

THE GENE POOL OF NANAI FROM RUSSIAN FAR EAST: POPULATION AND CLAN STRUCTURES

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Nanai population is 'a white spot' for both genetics and demography, despite it is the largest indigenous ethnic group of the Amur region. The variety of dialects of Nanai language (which belongs to Manchu-Tungus branch of the Altaic family), and Nanai cultural diversity indicate the complex population structure of the ethnos, which was formed on the ancient genetic background by following multiple migrations waves. To determinate the modern demographic structure of Nanais, we analyzed the information from the household books. 8 villages from 3 districts of the Khabarovsk region were studied (more than 5000 records). The villages in Nanai and Solnechny districts (the initial Nanai-area) are mono-ethnic (80% of their population are ethnic Nanais), while in the villages of the Komsomolsky district the proportion of Nanais is twice lower. However, the level of cross-breeding is low (4–11%) in all villages. The obtained results indicate that Nanai population presents a closed demographic system, and the probability of its miscegenation by mixing with other ethnic groups is not significant. The Nanai surnames emerged from their clan names and therefore represent the patrilinear structure of the population. The present day number of clans (13) is twice lower as compared to the 19th century. In every village about half of its population belongs to six clans: Beldy – 23%, Kiel – 9%, Onenko – 8%, Samar – 8%, Khodzher – 7%, Gayker and Passar – 6%. Clans have clear geographical areas: for example, Beldy is frequent in the 'Upper' Nanais while Samar is frequent in the 'Gorin' Nanais. These demographic data are in agreement with the genetic ones, which we analyzed in the same populations. The four Y-chromosomal haplogroups are the most frequent in the Nanais: C3-M217, C3c-M48, N1c1-M178, O3-M122. The greatest genetic diversity was found in the Beldy clan. It confirms that Beldy is a conglomerate of smaller clans. The gene pools of other clans are so homogeneous that Y-chromosomal haplotype of the clan's ancestor could be reconstructed. The results show that studying the correlation between clan structure and polymorphism of the Y-chromosome is a promising way to reconstruct the Nanai ethnogenesis. This study was supported by RFBR grants 14-06-00384a, 14-06-10026-к, 13-06-00670.

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