

A.N. Bitkeyeva (2006), B. Nanzatov, and M. Sodnompilova (2012). The Sart Kalmyks rarely became the object of bioanthropological research. The few studies include that by D.O. Ashilova (1976), who made a number of conclusions based on anthropometric data. Though the ethnographic group of Sart Kalmyks incorporated into the Kirghiz nation in the past was related to the Western Mongolian ethnic group by common ancestry, language, and culture, now they differ in appearance from groups belonging to the Central Asian anthropological type (Kalmyks, Mongols, and Buryats) and show the closest affinity with Kirghizes. During our expedition in 2013, we conducted a comprehensive anthropometric and genetic study among the Sart Kalmyks. We have collected anthropometric data on 84 women and 119 men, made 830 photographs for creating generalized portraits, and studied the diagnostically important descriptive characteristics of the face. We also collected material for genetic analysis – 197 blood samples of 101 women and 96 men. Regarding ethnicity, the following distribution was observed: 111 persons stated that both their parents were Sart Kalmyks, and about a half of them (51 persons) knew the tribal affiliation of parents. Forty individuals are hybrids between Sart Kalmyks and Kirghizes, 29 have both parents of Kirghiz origin, and 8 people mentioned Kazakhs, Uyghurs, Tatars, and Bashkirs among their ancestors. Based on these materials, we will trace the origin and history of the Issyk Kul Kalmyks in comparison with Kalmyks living in Russia and China; assess the demographic and genetic structure of Karakol Kalmyks; and calculate genetic distances and the degree of relationship with Russian Kalmyks. Based on individual photographs, generalized portraits of the Sart Kalmyk men and women will be created. In sum, this research will highlight the most recent trends in the development of this ethnic group. This study was partly supported by a grant from the Russian Foundation for the Humanities, # 12-01-00063a.

Key words: *physical anthropology, anthropometry, population history, Sart Kalmyks*

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GENETIC DIVERSITY AND LINKAGE DISEQUILIBRIUM PATTERNS IN ROMA POPULATIONS LIVING IN CROATIA BASED ON X CHROMOSOME STR LOCI

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The aims of the study were to evaluate the genetic diversity and explore linkage disequilibrium (LD) patterns in three Roma populations of different migration origin, socio-cultural and dialect category using seven microsatellite (STR) loci in the Xq13.3 region of the X chromosome. These loci (DXS983, DXS8037, DXS8092, DXS1225, DXS8082, DXS1066 and DXS986) were analyzed in 189 Roma males from three populations in Croatia (Međimurje, Baranja and Zagreb), who belong to different migration and dialect groups. Several diversity indices (e.g. gene diversity, expected heterozygosity, mean number of pairwise differences) were calculated and the level of LD was inferred using exact test and D' statistics. Results suggest that Međimurje Roma population has the lowest genetic diversity ($\pi = 4.756$) and is significantly different from Baranja ($\pi = 5.395$) and Zagreb ($\pi = 5.429$) populations. Linkage disequilibrium analyses showed that Međimurje Roma population has the highest level of linkage disequilibrium while Zagreb population has the lowest. When compared to other isolates, Međimurje population shows highest similarity to small and stable isolated populations while Baranja and Zagreb Roma populations resemble large, more open isolated populations. In addition, results point to possible early separation of all the three populations despite the fact that Međimurje and Baranja populations belong to the same migration category and speak the same dialect. All three populations were most likely separated as early as the beginning of slavery in Romania, which was approximately 500 years ago.

Key words: *Vlax Roma, Balkan Roma, Bayash, microsatellites, X chromosome*

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