

Y-Chromosome Haplotypes in the Populations of Tatar in Russia

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Abstract: In recent years the study of the evolution and diversity of the human genome in the population had a rapid development, but the question of the demographic history of certain ethnic groups, such as the Tatars, remains open. The purpose of this paper is to compare the frequencies of Y-chromosome haplogroups in the population of the Kazan Tatars, Russian Federation and ethnic populations of the Volga-Ural region (VUR). The study of the genetic structure of the Tatar population from the data on the frequencies of Y-chromosome haplogroup reflects not only the probable participation of the Finno-Ugric component in the development of a particular ethnic group, but also the fact that in the content of major haplogroups Tatars did not stand out among other populations of the Volga-Ural region.

Key words: Evolution • Human genome • Population • Y-chromosome

INTRODUCTION

In recent years the study of the evolution and diversity of the human genome in the population had a rapid development, but the question of the demographic history of certain ethnic groups, such as the Tatars, remains open.

The Y-chromosome is one of the most convenient and reliable marker systems for molecular genetic analysis of populations. The reasons why the Y-chromosome has been successfully used in studies of human evolution, defined by its unique differences from other chromosomes. The Y-chromosome is specific to men, passed from father to son and is characterized by the lack of recombination. Mutations arising in the Y-chromosome are preserved and transferred en bloc from generation to generation [1].

The purpose of this paper is to compare the frequencies of Y-chromosome haplogroups in the population of the Kazan Tatars, Russian Federation and ethnic populations of the Volga-Ural region (VUR).

MATERIALS AND METHODS

The material for the population genetic analysis were 96 DNA samples from unrelated individuals - representatives of Tatar nationality, Russia. Data on

ethnicity was found out by the survey, blood sampling was carried out on a voluntary basis with signed informed consent.

DNA was isolated from peripheral blood by phenol-chloroform extraction. Polymorphism 15 Y-chromosome loci (M9, M89, YAP (M1), M35, M130, 12f2, M172, M231, M207, Tat (M46), M20, M175, 92R7, SRY1532, M269) were determined by PCR amplification, followed by restriction analysis and gel electrophoresis. Statistical analysis was carried out using Genepop and popSTR software.

RESULTS AND DISCUSSION

Genotyping experiments revealed that out of all the detected haplogroups, the highest frequency of haplogroup accounts for N1s (23.5%), typical for the populations of Northern Europe and the North-Eastern Siberia [2, 3]. Previously, it was shown that among the peoples of the Volga-Ural region N1c is quite common in Mari, Komi Zyryan and Komi - Perm and the maximum frequency is characteristic for the Udmurt. Notable is the fact of finding it with a rather high frequency of the Tatars (0.185), which seems to reflect the participation of Finno-Ugric significant component in the formation of this ethnic group. Based on these results it can be assumed that the source of origin of Y-chromosomes with

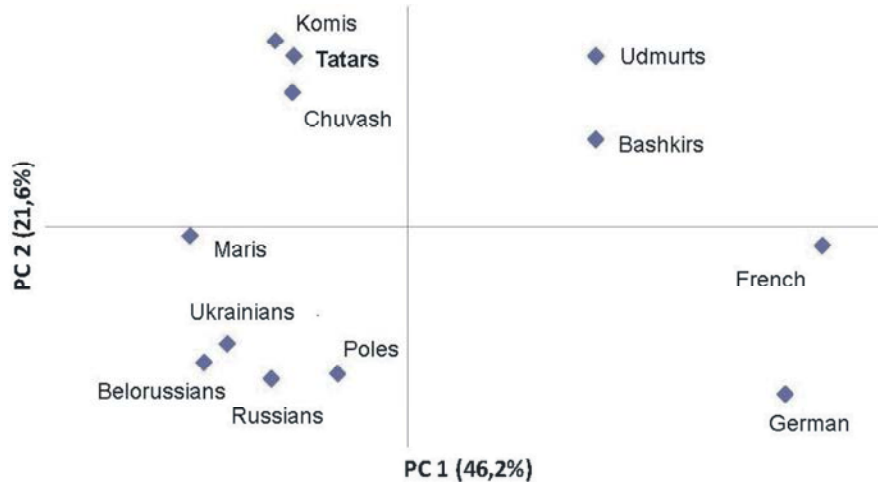


Fig. 1: The situation of populations in the space of the first two principal components from the data on the frequencies of haplogroups (R1a, N1s, N (xN1s), O, E1b1, J2, C) Y-chromosome

Tat- mutation is a Finno-Ugric commonality within the people of the Volga region [4, 5]. However, we can not exclude that the high frequency of N1s in Udmurt may be due to a founder effect and genetic drift. According to the literature is ancestral to N1s haplogroup N, Carrier G – A- transitions locus LLY22 [6]. In populations of Bashkirs, Mordvy, Udmurt and Komi Zyryan almost all chromosomes carrying the mutation of Tat- containing this transitions, indicating a single source of origin of Tat- mutations in these ethnic groups. High frequency of G- allele locus on chromosome LLY22 with Tat- mutation of the Tatars, Chuvash and Mari can, on the one hand, indicate the presence of different ancestral lines N1s in these ethnic groups, on the other side – the evidence of re- occurred Tat- mutation [7].

Also, with a high frequency in the studied population of the Tatars haplogroup R1 was found. Haplogroup R1 is represented by a branch of R1a (21.6%) and determined by a mutation in the locus SRY1532. It was previously shown that the R1 lines appear with the highest frequencies in populations of Eastern Europe and Central Asia [8, 9]. But other ethnic groups of the Volga- Ural region and the population of Central Asia and Southern Siberia are characterized by the high frequency of this haplogroup. In other words, the population of the Tatar in this respect has no exception considering local genetic landscape. However, clearly indication the source of origin of this haplogroup in the region as a whole and the Tatars in particular, will be possible only after discovery of new markers for assessing the structure of R1a with a higher degree of phylogenetic resolution [4].

Figure 1 shows the position of the Tatar population

and some other populations in the space of the first two principal components from the data on the frequencies of Y-chromosome haplogroup, explaining 67.8% of the variability of the latter. We see the separation of populations into three clusters: the population of the Volga- Ural region, Eastern European and Western European population.

Thus, the study of the genetic structure of the Tatar population from the data on the frequencies of Y-chromosome haplogroup reflects not only the probable participation of the Finno-Ugric component in the development of a particular ethnic group, but also the fact that in the content of major haplogroups Tatars did not stand out among other populations of the Volga-Ural region.

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