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Ethno-Territorial Groups of the Yakuts: Genetic Structure Characteristics

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ABSTRACT

This paper presents the characteristics of the gene pool of the three Yakuts ethno-territorial groups (Central, Vilui and Northern) through the lines of mitochondrial DNA and Y-chromosome. Data for study was collected in expeditions carried by Yakut Research Center of Complex Medical Problems, Siberian Branch of Russian Academy of Medical Sciences, during 2002-2004. The population sample included healthy unrelated individuals whose ethnicity was considered mainly until the third generation. The results mainly correspond with the historians' opinion of the close relationship between Vilyuy and Central Yakuts, and Northern Sakha with the immigrants from Central Yakutia. Special characteristics of different ethnic geographical groups of the Yakuts can be observed through Y-chromosome.

Keywords: mitochondrial DNA, Y-chromosome, ethno-territorial groups, Yakuts.

INTRODUCTION

A considerable number of studies on genetic history of the Yakuts were published over the past decade [1,8,10,12-15,17-19]. Geneticists gave close attention to the history of Yakut ethnic group due to special characteristics of the male population's gene pool which had been firstly mentioned by Tatiana Zerjal [16]. Most of the Sakha males (over 80%) are descendants of one ancestor with N1c Y-chromosome, which is quite uncommon for such a numerous ethnic groups [8,10,12,14,16,17]. Extremely low diversity of the Yakuts' male lineages is balanced by heterogeneity of female gene pool, although the ancestor effect is still observed - a fifth part of the Sakha women comes from one ancestor with D5a2a2 mitochondrial lineage [1,14,17-19]. According to our research diversification of N1c-subcluster which are specific for the Yakuts began about 1600 years ago, followed by the expansion about 900 years ago [14]. The first date corresponds to the time of separation of the Yakut language from the ancient Turkic languages [5], and the second date coincides with supposed time of migration of the last and the most numerous group of Turkic ancestors of the Yakuts to the Middle Lena basin [4,6]. The Sakha people gene pool is mainly represented by genes of Asian origin (> 90%). The Caucasoid component is less than 10%: some part of these lineages was introduced by Russian-speaking population since the XVII century, the other part was brought from the Middle East through the steppe zone of Eurasia, Altai and South Siberia by the ancestors of Yakuts and Evenks [12,14]. According to genetic characteristics (mtDNA and autosomal loci testing) Yakuts are closest to Evenks [12,14,17], and then, according to the level of genetic proximity - to the peoples inhabiting southern areas – Buryats, Altaians, Khakassians, Tuvinians, Mongols [14]. Currently we can definitely say that the Yakuts is one of the most genetically studied ethnic group in the world, but sub-ethnic structure characteristics have not been sufficiently described yet.

The aim of the work is to define genetic characteristics of specific ethno-territorial groups of the Yakuts (Central, Northern and Vilyuy Yakuts).

Material and Methods: Data for study was collected in expeditions carried by Yakut Research Center of Complex Medical Problems, Siberian Branch of Russian Academy of Medical Sciences, during 2002-2004. The population sample included healthy unrelated individuals whose ethnicity was considered mainly until the third generation: Central Yakuts of Amginsky, Megino-Kangalassky, Namsky, Tattinsky, Ust-Aldansky, Khangalassky, Churapchinsky districts; Vilyuy Yakuts of Verkhnevilyuisky, Vilyuysky, Nyurbinsky, Suntarsky districts; Northern Yakuts of Verkhnekolymsky, Verkhoyansky, Zhigansky, Momsky, Srednekolymsky districts. MtDNA haplotypes were determined by sequencing of hypervariable segment I (HVSI) (16024-16390) and analysis of 95 sites of mtDNA coding region (n = 423). Y-chromosome haplotypes were identified by analysis of 28 diallel loci and 6 microsatellite loci of the nonrecombining region (n = 215). We used mtDNA haplogroups nomenclature according to http://www.phylotree.org/, and Y-chromosome haplogroups classification according to http://www.isogg.org/tree/. Calculations of genetic diversity (H) and genetic differentiation (Fst) were performed with ARLEQUIN software package, version 3.01. The analysis of genetic relationships between populations using principal component analysis was made through POPSTR program kindly provided by H.Harpending (Estonian Biocentre).

Results and Discussion

Table 1 shows the frequencies of mitochondrial DNA and Y-chromosome haplogroups in three ethno-territorial groups – Central, Northern and Vilyuy Yakuts. Statistically significant differences were detected between Northern and Vilyuy Yakuts (in Y-chromosome N1c haplogroup), between Northern and the other two groups (in mtDNA D5a2a2 haplogroup). Statistically significant differences in other haplogroups frequencies between populations have not been identified. Figure 1 shows European and Asian lineages ratio. European component is mainly represented in Vilyuy Yakuts (16% of mtDNA lineages) and Central Yakuts (11% of Y-chromosome lineages). The differences between populations mainly represented by Y-chromosome (4.1%) and less by mtDNA (0.5%). There are significant differences in genetic diversity of the male gene pool of different groups (Table 2). Analysis of genetic relationship shows the close genetic relationship of Central and Vilyuy Yakuts and the remoteness of Northern Yakuts (Fig. 2).

The Central Yakuts represent the core of the Yakut ethnic group and refer their ancestors to the sons of the legendary forefathers Elley and Omogoy. Such Yakut groups as the Khangalastsys, the Megintsys, the Baturustsys, the Borogontsys, the Namcys descended from Elley and the Bayagantaytsys are descendants of Omogoy. Genetic characteristics of the Yakut ethnic group described in the introduction are fully applicable to Central Yakuts. 86% of male natives of the central districts have one ancestor with N1c-chromosome. It is interesting that in contrast to other populations of Yakutia (Vilyuy and Northern Yakuts, Evenks, Evens and Yukagirs) phylogenetically older N1c-lineages have not been detected in the gene pool of the Yakuts of Leno-Amginskoe interstream area [14]. This is also confirmed by DNA analysis of skeletal remains from ancient burials in Tattinsky, Churapchinsky and Khangalassky districts [15]. This fact points to isolation of the Middle Lena Yakuts for a long period of time. The frequency of N1b haplogroup which is peculiar to the peoples of Urals language family is 2.2%. The presence of rare C3d haplogroup (1.1%) indicates close genetic linkages between the Yakuts and the peoples of South Siberia and Mongolia: this haplogroup was found in Buryats, Teleuts, Tuvinians, Soyots, Mongols, Hamnigans [20], and notably that its frequency reaches 29% in the Buryats [2]. C3c Y-chromosome haplogroup which is peculiar to the Tungus ethnic groups was not detected in the examined sample. The independent research conducted upon another samples estimated no more than 2% frequency of this haplogroup in Central Yakuts [8, 17]. The Caucasoid component is represented by clusters I1, R1a1a7, R1b1b2 which are specific to Europeans, and R1a1 *- lineages which are also found among the peoples of Southern Siberia.

The Vilyuy Yakuts have low diversity of the male gene pool. At the same time 90% of Y-chromosome lineages coincide with the lineages of Central Yakuts [12], which is agreed upon by the opinion of historians that the origin of the Vilyuy Sakha is closely linked with the Yakuts of central districts. According to the archives, the population of lower Vilyuy district was only a few hundred people in 1639, the number of immigrants from central districts increased only at the end of the XVII century [3, 7]. At the same time it should be noted that archaeologists found and studied settlements of cattle-breeders of kulun-atakhskaya culture of the XIV-XVI centuries on the territory of present Vilyuy district (unpublished data). Apparently the Yakuts had mastered not only the estuary part of the Vilyuy as it was previously considered, but much larger areas of the Vilyuy basin in its lower reaches by the arrival of the Russians in the 30s of the XVII century. According to G.V.Ksenofontov Vilyuy district was originally inhabited by "the Yakut reindeer herding people of mixed ethnic origin" who were later forced out to the north by the first Yakut cattle-breeders migrated from Verkhnelensky region [4]. According to the Vilyuy Yakuts legend “the Yakut indigenous population of Vilyuy area was formed not due to the russian refugees but due to refugees of the period of legendary Yakut king Tygyn" [4]. Y-chromosome C3c-lineage in the male gene pool of the Vilyuy people indicates the presence of Tungus component (3.4%). Indeed, historians have noted that the Vilyuy Yakuts included representatives of Sologon, Yugyuleet, Nyurbachaan clans who are descendants of such Tungus clans as Shelogon (Sologon), Fuglyad (Ugulyat) and Nyurmagat (Nyurbachan) of the XVII century [3,11]. The Vilyuy people Caucasoid component by Y-chromosome is only 3.4% (haplogroups I and R1a *), whereas it reaches 16% by mtDNA (haplogrous H, HV1, T, J, U, W).

The Northern Yakuts are characterized by high diversity of male gene pool lineages. It was determined that the Northern Yakuts have higher frequencies of haplogroups specific to the ethnic minorities of the North-East Eurasia (haplogroup G1b of mtDNA, haplogroups C3*, C3c of Y-chromosome). These data indicate a higher degree of miscegenation of Northern Yakuts with Evenks, Evens and Yukagirs. Frequency of N1c Y-chromosome haplogroup and D5a2a2 mtDNA peculiar to the Yakuts in general are lowered in the northern ethno-territorial group. The Northern Yakuts as well as Vilyuy Yakuts have phylogenetically older N1c-lineages in their gene pool [12,14]. The presence of N1b, C3d, R1a1 * haplogroups indicates a direct genetic linkages between Central and Northern Yakuts. According to historians, most of the northern Sakha descended from immigrants from Central Yakutia and they mainly include the same clans. The upper and the middle Jana was inhabited by the Yakuts long before the Russians’ arrival [3, 4, 7]. The territory of Verkhoyanskoe wintering was inhabited by the following Yakut clans in the 40s of the XVII century: the Duhaal (Yusaltsy), the Horo, the Bidy, the Kyure, the Enge, the Elget. Yasachnaya book dated 1640 mentioned the Betyuntsys and the book dated 1642 mentioned the Yakuts of Namskaya territory. The following years brought more newcomers from various Yakut districts to Verkhoyanskoe wintering [7]. Representatives of Verkhoyansk clans (the Bidys, the Enge, the Horo, the Tumat) and the central Yakuts began to move to the territory of future Abyisky and Momsky districts since the XVIII century. Interaction between Yakuts and Evens and Yukagirs contributed to diversity of dialect and customs of these northern districts. Kolymsky district comprised 11 Yakut communities in 1810: Verhnekilymsky district included Myatyuzhsky and Baydunsky communities; Srednekolymsky district included Baydunsky, Borogonsky, two Kangalassky, two Myatyuzhsky and Eginsky communities; Nizhnekolymsky district included Myatyuzhsky community [9].

Thus, the results mainly correspond with the historians' opinion of the close relationship between Vilyuy and Central Yakuts, and Northern Sakha with the immigrants from Central Yakutia. Special characteristics of different ethnic geographical groups of the Yakuts can be observed through Y-chromosome.

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Table 1

Frequencies of mtDNA and Y-chromosomal haplogroups in Central, Vilyuy, Northern Yakuts

MtDNA				
Haplogroups	CY (n=164)	VY (n=111)	NY (n=148)	SUM (n=423)
A	2,4 (1,0-6,1)	3,6 (1,5-8,9)	0 (0-2,4)	1,9
B	0,6 (0,1-3,3)	0 (0-3,2)	2,7 (1,1-6,7)	1,2
C4	33,5 (26,8-41,1)	32,4(24,4-41,6)	32,4 (25,4-40,4)	32,8
C5	11,6 (7,6-17,4)	3,6 (1,5-8,9)	8,1 (4,7-13,6)	8,3
C7	0,6 (0,1-3,3)	0 (0-3,2)	0 (0-2,4)	0,2
D4	15,9 (11,1-	11,7 (7,0-19,0)	17,6 (12,3-	15,4

	22,2)		24,5)	
D5a2a2	17,1 (12,1-23,6)	18 (12,0-26,2)	6,1 (3,3-11,2)	13,5
D5b1	0 (0-2,2)	0 (0-3,2)	2,0 (0,7-5,8)	0,7
F	3,7 (1,7-7,7)	5,4 (2,5-11,3)	4,7 (2,3-9,4)	4,5
G1b	0 (0-2,2)	0,9 (0,2-4,9)	1,4 (0,4-4,8)	0,7
G2a	4,9 (2,5-9,3)	2,7 (1,0-7,6)	5,4 (2,8-10,3)	4,5
M7	0 (0-2,2)	0,9 (0,2-4,9)	1,4 (0,4-4,8)	0,7
M13	1,8 (0,7-5,2)	1,8 (0,6-6,3)	6,8 (3,7-12,0)	3,5
Y	1,2 (0,4-4,3)	2,7 (1,0-7,6)	0 (0-2,4)	1,2
Z	0 (0-2,2)	0 (0-3,2)	2,7 (1,1-6,7)	0,9
R1b	0 (0-2,2)	0 (0-3,2)	1,4 (0,4-4,8)	0,5
H	3,7 (1,7-7,7)	6,3 (3,1-12,5)	1,4 (0,4-4,8)	3,6
HV1	0 (0-2,2)	1,8 (0,6-6,3)	2,0 (0,7-5,8)	1,2
T	0,6 (0,1-3,3)	3,6 (1,5-8,9)	0 (0-2,4)	1,2
J	0,6 (0,1-3,3)	2,7 (1,0-7,6)	1,4 (0,4-4,8)	1,4
U	0,6 (0,1-3,3)	0,9 (0,2-4,9)	0,7 (0,2-3,7)	0,7
W	1,2 (0,4-4,3)	0,9 (0,2-4,9)	2,0 (0,7-5,8)	1,4
Y-хромосома				
Haplogroups	ЦЯ (n=92)	ВЯ (n=58)	СЯ (n=66)	Суммарно (n=216)
N1b	2,2 (0,7-7,6)	0 (0-6,1)	10,6 (5,3-20,3)	4,2
N1c	85,9 (77,3-91,5)	93,1 (83,5-97,2)	71,2 (59,3-80,7)	83,3
C3*	0 (0-3,9)	0 (0-6,1)	3,0 (0,9-10,4)	0,9
C3c	0 (0-3,9)	3,4 (1,1-11,7)	6,1 (2,5-14,6)	2,8
C3d	1,1 (0,3-5,8)	0 (0-6,1)	4,5 (1,7-12,5)	1,8
I1	2,2 (0,7-7,6)	1,7 (0,4-9,1)	0 (0-5,4)	1,4
R1a1*	4,3 (1,8-10,6)	1,7 (0,4-9,1)	4,5 (1,7-12,5)	3,7
R1a1a7	2,2 (0,7-7,6)	0 (0-6,1)	0 (0-5,4)	0,9
R1b1b2	2,2 (0,7-7,6)	0 (0-6,1)	0 (0-5,4)	0,9

Table 2

Indexes of genetic differentiation (Fst) and genetic diversity (H) of three populations of Yakuts by mtDNA and Y-chromosomal haplogroups

Population	Fst	H
mtDNA		
CY (n=164)	0.0052	0.82±0.02
VY (n=111)		0.84±0.02
NY (n=148)		0.85±0.02
Y chromosome		
CY (n=92)	0.0408	0.26±0.06
VY (n=58)		0.13±0.06
NY (n=66)		0.48±0.07