

THE ANALYSIS OF THE GENETIC STRUCTURE OF THE KAZAKH POPULATION AS ESTIMATED FROM MITOCHONDRIAL DNA POLYMORPHISM

The study polymorphism of mitochondrial DNA carried out in population of Kazakhs (N=304). The analysis shows that Western Europe (55%) and Eastern Europe (41%) mtDNA lineages exist in the Kazakhs population. A high genetic diversity was observed in the Kazakhs population ($h=0.996$). Nei's genetic distances using mtDNA haplogroups frequencies are calculated and the situation of the Kazakhs among other peoples is determined. The paper offers analysis of the genetic structure of the Kazakh population using data of the frequencies of mtDNA haplogroups. It is noted a high degree of intensity of gene exchange between the Kazakh population and frontier populations of Russia on the North-West, North, Northeast and East of Kazakhstan.

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Introduction

A study the structure of the gene pool of modern human populations is one of the key problems of population genetics. Contemporary molecular and genetic methods of research allow studying genetic polymorphism in human populations at the DNA level. The Mitochondrial DNA became one of the markers widely applied in such kind of studies. MtDNA refers to highly polymorphous genetic systems. Wallace et al. (1995) believe that maternal inheritance character, absence of recombination and high level of variability allow using MtDNA as a highly informative tool in solution of questions concerning evolutionary, population and medical genetics.

Limborskaya et al. (2002) state that the mitochondrial genome evolves only through the successive accumulation of mutations in generations. According to Torroni et al. (1993), Ward et al. (1991) observed disbalance in linkage between mutations in the mitochondrial genome allows to consider a mtDNA molecule as a single locus presented by a set of alleles - mitotypes, certain groups of which correspond to linkage groups between specific mutations.

Rychkov and Balanovskaya (1992) in studies of the genetic structure of human populations indicate that genetic polymorphism is a normal state of any local population and of humanity as a whole, but it does not arise instantly. On the contrary, it represents the result of genetic variation taking place at all levels of the organization - from molecular to population. These processes are generated by the impact of the mutation, selective, migration and other factors on the genetic structure of populations and in the complex interaction merge into a single population genetic mechanism that differentiates or, on the contrary, brings together populations, and, simultaneously, changes their genetic properties.

Thus, analysis of mtDNA variation provides information on the genetic structure of human populations, to identify similarities and differences between ethnic and racial groups of people, which is a prerequisite both for studying the processes of differentiation of humanity far back in the past during periods of race formation and relatively recent demographic history of countries and continents.

Populations of Kazakhstan practically are not involved in the orbit of contemporary population and molecular genetic studies based on the highly informative DNA technologies. Modern populations of Kazakhs, inhabiting the territory from the Urals, the Caspian Sea to Siberia are interesting from the population genetic point of view due to the peculiarities of their ethnic history.

Due to complexity of ethnic and genetic processes in the age of broad migration and genetic interaction of Asian tribes with Slavic, Finno-Ugric and Turkic ethnic groups in Central Asia, it is impossible to establish authentically the basic components that formed the basis for the formation of the gene pool of indigenous population - Kazakhs by using traditional historical methods. The results of our population-based molecular genetic studies of mitochondrial DNA polymorphism of Kazakhs will make an important contribution to in solution of these issues. The aim of the study was to evaluate the genetic diversity of modern mitochondrial gene pool of Kazakhs.

Material and methods

DNA separated from peripheral blood of 304 volunteers (unrelated persons of Kazakh nationality) served as material for the research. All people (volunteers) were informed about the conduct of population genetic studies.

DNA was separated from 10 ml of peripheral blood with a salt method by the standard technique described in the work of Miller et al. (1988). The fragment 16024-16400 p.n. I/BCI of mtDNA control area was sequenced by ABI 377 DNA Sequencer "Perkin-Elmer" using DYEnamic™ ET terminator cycle sequencing premix kit "Amersham Pharmacia Biotech". MtDNA haplogroups were determined using RFLP-analysis. Mutations in mtDNA were numbered according to the Cambridge reference sequence (CRS) represented in the work of Anderson et al. (1981). Indicators of haplotype diversity h , the genetic distances based on frequencies of mtDNA haplogroups for determination of the phylogenetic relationships of the Kazakhs with other nations were determined according to the work of (Nei, 1988). Geogeographic analysis was performed using original software packages "GENE-MAP" and "GENE-STAT" created in the laboratory of human genetics in IOGene (Moscow) under the supervision of Rychkov and Balanovskaya (1992).

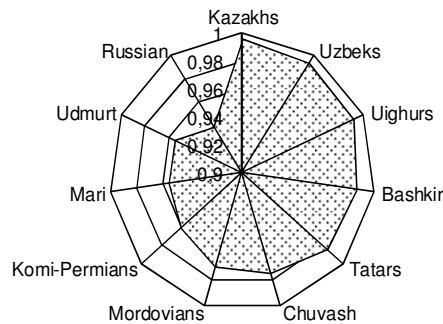
Results and discussion

For Kazakh population there have been discovered a wide diversity of mtDNA haplotypes and haplogroups based on them. To assess the degree of mtDNA heterogeneity we used the indicator of haplotype diversity. According to Kolman et al. (1996), indicators of haplotype diversity of Caucasoids are characterized by essentially lower heterogeneity, whereas populations of Mongoloids and the Middle East have the highest values of levels of haplotype diversity.

The indicators of haplotype diversity of mtDNA nucleotide sequences for Kazakhs and other nations according to the monograph of Khusnutdinova (1999) are represented in the Figure 1. The index of haplotype diversity (h) of mtDNA for Kazakhs was 0.996. It can be compared with the values of h in Uzbek (0.993) and Uighur (0.992) populations, according to the data provided by Batyrova (2004).

In Khusnutdinova (1999) the average index of haplotype diversity of mtDNA for the Turkic ethnic groups of the Volga-Urals region was 0.981, for the Finno-Ugric nations - 0.962, reflecting the lower heterogeneity of mtDNA types of the latter. High rates of h were found in the Volga-Urals region for the Bashkirs (0.986), the Chuvashs (0.975), the Tatars (0.985) and the Mordovians (0.971). In ethnic groups of Udmurts, Maris and Komi-Permyaks we can observe the intermediate values of h (0,955; 0,956; 0,961, respectively), and lower values were found out in the Russian nation (0.939).

FIGURE 1. THE INDEX OF HAPLOTYPE DIVERSITY IN DIFFERENT ETHNIC GROUPS



The results of the study of genetic diversity of mitochondrial gene pool of the Kazakhs showed their high heterogeneity. These results agree with the data of ethnographers and anthropologists, pointing to the great complexity of the ethnogenesis of the Kazakh population, characterized by mixing of many ethnic components in different proportions.

To analyze the polymorphism of the nucleotide sequences ГBCI of mtDNA among the Kazakhs the identified haplotypes have been attributed to haplogroups in accordance with the classification of Macaulay et al. (1999). There has been identified 44 haplogroups. There is a considerable scope of changes of frequencies of mtDNA haplogroups from 0.003 to 0.181 in the Kazakh population.

The contribution of Caucasoid and Mongoloid components in the formation of the anthropological type of the Kazakhs was proved earlier by Ismagulov (1970) on the basis of a comprehensive study of paleoanthropological and craniological materials.

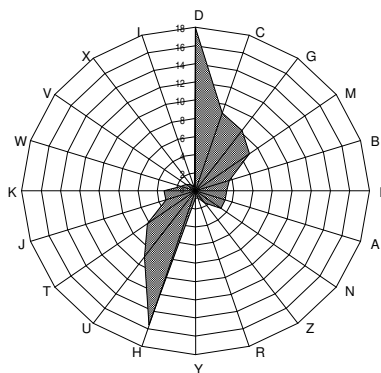
On the basis of the analysis of the results we have made the following conclusion: a centuries-old layering of the Mongoloid component on the Old Kazakhstanian anthropological layer of Proto-European race took place on the territory of Kazakhstan; anthropological type of the Kazakhs taking into account the main differentiating features of Caucasoid and Mongoloid race occupies an intermediate position and refers to a mixed South Siberian race.

We have studied the relation between East Eurasian and West Eurasian lines in the gene pool of the Kazakhs using the data on polymorphism HVSI of mtDNA (frequencies of haplogroups). It was found out that the main contribution of East Eurasian lines (55% of the total gene pool) to the modern gene pool of mtDNA of the Kazakhs make haplogroups D, C, G and Z (36.2%), A and F (6.9%) and other haplogroups of Asian origin (11.9%). West Eurasian lines (41% of the total gene pool) in the Kazakh gene pool are most frequently represented by the haplogroups H (14.1%), K (2.6%), J (3.6%), T (5.5%), U5 (3%) and others (12.2%) (Figure 2).

According to the results of our own research and using the data of Khusnutdinova (1999) on frequency of occurrence of major East Eurasian and West Eurasian lines in the populations of Asia and Europe, we have calculated the values of genetic distances according to (Nei, 1988) on the frequency of occurrence of mtDNA haplogroups in order to determine the location of Kazakhs among other nations.

On the basis of genetic distances we have constructed phylogenetic tree.

FIGURE 2. THE RELATIVE CONTRIBUTION OF THE WESTERN AND EASTERN EURASIAN MTDNA HAPLOGROUPS IN THE FORMATION OF THE MODERN GENE POOL OF THE KAZAKHS



Taking into account localization, populations are differentiated on the phylogenetic tree into two large communities. Thus, all populations of Asia form a community consisting of two clusters. The most closely related populations are the Kazakhs and Uighurs, they are accompanied by the Uzbeks and the nation(s) of the southern Altai on one level. The Kyrgyz and Bashkir nations formed an independent taxonomic group in this cluster.

The second cluster in this community brings together the nations of Siberia. Most closely related populations are populations of the Evenks and Yakuts, and then they are adjoined consistently by the Buryats and Tuvinians.

The second community is also formed by two clusters. The first cluster is represented by two populations - the Mordovians and Tajiks; the Tatars are adjoining the first group. The second cluster is formed by the Maris and Russian; the Chuvashes accompany them. The most distant in this cluster are the Udmurts.

In order to make the genogeographic analysis we used digital models of distribution of haplogroups' frequencies on the territory of Kazakhstan, constructed by the interpolation procedures. We have calculated the average values of frequencies of haplogroups studied for the Kazakh ethnic group, which were used to construct the matrix of genetic distances by Nei (1988).

The results of our scientific research give us the right to suggest that the most intensive gene exchange occurs with the neighboring populations in the Northwest, North and Northeast of Kazakhstan. At the same time, the gene exchange with population of Altai in the east has, apparently, a lower intensity.

Conclusion

Thus, we have studied the diversity of nucleotide sequences of the mtDNA hypervariable segment 1 of Kazakh ethnic group. This allowed us to estimate the genetic structure of their mitochondrial gene pool. In the investigated Kazakh population we have found out a high level of diversity of mtDNA haplotypes and haplogroups based on them. The index of haplotype diversity index is 0.996.

The genogeographic analysis of the genetic structure of the Kazakh population on the frequencies of mtDNA haplogroups revealed the extent of intensity of gene exchange of the Kazakh population with neighboring populations of Russia in the Northwest, North, Northeast and East of Kazakhstan.

The quantitative estimation of proportion of the basic racial components on mtDNA haplogroups for the Kazakhs was made for the time. In the mtDNA gene pool of Kazakhs we can trace the features both of East Euroasian (55%) and Western Euroasian (41%) trunks. All these gives the new information about the difficult process of formation of the Kazakh ethnic group and contribute greatly to the study of genetic structure of the Kazakh populations and can be used in anthropology, history and ethnography.

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