

CLADISTIC ANALYSIS OF ANCIENT ANATOLIAN POPULATIONS: MOUND OF VAN FORTRESS AND KARAGÜNDÜZ SAMPLES

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This study aims to compare craniometric traits of Van-Karagündüz and Mound of Van Fortress (MVF-Christian and MVF-Islamic) populations which lived during the Middle Ages, and to assess biological relationships between these groups and their affinities with other Anatolian populations. We used 8 measurements (maximum cranial length, maximum cranial breadth, basion-bregma height, porion-bregma height, bizygomatic breadth, upper facial height, nasal height, nasal breadth) and 3 indices (cranial index, upper facial index, nasal index) on crania of 191 skeletons belonging to three populations. SPSS 19 was used for calculating biological distances and for cluster analysis, from which phenograms were derived. Results of cluster analysis separate MVF-Christian and MVF-Islamic populations even though they lived in the same place and at the same time. In addition, we recognized two distinct subgroups within the populations (MVF-Christian and Karagündüz) and (MVF-Islamic and Tepecik). Both subgroups lived in Van. These populations were similar to other contemporary eastern and western Anatolian populations such as Dilkaya, Panaztepe, Datça, Nikolaos, Truva 2. However, they were distinct from Çatalhöyük, Boğazköy, Çayönü, Hisarlık, İznik and even farther from Tilkitepe, Sardis, Alişar and Lidar. The results suggest that contemporaneous groups tend to be closer to one another than chronologically diverse ones.

Key words: *craniometry, Mound of Van Fortress, Karagündüz, ancient Anatolia*

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GENETIC TRACES OF THE TURKIC INFLUENCE IN ARMENIANS AND NEIGHBORING POPULATIONS

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We intended to evaluate the rate of genetic signals from Turkic tribes in the gene pool of various groups of modern Armenians and compare it with the corresponding rate in neighboring populations. The most frequent Y-chromosomal haplogroups in Central Asia were considered as genetic markers of Turkic expansion. The rate of Turkic genetic signal in different territorial groups of Armenians representing almost the whole area of historical Armenia varies in the range of 0–1%, with 0.5% on average for the general population. Comparable rate of Turkic genetic input is also detected in Georgians and non-Turkic speaking ethnic groups of Iran. This level contrasts sharply with that found in other neighboring populations: 6% in modern Turkey, 10–12% in Iranian Azeris, and 10% in Lezgins. These results are consistent with the historical records indicating the main routes of Turkic expansion south of the Caspian Sea and along its western coast. In many cases, the expansion has also resulted in language replacement through the elite dominance model. The virtual lack of Turkic genetic traces observed in Armenians or Georgians as well as the preservation of their language indicates the conservation of their genetic structure despite the centuries of Turkic expansion in southern Caucasus. This genetic evaluation raises questions about the reasons that have impeded genetic contact of Armenians with Turkic tribes. The reason that is most likely a priori is the adoption of Christianity and the formation of a strong ethnic and cultural identity long before the Turkic migration into the region.

Key words: *Armenian population, Turkic expansion, genetic signals*

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