

INTEGRATIVE ARCHAEOLOGICAL AND ARCHAEOGENOMIC DATABASE FOR STUDYING THE POPULATION HISTORY OF THE HUN PERIOD

Leonid Vyazov¹, Pavel Flegontov^{1,2}, Ulaş Işıldak^{1,3}, Olga Flegontova¹, Gulnaz Sagmanova¹

¹ *University of Ostrava, Ostrava, Czech Republic*

² *Harvard University, Cambridge, MA, USA*

³ *Middle East Technical University, Ankara, Turkey*

The Migration period in the Eurasian steppe and forest-steppe is a bizarre pattern of population processes. Hunnic invasion to the East European steppes in the 3rd started dramatic and wide-scale relocations of the local groups of different origins. It resulted in intensive population admixture and formation of heterogeneous societies, which were the main actors during the whole period. The sophisticated nature of the migrations process caused by the Huns and the associated groups requires a multi-proxi study based on integrated archeogenomic and archaeological records.

To perform multidisciplinary analysis, we developed a Web-based and GIS-driven database, integrating archaeogenomic and archaeological data. From the archeological side, our database deals with both cultural and stylistic interpretations and relative chronological sequences as well as absolute datings. It is based on the use of a graph database (Neo4j) that allows us to store, analyze and manage complex relationships between the archaeological evidence, its context, and interpretations. The functionality of our multi-user system includes data mapping, visualization, selection, and processing. Published genome-wide archaeogenetic data from the Allen Ancient DNA Resource are stored in the database and linked to respective burials. The web-GIS toolkit enables users to select certain groups of burials and archaeological sites and perform simple analyses of genetic data: hierarchical clustering of genetic distances, PCA (both basic and with projection on user-defined axes), ADMIXTURE, f-statistics, and qpWave/qpAdm. The database also enables users to store connections between ancient individuals revealed by the identity by descent (IBD) methodology. IBD sharing (autosomal haplotype sharing) is a high-resolution method of genetic analysis that recently became applicable to ancient DNA samples due to advances in genotype imputation and phasing for ancient DNA data in the Reich Lab.

We hope that this database and a simple toolkit will help to cross the divide between research in archaeology and archaeogenetics.

Keywords

aDNA, Migration period, Web-GIS, IBD sharing, genetic analysis toolkit

Note/comment