GENE POOL OF TURKIC SPEAKERS OF THE CAUCASUS IN THE EURASIAN CONTEXT (Y-CHROMOSOMAL PERSPECTIVE)

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The complex ethnogenesis of the Turkic populations of the Caucasus included both the pronounced autochthonous component and influence of the incoming Turkic speakers. This pattern was reflected not only in the high anthropological differentiation of the Turkic populations from the Caucasus but also in their gene pool. We studied Y-chromosomal polymorphism in all Turkic ethnic groups of the Caucasus (N=870): Azerbaijanians, Balkars, Karanogais, Karachays, Kuban Nogais, and Kumyks. We identified 39 Y-chromosomal haplogroups, four of which were the most frequent in the gene pool of Turkic peoples: R1a1a-M198 (24%), G2a-P15 (16%), R1b1a2-M269 (14%), and J2-M172 (12%). The phylogenetic analysis of rapidly mutating STRs markers showed high heterogeneity of the gene pool of Turkic peoples of the Caucasus. A number of phylogenetic networks including STR haplotypes not only from Turkic groups of the Caucasus, but also from multiple Turkic peoples of Eurasia were constructed for the first time. The phylogenetic network of haplogroup R1a1a-M198 showed an ancient genetic links between Turkic speakers of the Caucasus and Altai regions, thus indicating the 'steppe' component. The phylogenetic network of haplogroup N1-LLY22 revealed the proximity of gene pools of Kazakhs and Karanogais, and also the expressed genetic connection between Balkars and Bashkirs. This connection might indicate the Bashkiro-Nogai migration to the North Caucasus. The map of genetic distances from averaged gene pool of Turkic-speaking groups from the Caucasus to multiple Eurasian populations revealed the greatest genetic similarity in steppes near Black and Caspian seas. Some similarities could be also seen Southwest Asia particularly in North Anatolia and Iran. The Eastern European populations, Turkic peoples from Altai-Sayan and Volga-Uralic region are more genetically distant from Turkic populations from the Caucasus. Note, that indigenous populations of East Caucasus are genetically different from Turkic speakers of the region, despite Kumyks and Azerbaijans dwell the East Caucasus. This study was supported by RFBR grants 13-03-31331-mol a, 13-06-00670 a.

Key words: Y-chromosome, SNP markers, STR markers, Turkic peoples of the Caucasus, gene pool

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