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Haplogroup R1a-M198 in Turkic-speaking populations of the North Caucasus

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Objective: to study the genetic structure and diversity of gene pools of populations of the North Caucasus based on the variability of the haplogroup R1a-M198 of the Y chromosome.

Material and methods. The analysis of the genetic diversity of the Caucasian populations was carried out according to the results of the variability of the haplogroup R1a-M198 of the Y chromosome.

Results. Based on the results of genotyping, it was revealed that the haplogroup R1a-Z2123 is the major haplo group in the Turkic-speaking populations of the Central and Western regions of the North Caucasus, while it turned out to be uncharacteristic for the Turkic-speaking populations of Dagestan and the Kuban Nogai. We conducted an analysis of the frequency distribution of the branches of the haplogroup R1a-M198 of the Y chromosome in the Balkarian population, taking into account their belonging to different subethnic groups (Baksans, Chegemians, Kholamets, Bezengi, Malkars). **Conclusion.** The subethnic groups of Bezengis and Kholamets are characterized by the lowest frequency of lines of the haplogroup R1a-M198, and in the subpopulation of cholama, only haplogroup R1a-Z2123 is detected.

Keywords: genetic structure, gene pool, haplogroup R1a-M198, turkic-speaking population, North Caucasus

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ctive development of new lands and the aggressive campaigns of the Turkic-speaking tribes led to the settlement of the vast territories of the Eurasian continent by the peoples of this language group. Representatives of the Turkic group of languages in the Central and Western Caucasus are populations of Balkarians and Karachais living in the mountains and foothills of the region. In the course of many territorial transformations that took place in the Russian Empire and in the former Union of Soviet Socialist Re-

publics (USSR), the single Karachay-Balkarian people (endo-ethnonym - taulu) was administratively divided into two entities. Currently, most Karachais and Balkars live compactly in the Karachay-Cherkess and Kabardino-Balkarian republics, which are part of the Russian Federation. Among the Balkars, 5 sub-ethnic groups are distinguished: Baksans, Chegemians, Kholamts, Bezengis and Malkars. In some early works, the population of various subpopulations of Balkars is referred to as peoples at all [1]. At different times, linguists distin-

guished up to 4 different dialects in the Balkar language [5-10]. According to the 2010 census, the number of Balkars in Russia is 112.9 thousand people, Karachais - 218.4 thousand people [11]. For the period between the censuses of 1897 and 2010 the number of Balkars and Karachais (in general) increased from 50 thousand to 331,327, i.e. more than 6 times. In general, the number of Balkars and Karachais in Russia and foreign countries totals about 460 thousand people [12]. As a result of greater interest on the part of historians in the problems of ethnogenesis of the Balkarians and Karachais. 2 conferences were devoted to this subject. The first one took place in 1959 in the city of Nalchik, with the participation of leading academic institutions of the USSR, where, comprehensively, with the involvement of specialists in the field of historiography, archeology and anthropology, the whole spectrum of the historical process of formation and development of these peoples was considered [14]. The second conference was held in 2014 at the Institute of Ethnology and Anthropology named after N.N. Miklouho-Maclay of Russian Academy of Sciences with the involvement of specialists in the field of human population genetics [15]. The results of these conferences testify in favor of the fact that various North Caucasian, Iranian-speaking and Turkic-speaking tribes played the main role in the ethnogenesis of these peoples [13, 14].

To date, a number of studies have been carried out on the anthropological characteristics of the Balkars and Karachaystsevs [15-17]. They studied a wide range of anthropological disciplines, such as: craniology (studying the variation in the shape of the skull), somatology (studying the anthropometric characteristics), odontology dentoalveolar (studying the system), dermato-glyphics (studying the pattern of the skin). As a result of a comprehensive study, conclusions were drawn about: the Caucasian physical type of the Balkars and Karachays, the indigenous origin of the Balkars and Karachays and their kinship with representatives of neighboring peoples [14-16].

To assess the genetic relationship of the studied populations with the neighboring peoples of the region, as well as to better understand the processes of ethnogenesis, we considered it necessary to conduct a detailed study of the Karachai population and sub-ethnic groups of the Balkars using the latest markers of the haplogroup R1a-M198 of the Y chromosome.

Objective: to study the genetic structure and diversity of the gene pools of the populations of the North Caucasus according to the results of the variability of the haplogroup R1a-M198 of the Y chromosome.

Materials and methods

The study used samples from 2002-2015 from 22 populations of the Caucasus from the "Collection of Human Biological Materials" Institute of Bioregulation and Gerontology Ufim Federal Research Center of the Russian Academy of Sciences, supported by the Program of Bioresource Collections Federal Agency of the Russian Federation, a total of 1942 samples belonging to populations of the North and South Caucasus. As a result of the questionnaire, the ethnicity of the subjects was established, indicating ancestors up to the third generation. All participants received informed consent to participate in the study.

DNA was isolated from peripheral blood phenol-chloroform bv the standard extraction method [18]. To determine the haplogroups of the Y chromosome, 13 markers of the non-recombining region of the Y chromosome were analyzed: M9, M198, PAGE07, Z282, Z93, Z95, M458, M558, M582, Z2125, Z2123, Z2122, M207. These polymorphisms were analyzed for the most part using appropriate restriction enzymes. In their absence, the analysis was carried out by sequencing. Sequencing was performed on an automated sequencer Applied Biosistems (ABI) 3730 XL DNA Analyzer or Applied Biosistems (ABI) 3500. The sequencing results were analyzed using ChromasPro 2.4.1 software and Sequencer 5.1 (GeneCode Corp).

Results and discussion

Genotyping data indicate that 7 out of 33 haplogroups found in the studied samples belong to the branch of one of the most widespread haplogroups in the world - R1a. More than 10% of men living in the territory from South Asia to Scandinavia belong to

this haplogroup. The distribution of R1a subhaplogroups in the world shows its clear division into two main branches: the European (R1a-Z282) and the Central and South Asian (R1a-Z93) [20]. We also studied additional markers within the haplogroup R1a, the distribution data of which were not previously published in the study of the genetic structure of the peoples of the world. In view of this, we activated samples from the genetic bank of the Institute of Bioregulation and Gerontology Ufim Federal Research Center of the Russian Academy of Sciences - 1942 sample from 22 populations of the North and South Caucasus. It was revealed that the dominant line of the haplogroup R1a-M198 of the Y chromosome in the populations of Karachais (30.1%) and Balkars (16.2%) is R1a-Z2123 (table 1). In other peoples of the region, this haplogroup is much less common, and maximum frequencies are observed among representatives of the Adyghe-Abkhaz language group: Circassians (7.9%), Abazin (7.9%), Q-Bardins (6.4%), Advghe people (4.5%) and Abkhazians (1.8%). Speaking about other Turkicspeaking peoples of the North Caucasus, this haplogroup has the maximum value among the Karanogais (3.9%), while in the Kumyks its frequency is 1.4%, and it was not found at all in the Kuban Nogai population. In other populations, the haplogroup R1a-Z2123 is found in isolated cases. In the sub-populations of the Balkars, it is distributed almost evenly, demonstrating the maximum value among the Chegemians (20.3%) and the minimum among the Kholamets (10.7%).

Of particular interest is the high frequency of the haplo group R1a-Z2123 in the Bashkir population, which reaches 44% in some ethno-geographical groups (our unpublished data). But the data obtained by sequencing the complete sequence of the Y chromosome in the Bashkir and Balkars attributed them to the various branches of this haplo group, combining, in turn, the Bashkir with a representative of the Jewish community from India [20]. Despite the poor knowledge of this marker in world populations and the lack of large-scale population studies on it, relying on data on

the frequency distribution of the ancestral haplogroup R1a-Z2125, which was found with high frequencies in populations of Kyrgyz and Uzbeks, Turks, Afghan Pashtuns (40%), and among other peoples of Afghanistan, and in some Iranian populations [19], we can assume that the presence of the haplogroup R1a-Z2123 in the populations of Karachais and Balkars South and Central Asian influence. On the other hand, analysis of the complete sequence of the Y-chromosome with R1a-Z2123 in the Balkar showed the presence of a separate deep branch [20], which indicates the earlier presence of this haplogroup in the Caucasus. In this regard, the data obtained as a result of the study of the remains of representatives of the Srub-Scythian archaeological cultures, which are direct descendants of the so-called Kurgan historical and archaeological community and the identification of East Eurasian haplogroups in their environment, are of particular interest. R1a (Z93, Z94, as well as Z2123) [21-25]. Considering the fact that the major haplogroup in the populations of Karachais, Balkarians, and Bashkirs living in the ancient distribution area of the Srub and Scythian cultures is haplogroup R1a-Z2123, the probable connection of these peoples with Balkars and the Karachais look logical. The opinion existing in historical literature about the ubiquitous Iranian language of the Scythians does not seem so correct, especially in the light of recent works showing the exceptional connection of the Eastern Scythians with Turkic-speaking peoples, especially those whose languages belong to the Kypchak group of the Altai language family [26].

At the same time, groups of western Scythians have much in common with populations of the Caucasus and Central Asia [26–33]. In populations of North and South Ossetians, which, according to historiography, are direct descendants of Scythians and Alans, the haplo group R1a-Z2123 was found only in a single case. A similar picture is also observed in the work devoted to the Don Alans, where, in addition to the haplogroups of the Y chromosome characteristic for the Caucasus cascade, haplogroups R1a-Z94 and R1a-Z95 were also

found [34]. This hypothesis still needs to be taken with caution, since the haplogroup R1a-Z2123 with extremely low frequencies was found in the population of Turkic-speaking Volga Tatars and Chuvashs and, at the same time, the ancestral haplogroup for R1a-Z2123-R1a-Z2125, albeit with lower frequencies than the Kyrgyz, found among Iranian-speaking Tajiks and Pashtuns. The presence and continuity of R1a-Z2123 from the designated ancient cultures requires a detailed study using new homogenous markers, as well as the results of the complete Y-chromosome sequencing of ancient samples of designated cultures.

With a much lower frequency, the haplogroup R1a-Z2122 is found in the studied populations. With a frequency of 2.4%, she was found in the Karachai population and 3.4% in the Balkarian population. Interestingly, in the Chegemian sub-population, the frequency R1a-Z2122 is 6.8%, which is the absolute maximum for all the studied peoples of the region. All samples were genotyped for the M582 marker, but the results were negative. Previously, the haplogroup R1a-Z2122 (xM582) was found in native speakers of the New Aramaic, while R1a-M582 was characteristic of the Jewish population with their bifurcation about 4000 years ago [20, 35]. For an in-depth study of this haplogroup, 23 Y-STR haplotyping was performed, followed by the construction of a median network. The extremely scarce Y-STR data with haplotypes from populations of other regions did not allow us to determine the genetic relationship with other regions, but nevertheless a rather significant variability was revealed within our sample. Separately, it is necessary to say about the frequency distribution of the haplogroups R1a-M458 and R1a-M558, which are mainly found in Central and Eastern Europe. In this case, the peak of occurrence of the haplogroup R1a-M458 falls on Central Europe, and its frequency decreases to the Urals, while R1a-M558 has several peaks, including in the Volga-Ural region [19]. In this regard, these haplogroups can be used

as markers for the distribution of the East European gene pool. In the populations studied by us, these haplogroups were detected with low frequencies or were not detected at all. This testifies in favor of a slight East European influence on the studied populations along the male line.

Conclusions

Thus, we can conclude that the major haplogroup in the Turkic-speaking populations of the Central and Western Caucasus (Balkars and Karachays) is the haplogroup R1a-Z2123, which is not typical for the Turkic-speaking populations of Dagestan, as well as the Kuban Nogais.

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