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S.A. Fedorova

ORIGIN OF THE YAKUTS: MOLECULAR-GENETIC RECONSTRUCTIONS IN COMPARISON WITH THE HYPOTHESES OF HISTORIANS

ABSTRACT

This review presents the results of studies of the genetic history of the Yakut (Sakha) people conducted by researchers of the Yakut Scientific Centre of Complex Medical Problems and M. K. Ammosov North-Eastern Federal University (Yakutsk, Russia) in collaboration with the researchers of the Estonian Biocentre (Tartu, Estonia) and the Institute of Biochemistry and Genetics (Ufa Scientific Centre of RAS, Ufa, Russia), over the period 2002-2016. The obtained results are compared and contrasted with the reconstructions proposed by other groups of geneticists and with historical and archaeological hypotheses on the ethnogenesis of the Yakut (Sakha) people.

Keywords: Yakut (Sakha) people, genes, ethnogenesis, mitochondrial DNA, Y-chromosome.

INTRODUCTION

It is generally believed that the formation of the Yakut (Sakha) ethnic group in the territory of Yakutia occurred as a result of the gradual mixing of Turkic-speaking cattle-breeding tribes migrated from the south to the middle Lena River with local tribes over a long period of time. During the Soviet period, archaeological surveys were conducted in the Baikal region and Yakutia to study the earliest stages of the history of the Yakut (Sakha) people. Most modern scholars see the relation of the Yakuts to the Kurumchi culture of the Baikal region (6th to 10th centuries) [7,16,23,29]. Traditionally, the tribes of the Baikal Kurykans are considered to be the immediate ancestors of the Yakuts; apparently, they represented a union of three Turkic tribes, since they are referred to as *Uch-Kurykan* – 'three kurykans' in ancient sources [23]. Kurykans as a separate ethnic group appeared as a result of the assimilation of the aboriginal population and some Mongol-speaking groups by Turkic-speaking Teles tribes who moved to the Baikal region in the 5th-6th centuries [7].

Historians and archaeologists differ significantly in their opinions on the time when the ancestors of the Yakut people migrated to the north. Outstanding Yakut ethnographer G.V. Ksenofontov believed that the Yakuts are an ethnic group of mixed origin, which included three waves of Turkic-speaking immigrants. In his opinion, the first Yakuts began settling in the Vilyui River basin at the end of the 1st century AD; the second wave of the Yakuts migrated to the middle Lena and Vilyui from the Baikal region in the 6th-7th centuries AD; and finally, the last stage of the Yakut settlement occurred in the 11th-12th centuries, triggered by the strengthening of Mongol tribes and the complete displacement of the Yakuts' ancestors from the original place of living [20]. A.P. Okladnikov assumed two "decisive stages" in the settlement of the Yakuts' ancestors in the north. The first, in his opinion, began in the early Iron Age and ended in the 10th-11th centuries; the second stage dates back to the 15th-16th centuries [23]. According to archaeologist I.V. Konstantinov, the migration of the Yakuts' ancestors from the Baikal region occurred in the 15th century, as a compact group, which represented a fully developed ethnic community [19]. More recent researchers believe that the mass migration of the Yakuts' ancestors to the north occurred at the beginning of the 2nd millennium AD and is characterized by the appearance of the Small Houses Culture in Yakutia in the 13th century, which was later replaced by the Kulun-Atakh cattle-breeding culture. [16] On the other hand, archaeological findings (specific arrowheads, details of the bow, armor plates, cult pendant amulets, bull bones) and the appearance of runic inscriptions on the Lena petroglyphs testify to the penetration into Yakutia of, first, Hunn-Xianbi, (in the 3d - first half of the 4th centuries AD), and later, from the 5th-6th centuries, Turkic-Mongolian groups [3].

The ratio of different-origin elements in the Yakut (Sakha) gene pool, their composition and the process of the traditional culture formation still require further research. Regarding the ethnic background of the local tribes who contributed to the formation of the Yakut ethnic group, historians have two points of view. Most researchers believe that these were the Tungusic tribes [16,20,23], although the small number (only about 4%) of Tungus words in the Yakut language testifies to the contrary. According to the anthroponymic data, out of 1,083 Yakut pagan names, there are 47% of Turkic, 37% of Mongolian, 6% of Turkic-Mongolian, and 10% of Evenki origin [24]. Thus, the linguistic data indicate a weak interaction between the Yakut and Tungusic languages.

By the opinion of Prof.A. N. Alekseev, the active settlement of the Tungus in North Asia, including Yakutia, began only at the end of the 1st and the beginning of the 2nd millennium AD, and the important contribution to the formation of the Yakut (Sakha) gene pool was made by the ancient non-Tungusic population of Yakutia, most likely by proto-Yukaghirs, proto-Samodeic or other ancient tribes whose ethnonyms were not preserved [3]. According to a legend, when Tungus and Yakut people came to the territory of Yakutia, they met local tribes - Sortols, Dirikineis, Khara Sagyls. The legends mention various ethnic groups who allegedly inhabited the territory of Yakutia, including Tumats and even the Kyrgyz [8], which indicates a sufficient diversity of the local and migrant populations of the time. A. N. Alekseev proposes that the local tribes inhabiting the middle Lena River since the ancient times and 'turkized' after the migration of small groups of southern cattle-breeders formed a significant layer of proto-Yakuts: "It was not newcomers who reproduced; the number of people who spoke their language grew ... the entire Eurasia experienced such turkization; that is why the Turkic-speaking ethnic groups are now so numerous nowadays ... "[3].

Since the 1990s, to answer the questions about the origins of individual ethnic groups, the molecular genetics methods have been widely used in addition to the generally accepted ethnographic, archaeological, and linguistic approaches. There appeared a new scientific branch - Genetic Archaeology, which allows modelling of past events basing on the study of human genome in modern populations. The intensive studies of the genetic structure of the modern Yakut (Sakha) population and the genetic relationships of the Yakuts with other peoples of Siberia were undertaken in the 2000s by three groups of researchers - scientists of the Research Institute of Medical Genetics, Siberian Branch of the Russian Academy of Medical Sciences (Tomsk, Russia) [26,28]; researchers of the Max Planck Institute for Evolutionary Anthropology (Leipzig, Germany) and the Institute of Health, Academy of Sciences of the Sakha Republic (Yakutia) (Yakutsk, Russia) [6,9,18] and scientists of the Yakutsk Scientific Centre of Complex Medical Problems, M. K. Ammosov NEFU (Yakutsk), in cooperation with colleagues from the Institute of Biochemistry and Genetics of the Ufa Scientific Center, Russian Academy of Sciences (Ufa, Russia) and the Estonian Biocenter (Tartu, Estonia) [1,2,4,5,10-13,15,17,27] These studies were carried out mainly using two complementary genetic systems - Y-chromosome and mtDNA, which allow describing the features of the male and female gene pool and autosomal markers panels. In recent years, the development of new molecular genetic technologies has enabled the whole genome analysis.

This review presents the results of our studies of the genetic history of the Yakut (Sakha) people in comparison and contrast with the reconstructions proposed by other groups of geneticists and with the hypothesis about the ethnogenesis of the Yakut (Sakha) people, proposed earlier by historians and archaeologists.

The origins of the Yakut (Sakha) people in the light of genetic archaeology data

The analysis of the lineages of Central, Vilyui and Northern Yakuts from 16 regions of the Sakha Republic (Yakutia) (n=215) showed that the vast majority of male Sakha (over 80%) are descendants of one male founder with a Y-chromosome lineage belonging to haplogroup N3 [5,11-13,15]. Our data confirmed the results of studies by other groups of geneticists on the analysis of the Yakut lineages of Ust-Aldan region (n=109) [26,28] and eight central, Vilyui and northern regions of the SR (Y) (n=178) [18]. It was also found out that the extremely low diversity of male lineages in the Yakuts is compensated by the high diversity of the female gene pool lineages [5,10-13,15], which was later confirmed by studies of other authors [6,9,18].

On the Y-chromosome phylogenetic tree, the N3-lineages of the Yakuts are combined into one specific branch [1] In previous works, the structure of this branch was considered as "star-like", that is having one ancestral haplotype [18,26,28]. According to Kharkov et al., 2008, the generation time of specific N3-lineages in the Yakut population is 4.45 ± 1.96 thousand years; according to B. Pakendorf, 2006 - 880 ± 440 years. Unlike the other authors, we consider the Yakut branch in the structure of the N3-network of neighboring ethnic groups of Southern and Western Siberia, Chukotka and Kamchatka, as one containing two closely related dominant haplotypes (Fig.1) and, accordingly, undergone **to two successive expansions** [5] According to our estimates, the separation of N3-branch, specific of the Yakuts, of Y-chromosome tree and the first expansion began ~ in the 4th-5th centuries A [5]. After the separation of the Yakut branch ~ 1,600-1,700 years ago, a secondary expansion followed ~ 900 years ago. The first date corresponds to the time when the Yakut language started to separate from the ancient Turkic languages, according to G. G. Levin [21]; the second one coincides with the estimated time of migration of the last, most extensive wave of the Turkic-speaking ancestors of the Yakuts into the Middle Lena basin. The time of the secondary expansion of N3-lineages, according to our estimate, corresponds to the values proposed by B. Pakendorf. We assume that the Turkic-speaking ancestors of the Yakuts could have migrated to the north long before the rise of the Genghis Khan Empire. An indirect confirmation of this supposition can be the fact that the Yakuts do not have the so-called 'C3-lineage of Genghisides', widespread in the territories that were under the rule of the great Khan [5]. Apparently, in the ancestral tribe in the 4th-5th centuries the men of one kin were dominated, while the ancient Yakut population whose expansion began ~ 900 years ago should have carried the both dominant haplotypes.

What region did the Yakut (Sakha) N3-lineage appear in? The maximum frequency of the "Yakut" N3-lineage is characteristic only for Yakutia: from 70 to 90% in various ethnogeographical groups of the Yakuts, Dolgan (50%), Evenks (47%), and Evens (29%) [5,12,17]. Phylogenetic studies established that the "Yakut" lineage is not a derivative of the N3-lineages of the neighboring peoples - Mongols, Buryats, Chukchi, Eskimos, Koryaks, Nanais, Japanese and Han Chinese [2,17]; thus, the origin of this lineage, apparently, is not connected with the territories adjacent to Baikal from the east and south (Buryatia, Mongolia, the Amur River basin, China), either with the territory of ancient Beringia (Chukotka and Kamchatka). The N3-lineages of the Yakuts are also different from the N3-lineages of the peoples of the Volga-Ural region and Scandinavia. The appearance of the more ancient dominant "Yakut" haplotype (haplotype 1 in Fig.1) in Southern Siberia, in regions west of Baikal seems to be more likely, since its close phylogenetic derivatives are present in Tuvinians, Tofalars, and Soyots. The second dominant haplotype (haplotype 2 in Fig.1) and its derivatives are found only in the populations of Yakutia, respectively, its multiplication and secondary expansion occurred in the territory of Yakutia.

Researchers of the Institute of Medical Genetics (Tomsk) previously hypothesized on the autochthonous origin of the N3-Yakut lineages. Prof. V.A. Stepanov suggested that the male Yakut gene pool was formed on the basis of the local Evenk component, and the Turkic language was acquired as a result of the cultural dominance of the Turkic-speaking elite, which left no significant trace in the Y-chromosome pool [26]. Later, the authors expressed the opinion that these lineages were acquired by the Yakuts indirectly through the Evens from even more ancient aboriginal tribes that had formerly lived in the territory of modern Yakutia and were assimilated by the Tungus [28]. The authors explain an unusually high frequency of N3-lineages in the male Yakut gene pool (over 80% of the population as a whole), in contrast to the Evenks (25-33%), by a significant increase in the number of Yakuts in recent centuries, which led to a random sharp increase in the frequencies of individual lineages with the predominant founder haplotype in the population. Unlike this, we consider the emergence of a "Yakut" N3-lineage in Eastern Sayan region, rather than in the territory of modern Yakutia, since close STR-haplotypes are present among the ethnic groups living to the west of Baikal. However, in our view, the final answer to the question "where and when did the N3-lineage of the Yakuts originate?" could only be given in the future by DNA analysis of the ancient populations of Yakutia and Southern Siberia.

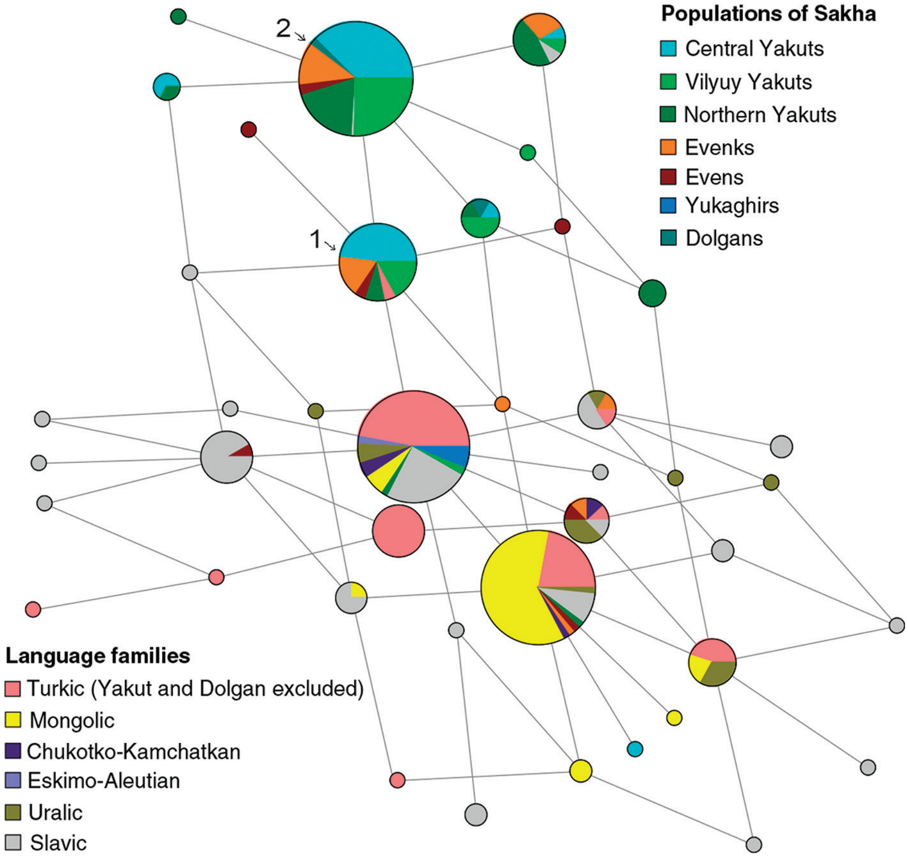

Fig.1. Phylogenetic network of N3-haplotypes of Y-chromosome of the ethnic groups in Yakutia and adjacent regions. [5] The circles indicate microsatellite haplotypes, the area of the circle and the sectors inside the circle is proportional to the haplotype frequency. The dominant "Yakut" haplotypes 1 and 2 are marked by the arrows.

What ethnic groups are the closest to the Yakut (Sakha people?

The study of the genetic relationships of the Yakuts with neighboring peoples showed a close genetic similarity of the Yakuts with the Evenks of Yakutia [5,12,13,15]. We propose that the close genetic relationship of the Yakuts to the Evenks of Yakutia is primarily due to the origin of these peoples from the common South Siberian genetic pool (and if the origin of the Yakuts is connected with the regions west of Lake Baikal, then the Tungus - most likely with the territories east of Lake Baikal), as well as the mixing of territorially close ethnic groups to Yakutia over a period of at least 900 years. Some ethnographic studies noted that Yakut men often and willingly married Evenk women, while Yakut women rarely married Evenks [25]. Most likely, these marriage traditions explain the high content of the common lineages in the female gene pool (50-65%) in different ethnogeographic groups of the Yakuts and Evenks [12] and the relatively low content of the N3-lineages in the male gene pool of the Evenks.

It is curious that we found the "Genghis Khan" haplotype in the Evenks of Yakutia; it occurs with high frequency among the ethnic groups that were under the power of Genghisides, which indicates a relatively recent male flow of genes from Mongols to Evenks [5]. The obtained genetic evidence supports the hypothesis of the relatively recent (in the beginning of the 2nd millennium AD) appearance of the Tungus in the territory of Yakutia., proposed by Prof.A. N. Alekseev [3]. The large-scale expansion of the Tungus and Turks through Siberia, which apparently occurred within the last 2,000 years, assimilated and/or displaced the ancient population of Yakutia to even more northern territories. Therefore, it is not surprising that in comparison with the Evenks of Yakutia, the peoples of the Arctic (Yukaghirs, Evens, Dolgans, and Nganasans) differ significantly from the Yakuts in the composition of the gene pool components and the content of specific mtDNA and Y-chromosome [5,12].

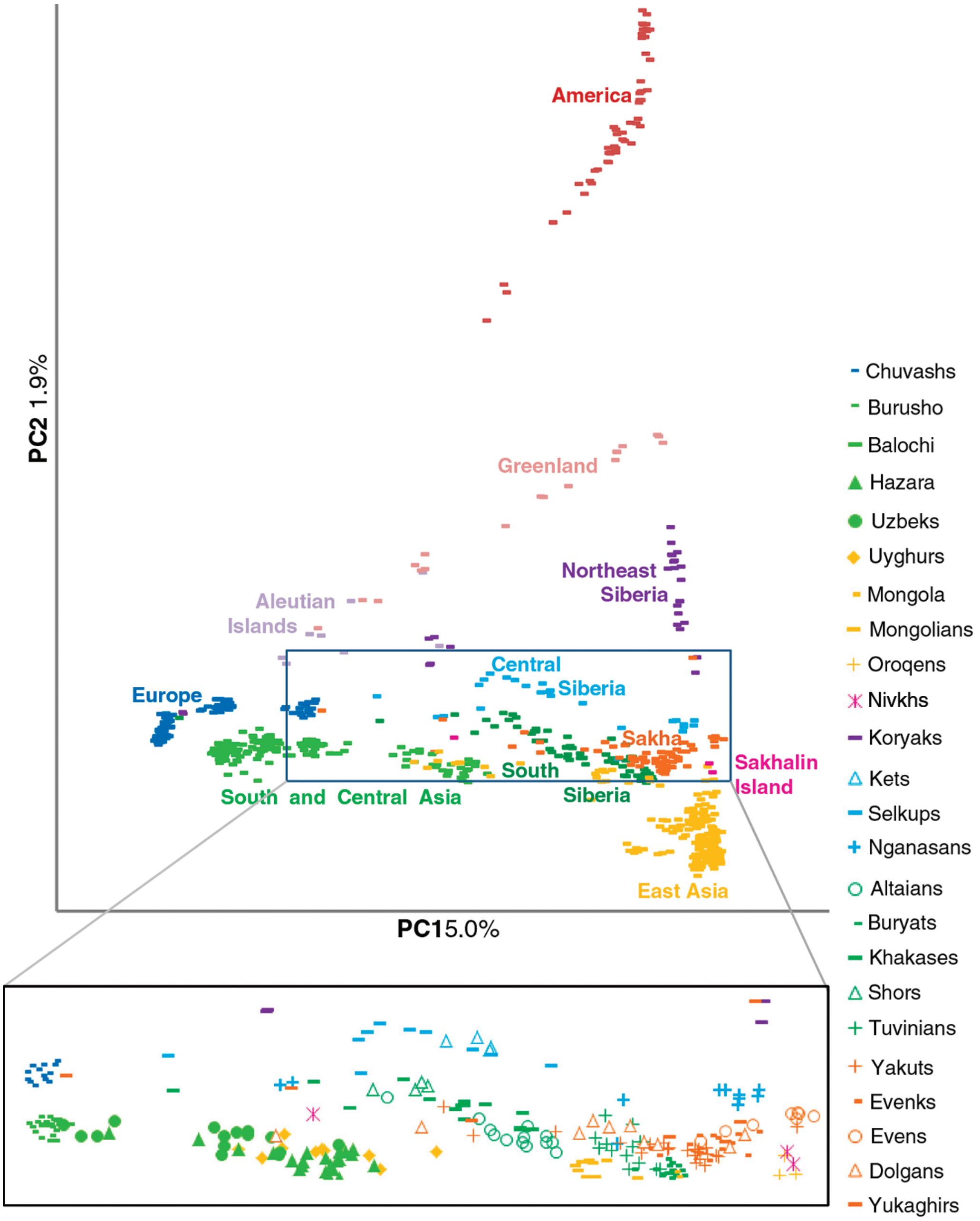

Fig.2. PC-map of the locations of populations in Yakutia among other populations in Eurasia and America, compiled with the use of 600,000 autosome SNP. [5]

Further, by the degree of genetic proximity and their genetic characteristics, the peoples of Southern Siberia - the Buryats, Tuvinians, Altaians, Mongols, Khakases - are closer to the Yakuts. Unlike the Yakuts, the Turkic-speaking peoples of Southern Siberia have a greater proportion of the European and South Asian components in their gene pool [5,27]. Even greater genetic distances separates the Yakuts from the peoples of western Siberia (Kets and Selkups), Southeast Asia (Han Chinese, Koreans, Japanese), Central Asia (Uzbeks, Uighurs), Chukotka and Kamchatka (Chukchi, Eskimos, Koryaks, Itelmen) (Fig. 2).

How large is the European component in the Yakut (Sakha) gene pool? How does the hypothesis of the Aryan origin of the Yakut (Sakha) people look in the light of the genetic archaeology data?

In the 1990s, the hypothesis about the "Aryan" origin of the Yakut (Sakha) people was brought about by the geneticist V. V. Fefelova on the basis of the analysis of two markers of the HLA system (HLA-A and HLA-B on the human 6th chromosome) was popular [14]. According to the results of immunogenetic studies, the Yakuts demonstrated a high frequency of the "Indo-European" gene HLA-A1 and haplotype HLA-A1, B17 was established, which was considered by the author of the hypothesis as the presence of a powerful ancient Caucasoid component in the Yakut gene pool, the content of which reaches 30%.

At the beginning of the 21st century, when first studying the female gene pool of the Vilyui Yakuts gene pool, indeed, the data were obtained on the high content of mtDNA lineages of European origin (17%), but the authors explained this fact by intensive processes of assimilation by the Russian-speaking population [22].

According to our data, the analysis of the mtDNA of 423 people from the Central, Vilyui and Northern ethnogeographical groups showed that the high content of the mother lineages of European origin is characteristic primarily of the Vilyui Yakuts (16%), for Central and Northern it accounts for 7%; thus, on average for the three ethnogeographic groups of Yakuts it makes 10%. The Caucasoid component of the Yakut gene pool is also low on paternal lineages - from 4% in the Vilyui Yakuts to 11% in Central Yakuts, with the average at 7% of the total pool [11,12]. It was found that the content of these lineages in the Yakut (Sakha) gene pool is explained not only by mixing with the Russian-speaking population who have been migrating to Eastern Siberia since the 17th century, but also by the presence of an ancient European component in the ancestral Yakut population, characteristic of all the Turkic-speaking peoples of Southern Siberia [5,12]. It is known that the formation of ancient Türkic groups equally involved both Caucasoid and Mongoloid populations. The origin of the ancient West-Eurasian lineages in the gene pool of the Yakut ethnos is apparently connected with the pre-ethnic stage of the formation of the Yakuts as a separate ethnic group - the Scythian-Siberian, subsequent Hunn-Sarmatian and ancient Turkic times. Some of these lineages originated in the Middle East, migrated along the Eurasian Steppe Corridor through Central Asia and Southern Siberia, and appeared in the territory of Yakutia with the Turkic-speaking ancestors of the Yakuts (Sakha) [5].

Thus, the genetic archeology data confirm the presence of the ancient Caucasoid component in the Yakut (Sakha) gene pool, which was proposed by Prof. V. V. Fefelova basing of the results of HLA system studies; however, we estimate the content of this component as being much lower at less than 10%, rather that 30%.

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