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STR and SNP Markers of Y-Chromosome Unveil Similarity between the Gene Pool of Kurds and Yezidis

Authors : M. Chukhryaeva, R. Skhalyakho, J. Kagazegeva, E. Pocheshkhova, L. Yepiskopossyan, O. Balanovsky, E. Balanovska

Abstract : The Middle East is crossroad of different populations at different times. The Kurds are of particular interest in this region. Historical sources suggested that the origin of the Kurds is associated with Medes. Therefore, it was especially interesting to compare gene pool of Kurds with other supposed descendants of Medes-Tats. Yezidis are ethno confessional group of Kurds. Yezidism as a confessional teaching was formed in the XI-XIII centuries in Iraq. Yezidism has caused reproductively isolation of Yezidis from neighboring populations for centuries. Also, isolation helps to retain Yezidian caste system. It is unknown how the history of Yezidis affected its geny pool because it has never been the object of researching. We have examined the Y-chromosome variation in Yezidis and Kurdish males to understand their gene pool. We collected DNA samples from 90 Yezidi males and 24 Kurdish males together with their pedigrees. We performed Y-STR analysis of 17 loci in the samples collected (Yfiler system from Applied Biosystems) and analysis of 42 Y-SNPs by real-time PCR. We compared our data with published data from other Kurdish groups and from European, Caucasian, and West Asian populations. We found that gene pool of Yezidis contains haplogroups common in the Middle East (J-M172(xM67,M12)- 24%, E-M35(xM78)- 9%) and in South Western Asia (R-M124- 8%) and variant with wide distribution area - R-M198(xM458- 9%). The gene pool of Kurdish has higher genetic diversity than Yezidis. Their dominants haplogroups are R-M198- 20,3 %, E-M35- 9%, J-M172- 9%. Multidimensional scaling also shows that the Kurds and Yezidis are part of the same frontier Asian cluster, which, in addition, included Armenians, Iranians, Turks, and Greeks. At the same time, the peoples of the Caucasus and Europe form isolated clusters that do not overlap with the Asian clusters. It is noteworthy that Kurds from our study gravitate towards Tats, which indicates that most likely these two populations are descendants of ancient Medes population. Multidimensional scaling also reveals similarity between gene pool of Yezidis, Kurds with Armenians and Iranians. The analysis of Yezidis pedigrees and their STR variability did not reveal a reliable connection between genetic diversity and caste system. This indicates that the Yezidis caste system is a social division and not a biological one. Thus, we showed that, despite many years of isolation, the gene pool of Yezidis retained a common layer with the gene pool of Kurds, these populations have common spectrum of haplogroups, but Yezidis have lower genetic diversity than Kurds. This study received primary support from the RSF grant No. 16-36-00122 to MC and grant No. 16-06-00364 to EP.

Keywords : gene pool, haplogroup, Kurds, SNP and STR markers, Yezidis
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