific haplotypes. The highest (89%) frequency of the Caucasian component has been observed in the gene pools of Chuvash and Tatars, indigenous populations of the Volga–Ural region located at the boundary between Europe and Asia [11]. The Mongoloid component increases up to 68% (in Kyrgyz) in Central Asian ethnic groups (Kazakhs, Kyrgyz, Uighurs) [12]. Only Mongoloid mtDNA haplotypes (frequency 100%) have been

found in North-East Asian ethnic groups of Kamchatka (Koryaks, Itelmen) and the Chukotka Peninsula (Chukcha, Eskimo) [13, 14].

The gene pools of Turkic ethnic groups have a high genetic diversity (*H*), which is maximal in Kazakhs and Kyrgyz. Yakuts have the lowest genetic diversity among the Turkic populations. Small populations of Northeastern Asia have even a lower diversity, as characteristic of ethnic groups originating from a small ancestral population and being to some extent isolated for a prolonged period.

We analyzed the frequencies of individual mtDNA haplogroups in Yakuts; in Turkic ethnic groups of the Volga–Ural region, Central Asia, and the Altai–Sayan Highlands; in Mongols; and in the indigenous populations of Northeastern Asia (Table 3).

The highest (44%) frequency in the Yakut mitochondrial gene pool was observed for haplogroup C, which is widespread in Asian ethnic groups and especially in the indigenous populations of Siberia. Frequency of this haplogroup is high in Evenks (84.3%)



**Fig. 2.** Phylogenetic tree of the mtDNA haplotypes observed in Yakuts. Haplotypes are shown with circles, with the number of carriers indicated. Caucasian haplotypes are shown black. Here and in Fig. 3: Distinguishing nucleotide polymorphisms of HVSI or RFLPs of the coding region are indicated on the links.

[15], Tuvinians (48.9%) [16], Koryaks (36.1%) [13], and Khakassians (35.2%) [17], and falls to 10% or lower in Chukcha and Eskimo in the east, Kazakhs and Uighurs in the south, or Tatars and Chuvash in the west. Haplogroup C occurs rarely or sporadically in South Asian populations, which has been explained by their recent migration from Central Asia [18].

Cluster D (30%) was the second most frequent Asian haplogroup in Yakuts. Compared with haplogroup C, it has much the same distribution through Asian populations, being widespread in the indigenous populations of Siberia and in Central Asian ethnic groups. Haplogroup D accounts for more than one-fourth of the mtDNA haplotypes observed in

**Table 2.** Diversity of mtDNA haplotypes and frequencies of race-specific mtDNA haplogroups in the gene pools of Turkic ethnic groups and North-East Asian indigenous populations

Population	<i>n</i>	Total HVSI haplotypes	<i>H</i>	Gene pool component, %		
				Caucasian	Mongoloid	Unidentified
Yakuts	191	67	0.964	8.4	91.6	0
Turkic ethnic groups						
Chuvash	55	39	0.988	89.1	9.1	1.8
Tatars	174	91	0.976	89.1	10.3	0.6
Bashkirs	211	105	0.988	60.7	39.3	0
Uighurs [12]	55	46	0.993	34.5	54.5	10.9
Kazakhs [12]	55	45	0.990	40.0	56.4	3.6
Kyrgyz [12]	95	70	0.990	27.4	68.4	4.2
Altai-kizhi [17]	92	nd	nd	23.9	67.4	8.7
Shorians [17]	42	nd	nd	35.7	64.3	0
Khakassians [17]	54	nd	nd	18.5	75.9	5.6
Soyots [17]	34	nd	nd	5.9	88.2	5.9
Tuvinians [21]	36	nd	nd	5.6	94.4	0
North-East Asian populations						
Evens [4]	65	33	0.962	0	90.8	9.2
Koryaks [13]	147	41	0.945	0	100	0
Itelmen [13]	46	19	0.931	0	100	0
Chukcha [14]	65	19	0.883	0	100	0
Eskimo [14]	77	12	0.819	0	100	0
Mongolia						
Mongols [19]	103	83	0.990	13.6	86.4	0

Note: The number of HVSI haplotypes has not been determined (nd) in some cases, as mtDNA haplogroups have been established by RFLP analysis without HVSI sequencing.

Mongols [19]. The highest (up to 50%) frequency of this haplogroup has been reported for Soyots [17]. Interestingly, Yakuts proved to have a high (12%) frequency of haplotype 16,092-16,172-16,189-16,223-16,266-16,362, which belongs to subcluster D5a. This frequency was far greater than that of any other mtDNA haplotype in our sample. Subcluster D5a is specific for populations of North China and is extremely rare in Central Asia or Siberia [20].

Haplogroup A, which is common for virtually all Siberian ethnic groups examined, occurred at a frequency 2.1% in Yakuts. This haplogroup is the major component of the mitochondrial gene pool in Chukcha and Eskimo (68 and 77%, respectively) [14].

Haplogroup G contains two subclusters: G1, which is characteristic of North-East Siberian populations and occurs at the maximal frequency in Koryaks (42%) and Itelmen (68%), and G2a, the highest (8.8%) frequency of which has been detected in Central Asia [20]. In Yakuts, haplotypes of subcluster G2a were found at a relatively low (4.2%) frequency.

Haplogroup F originates from South Asia and occurs at a high frequency in Vietnamese (32%), Malays (28%), Koreans (15%), and in Chinese populations [18]. Possibly, this haplogroup spread from Southeastern to Central Asia. The HVSI motif 16,172-16,304, which is characteristic of haplogroup F, has been found in Mongols [19], Kazakhs, Kyrgyz, and Uighurs [12]. Yakuts (6.3%) also proved to possess the mtDNA haplotypes of this group. In the Yakut mitochondrial gene pool, haplogroup F is represented by two subclusters F1b and F2a. The former (Fig. 2) is most common in Central Asia, Mongolia, Korea, and Japan [20]. Subcluster F2a lacks specificity to a particular geographic region and occurs at a low frequency in numerous Asian populations.

South Asian haplogroup B, which is similar in distribution to haplogroup F, occurred at an extremely low (0.5%) frequency in Yakuts.

A low (1.6%) frequency was also observed for haplogroup Y, which has recently been characterized [13] and is thought to originate from the Far East.

**Table 3.** Haplogroup frequency distribution in the gene pools of Turkic ethnic groups and North-East Asian indigenous populations

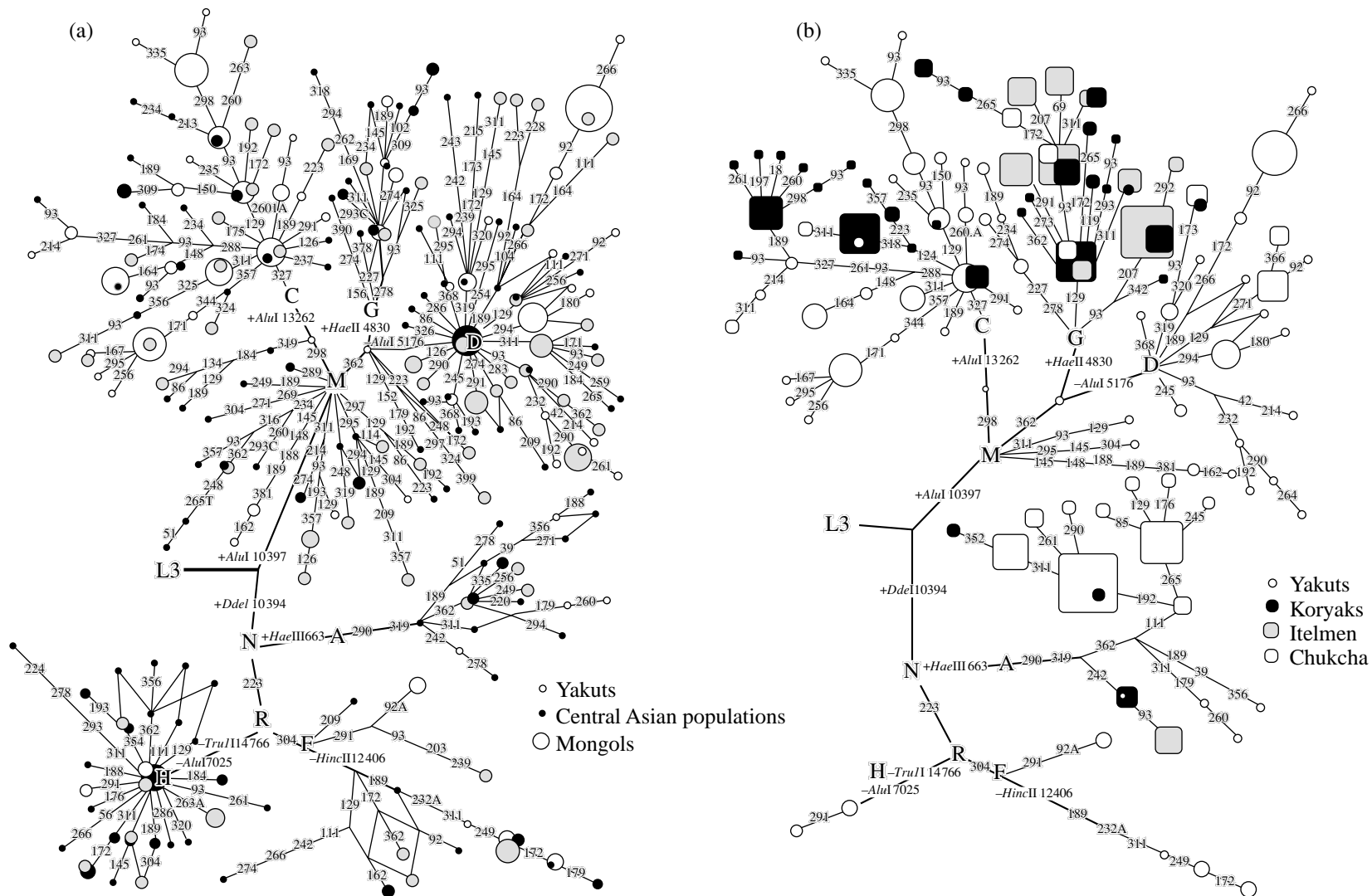
Population	<i>n</i>	Haplogroup frequency, %											
		A	B	C	D	G	F	M*	J	T	U	H	Others
Yakuts	191	2.1	0.5	44.0	30.4	4.2	6.3	2.6	1.1	1.1	1.1	2.6	4.0
Turkic ethnic groups													
Chuvash	55	1.8	0	1.8	3.6	0	0	1.8	5.5	3.7	36.4	25.5	19.9
Tatars	174	2.3	0	1.7	2.9	1.2	0	2.3	8.1	8.1	24.7	31.6	17.1
Bashkirs	211	4.3	0	12.8	8.1	4.7	6.2	1.0	3.3	5.2	27.5	14.2	12.7
Uighurs [12]	55	7.3	7.3	1.8	16.4	0	7.3	7.3	0	1.8	16.4	20.0	14.4
Kazakhs [12]	52	9.6	5.8	7.7	19.2	5.8	1.9	5.8	0	7.7	5.7	15.4	15.4
Kyrgyz [12]	92	3.3	6.5	14.1	19.6	7.6	3.3	6.5	5.4	3.3	3.3	18.5	8.6
Altai-kizhi [17]	92	3.3	3.3	30.4	9.8	4.4	5.4	9.8	5.4	0	5.4	5.4	17.4
Shorians [17]	42	0	2.4	7.1	9.5	0	43.0	2.4	11.9	0	0	21.4	2.3
Khakassians [17]	54	3.7	5.6	35.2	9.3	0	22.0	0	1.9	1.9	11.1	3.7	5.6
Soyots [17]	34	8.8	2.9	17.6	50.0	0	0	0	0	0	5.9	0	14.8
Tuvinians [21]	36	5.6	14.0	36.1	16.7	5.6	8.3	0	0	0	2.8	2.8	8.1
Tuvinians [16]	458	3.1	3.7	48.9	9.9	nd	nd	nd	nd	nd	nd	nd	nd
North-East Asian populations													
Koryaks [13]	155	5.2	0	36.1	1.3	41.9	0	0	0	0	0	0	15.5
Itelmen [13]	47	6.4	0	14.9	0	68.1	0	0	0	0	0	0	10.6
Chukcha [14]	66	68.2	0	10.6	12.1	9.1	0	0	0	0	0	0	0
Eskimo [14]	79	77.2	0	2.5	20.3	0	0	0	0	0	0	0	0
Evenks [15]	51	3.9	0	84.3	9.8	0	2.0	0	0	0	0	0	0
Evens [4]	65	4.6	0	26.2	15.4	0	1.5	0	0	0	0	0	52.3
Mongolia													
Mongols [19]	103	3.9	9.7	14.6	30.1	2.9	5.8	11.7	0	1.0	3.9	7.8	8.6

Note: Cases when a haplogroup has not been determined (nd) are indicated. Shaded are populations with mtDNA haplotypes established by a set of HVSI mutations without performing RFLP analysis.

A relatively broad spectrum of Caucasian haplogroups (H, HV1, J, T, U, W) was found in Yakuts. Yet these haplogroups each occurred at a low (1–2.6%) frequency, which was maximal in the case of cluster H.

Thus, the mitochondrial gene pool of Yakuts is diverse and has a highly specific haplogroup spectrum. Its peculiar feature is a great prevalence of haplogroups C and D (total frequency 74%). In mtDNA haplotype frequencies, Yakuts strikingly differ from the Turkic populations of the Volga–Ural region, Mongols, and the indigenous populations of Chukotka and Kamchatka. In high frequency of haplogroup C, Yakuts are similar to Evens and Tuvinians; yet additional data on HVSI polymorphism are necessary for elucidating their phylogenetic relationships. The mtDNA haplotypes characteristic of the populations living to the south of Yakuts testify to the southern contribution to the Yakut gene pool.

To assess the genetic relationships of Yakuts with Mongols and ethnic groups of Central Asia, we used phylogenetic analysis of their mtDNA haplotypes. A phylogenetic tree of mtDNA types of Yakuts, Mongols, and the pooled Central Asian population (Kazakhs, Kyrgyz, and Uighurs) is shown in Fig. 3a. Branches of the tree grow away from a trunk common for various Asian populations. Of all mtDNA haplogroups found in Yakuts, those occurring at a frequency less than 2% are not indicated in Fig. 3. Haplogroup C includes seven subclusters, which diverged from the major HVSI motif 16,223-16,298-16,327 as additional mutations accumulated in the course of evolution. Two of the subclusters proved to be specific for Yakuts. Of these, one has insertion of A in position 16,260 and the other, transition in position 16,291. The other subclusters of haplogroup C are common for Yakuts, Mongols, and Central Asian ethnic groups. In haplogroup D, most mtDNA haplotypes observed in Yakuts cluster with those characteristic of Mongols



**Fig. 3.** Phylogenetic trees of mtDNA haplotypes found in (a) Yakuts, Mongols, and the pooled sample of Central Asian populations (Kazakhs, Kyrgyz, Uighurs) or (b) Yakuts, Koryaks, Itelmen, and Chukcha. Haplotypes are shown with circles (Yakuts, Central Asian populations, Mongols) or squares (Paleoasian ethnic groups), with the area reflecting the haplotype frequency.



**Table 4.** Common mtDNA haplotypes in Yakuts, Central Asian populations, Mongols, and Paleoasian ethnic groups

Haplo-group	no.	Haplotype	Yakuts	Kazakhs [12, 22]	Kyrgyz [12]	Uighurs [12, 22]	Mongols [19]	Chukcha [14]	Eskimo [14]	Koryaks [13]	Itelmen [13]
			191	82	92	100	103	65	77	147	46
A	1	223, 242, 290, 319	1							4	
B	2	86, 136, 189, 217	1				2				
C	3	129, 150, 223, 298, 327	2								
	4	129, 223, 298, 327	6		1	1	1			1	
	5	148, 164, 223, 288, 298, 327	9	1							
	6	148, 223, 288, 298, 327	2		2						
	7	167, 171, 223, 298, 327, 344, 357	1				1				
	8	171, 223, 298, 327, 344, 357	12	1			1				
	9	189, 223, 298, 327	1								
	10	223, 298, 311, 327	8				1				
	11	223, 298, 327	10	1	1		1			6	
	12	223, 291, 298, 327	1								
	13	93, 129, 223, 298, 327	6	2		1					
D	14	223, 245, 362	2			1					
	15	223, 319, 362	4	1							
	16	223, 362, 368	1		2						
	17	92, 172, 189, 223, 266, 362	23				1				
	18	93, 223, 232, 290, 362	1				4				
F	19	189, 232A, 249, 304, 311	4	2		1	3				
	20	172, 189, 232A, 249, 304, 311	4			1					
G	21	223, 227, 278, 362	3		2		1				
	22	223, 227, 234, 278, 362	1	1							
H	23	CRS	3	4	5	3	1				
	24	223, 292	3	1		3					
Y	25	126, 231, 266	2	1							

and the pooled Central Asian sample. The only exception is a branch with nucleotide substitution in position 16,294. Similar results were obtained with other haplogroups, which are represented by a few haplotypes in the Yakut mitochondrial gene pool. This structure of the tree suggests a common genetic substrate, which was formed before the ethnic groups separated. Another evidence for this assumption is that the ethnic groups share many mtDNA haplotypes (Table 4). Of the 67 mtDNA haplotypes observed in Yakuts, 16 are present in the mitochondrial gene pool of the Central Asian population; their total frequency in Yakuts is 37.7%. Mongols and Yakuts share 11 mtDNA haplotypes, the total frequency of which is 37.7% in the latter. In total, 55.5% (21) of the Yakut mtDNA haplotypes have been found in the gene pools of the Central Asian and Mongol populations, which

agrees with the hypothesis of the southern origin of Yakuts.

Comparison of the mitochondrial gene pool for Yakuts and modern Paleoasian ethnic groups (Chukcha, Itelmen, Koryaks) revealed three (8.9%) haplotypes common for Yakuts and Koryaks. None of the Chukcha or Itelmen mtDNA haplotypes was found in Yakuts. On a phylogenetic tree, Paleoasian mtDNA haplotype cluster separately to form Paleoasian-specific branches (Fig. 3b). The branches developed and diverged in isolation, having virtually no overlap with the mtDNA haplotypes of Yakuts, Mongols, or Central Asian populations. Thus, our results are contradictory to the hypothesis of a substantial Paleoasian contribution to the modern Yakut gene pool. To clarify this issue, it is necessary to analyze the mtDNA gene pool in Yukaghirs.

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