## THE ISSUE OF CONTINUITY OF POPULATION HISTORY BETWEEN 8-12TH CENTURIES IN CARPATHIAN BASIN BASED ON ARCHAEOGENETIC RESULTS OF FOUR CEMETERIES

<u>Veronika Csáky</u><sup>1</sup>, Bea Szeifert<sup>1,2</sup>, Dániel Gerber<sup>1,2</sup>, Béla Szőke<sup>3</sup>, Szabina Merva<sup>4</sup>, Sándor Évinger<sup>5</sup>, Csilla Líbor<sup>6</sup>, Zsolt Petkes<sup>7</sup>, Balázs Mende<sup>1,3</sup>, Anna Szécsényi-Nagy<sup>1</sup> *Institute of Archaeogenomics, Research Centre for the Humanities, Eötvös Lóránd Research Network, Budapest, Hungary* 

As the Carpathian Basin is reputed as the westernmost point of the Eurasian steppe, it was influenced by movements of many nomadic tribes during migration period, as well. One of the most important question for discussion in archaeology is the continuity or discontinuity of populations in the investigated region. Although the survival of population of e.g. 9th century in the 10th century is taken as evidence in Carpathian Basin (among others Avars and Slavs), based on only archaeological research these observations cannot provide unambiguous data to this day. For example, over half a dozen cemeteries are known in which conquering populations were excavated above or near of the late Avar tombs, and it could not be decided yet whether we could speak of population and/or place continuity in these cases. In this study we try to answer this question in a different extent by examining power centres of Transdanubia with a broader time range: late Avar period, Carolingian period, Hungarian Conquest period and the early Árpádian Age.

We investigated 172 individuals from four cemeteries using NGS sequencing methods: Zalavár-Vársziget (9-12th centuries), Himod-Káposztásföldek (9-11th centuries), Visegrád (8-11th centuries), Sárbogárd-Tringer tanya (10th century). At least two of them (Zalavár-Vársziget and Himod-Káposztásföldek) contain well-separable chronological phases, based on which we created groups for population genetic analysis. The statistic and phylogenetic analyses based on whole mitogenomes were completed by whole genomic shotgun results. According to the later one, more precise conclusions have been drawn at individual level, although the different composition of the investigated populations is seen based on mitogenomic results as well.

This research was supported by The House of Árpád Programme (2018–2023) Scientific Subproject: V.1. Anthropological-Genetic portrayal of Hungarians in the Árpádian Age.

## Kevwords

Power centres in Transdanubia, Population genetics, Migration period

<sup>&</sup>lt;sup>2</sup> Doctoral School of Biology, Institute of Biology, ELTE Eötvös Loránd University, Budapest, Hungary

<sup>&</sup>lt;sup>3</sup> Institute of Archaeology, Research Centre for the Humanities, Eötvös Lóránd Research Network, Budapest, Hungary

<sup>&</sup>lt;sup>4</sup> Freelancer

<sup>&</sup>lt;sup>5</sup> Department of Anthropology, Hungarian Natural History Museum, Budapest, Hungary

<sup>&</sup>lt;sup>6</sup> King St. Stephen Museum, Székesfehérvár, Hungary

<sup>&</sup>lt;sup>7</sup> Gyula Siklósi Research Centre for the History of the City of Székesfehérvár, Hungary

## Note/comment