

Reconstruction of genetic history in Southern Siberia by paleogenetic study of diachronic population samples

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Motivation and Aim: Several areas in the south of Siberia, including the Altai, the Minusinsk Basin and the Baraba forest-steppe, have been well studied archaeologically. Archaeological cultures associated with populations chronologically covering the last few thousand years – from the Neolithic to the Late Middle Ages – are known for these regions. Representative collections of paleoanthropological material accumulated to date open up the possibility of a detailed study of the genetic history of Southern Siberia using paleogenetics methods, namely, the study of the genetic structure of populations within several local diachronic samples, identifying local features of the dynamics of the genetic composition of populations over time and comparing local models with each other to obtain a reconstruction of the main genetic events, influenced the formation of the genetic features of the indigenous population in this region and adjacent areas of Eurasia.

Methods and Algorithms: Representative diachronic samples of the ancient population of the Barabinsk forest-steppe, Mountain Altai, Steppe Altai, Minusinsk basin with a total number of samples of more than 2000 were formed. This unique sample bank is well characterized in terms of archaeological context and anthropological characteristics. Diachronic samples are subjected to sequential genetic analysis in several stages: 1. Analysis of the variability of mitochondrial DNA (mtDNA); 2. Determination of gender; 3. Analysis of the variability of the Y chromosome (for samples from men); 4. Analysis of individual autosomal markers (or small sets of markers); 5. Genome-wide methods of analysis. The combination of these methods makes it possible to gradually detail various aspects of the genetic history of the region in different chronological periods. *Results:* Data on the structure of more than 1,500 mtDNA samples and more than 300 Y-chromosome samples from our diachronic samples were obtained. These representative data allowed us to reconstruct the main stages of the formation of the population's gene pool in terms of maternally and paternally inherited genetic markers. We found correlations of the main changes in the structure of the gene pool with changes in the material culture of the population, including those caused by migration waves to the south of Siberia. Typical phenotypic features of their representatives (including features of pigmentation signs) have been determined for a number of populations. The study of large series of samples also allows us to study the local-territorial features of population processes in various areas of southern Siberia in detail.

Conclusion: Thus, the picture of the genetic history of the population in southern Siberia over the past few thousand years has been reconstructed. We continue to refine our reconstructions, including using genome-wide analysis methods.

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