GENE POOL OF THE SOUTHWEST ASIA: REFLECTION OF GEOGRAPHICAL RELIEF AND LINGUISTIC STRATIFICATION

Chukhryaeva Marina^{1,2}, Dibirova Khadizhat^{1,2}, Teuchezh Irina^{1,2}, Kuznetsova Marina^{1,2}, Agdzhoyan Anastasiya², Yepiskoposyan Levon³, Pocheshkhova Elvira⁴, Balanovsky Oleg^{2,1}

Southwest Asia despite the predominance of mountainous and arid landscapes was not only the birthplace of the ancient states - according to the Anatolian hypothesis it was the homeland of the Indo-European language family. How similar are the gene pools of the Indo-European speaking populations of Southwest Asia to those who speak Semitic and Turkic languages? Is the geographical landscape a factor which shaped the genetic landscape? To answer these questions, we studied the Y-chromosomal gene pool of the Southwest Asia for published data (over 4000 individuals) and our new data on five Armenian populations, covering the area of historic Armenia (436 individuals). The multidimensional scaling (MDS) plot revealed two genetically different groups of the populations in Southwest Asia. The first group included mountain-dwelling populations: Turks, Armenians and different populations from Iran. The second group included populations of Syria, Lebanon, Iraq, and Arabian Peninsula, and thus could be called the "plain" group. The hierarchical analysis of the inter-population variability (AMOVA) confirms this pattern. Genetic differences between "highland" and "plain" groups of populations are nine times higher than the differentiation obtained by grouping populations by standard geographic parameters like latitude and longitude. Armenians formed a subcluster within the "highland" group of populations on the MDS plot. Note, that Georgians (geographical neighbors of Armenians) fall into another (the Caucasus) cluster together with the Abkhazians and the majority of the populations of the North Caucasus. The cartographic analysis confirmed that North Caucasus and Georgian populations are genetically distant from populations of "highland" cluster. Analysis of genetic differentiation of Southwest Asian populations under the linguistic stratification revealed significant differences between the gene pools of the Turkic, Semitic and Indo-European speaking groups. Indo-European groups – Armenians and Iranian populations – are clustered together while Semitic-speakers form a separate cluster. This corresponds well with the geographic division into "plain-dwelling" (Semitic) and "highland-dwelling" (other) populations and suggests that the linguistic stratification could be also considered as the possible factor shaping the structure of Southwest Asian gene pool. The research has been supported by The Presidium of RAS programs: "Molecular and cell biology", "Fundamental sciences for the medicine", "Gene pool dynamics", and RFBR grant 13-04-01711.

Key words: gene pool, Y-chromosome, genetic markers, Southwest Asia, Indo-European language family

Contact information: Chukhryaeva Marina, e-mail: m.chukhryaeva@yandex.ru.

¹Research Centre for Medical Genetics, Russian Academy of Medical Sciences, Moscow, Russia

²Vavilov Institute of General Genetics, Russian Academy of Sciences, Moscow, Russia

³Institute of Molecular Biology NAS AR, Yerevan, Armenia

⁴Kuban State Medical University, Federal Agency of Public Health and Social Development, Krasnodar, Russia