

**GENOME DIVERSITY AND EVOLUTION HISTORY OF ETHNIC GROUPS FROM EUROPEAN RUSSIA AND SUB-ARCTIC TRANSURALIC REGION**

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Understanding the genetic structure of the European population is very important from historical and anthropological points of view. Several studies have examined the fine-scale structure of human genetic variation in Europe. But populations of Northern-Eastern European area and Sub-Arctic Transuralic region are less investigated. These territories are inhabited by different indigenous Finno-Ugric peoples and ethnic Russians. To explore genetic structure of the region we analyzed single nucleotide polymorphisms using different versions of Illumina BeadChips. Principal components (PC) analysis, ADMIXTURE clustering and Wright's fixation indices (FST) were used to examine population structure of Khanty, Mansi, Komi, Veps and Russians. Mansi were indigenous inhabitants of Northern European area prior to 17th Century AD. This ethnic group undergone trans-Uralic migration and nowadays inhabits Sub-Arctic Region of Western Siberia. The Khanty, closely related to Mansi by linguistic classification, are the indigenous inhabitants of this region. Both the Mansi and the Khanty peoples have genomic characteristics that differentiated them from all others. Komi are also inhabitants of the territory at Northern-Eastern Europe. Two ethnographic groups of them were included in the study – Izhemski and Priluzski Komi. They formed two neighbored clusters at PC plot. The Veps are the Finno-Ugric minority that is one of the oldest people of northern Europe. They still inhabit some territories of northwest Russia. Veps gene pool reveals similarity with Finns and Komi. Russians are the most abundant people in Northern-Eastern Europe. Principal component analysis showed significant differences between Russians of Northern European region and Russian populations from the central part of Russian Plain. The later Russian populations formed a single cluster on PC plot. In contrast, Northern Russians demonstrated close relationships with Finno-Ugric populations. The results obtained demonstrate distinct ancestry components in the samples from Sub-Arctic Transuralic region, that significantly differs them from all other populations studied.

**Key words:** *genome diversity, population genomics, Eastern Europe, SNP analysis*

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