

**GENE POOL OF THE TWO GROUPS OF SIBERIAN (TOBOL-IRTYSH) TATARS:  
ANALYSIS OF THE Y-CHROMOSOMAL SNP-MARKERS**

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Gene pool of Siberian Tatars is a “terra incognita” – there is only data on mtDNA of one population, while the variability of the most informative Y-chromosome has not yet been studied. Siberian Tatars include three major ethno-territorial groups of Turkic speaking populations in Western Siberia: Tomsk Tatars, Barabinsk Tatars and Tobol-Irtysh Tatars. Ethnogenesis of Siberian Tatars included mixing of Ugric, Samoyed, Turkic and partly Mongol tribes in proportions, which were different in territorial groups of Siberian Tatars. Later Bukharian Uzbeks, Teleuts, Kazan Tatars, Bashkirs and Kazakhs were also included in Siberian Tatars. Tobol-Irtysh Tatars of Tyumen region is the largest group of Siberian Tatars. They occupy a central region within their natural area, which was historically the center of consolidation of the Turkic groups in Western Siberia. We examined 140 representatives of Tobol-Irtysh Siberian Tatars in Vagayskii and Tobolskii regions of Tyumen Oblast: Isker-Tobolsk (2 populations) and Ishtyaxsk-Toguzsk (2 populations) subgroups. One of the traits of the Isker-Tobolsk Tatars gene pool was its high diversity: none out of the 13 identified haplogroups was predominant. Six most frequent haplogroups (R1a-M198, N1c-LLY22g, Q-M242, H-M69, N1b-P43, R2-M124) cover 80% of the gene pool, with the frequency varying from 6% to 25%. Major Y-chromosomal haplogroup Q-M242 has been found in over one third of the Ishtyaxsk-Toguzsk Tatars' gene pool. In Western Siberia Q-M242 is frequent in Selkups (65%) and Kets (90%), and in Southern Siberia it was met in Altaians and Tuvinians (17%). It may indicate a genetic relationship between these ethnoses. Next to them, by their frequencies, haplogroups R1a-M198 and N1c-LLY22g add up to a quarter of the gene pool of both Ishtyaxsk-Toguzsk and Isker-Tobolsk Tatars, which indicate their common ethnogenetic roots. In general, both the spectrum and frequency of Y-chromosome haplogroups of Tobol-Irtysh Siberian Tatars demonstrate the similarity of their gene pool with those of Turkic peoples of Siberia. For example, haplogroups R1a1a, N1b, N1c1 and Q are typical for Shors, Altaians and Khakases. However, the ratio of these haplogroups varies depending on the population. The basis of this diversity may lie in particular features of ethnogenesis: unequal contribution from different (by origin) tribes. This study was supported by RFBR grants 13-06-00670, and 14-06-00272.

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