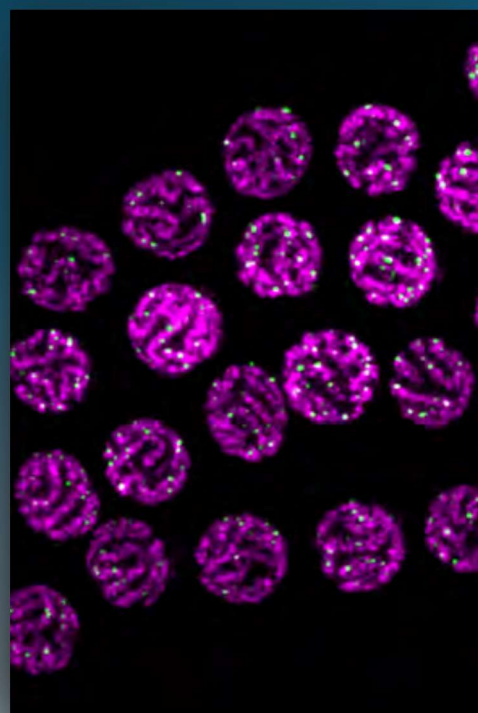
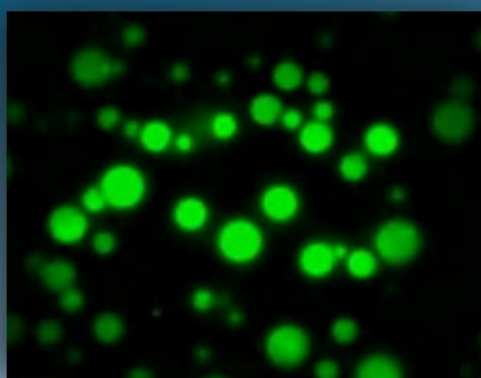
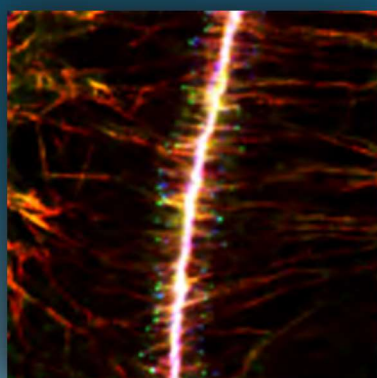


Book of Abstracts

Hungarian Molecular
Life Sciences 2021

5-7 November 2021
Eger, Hungary

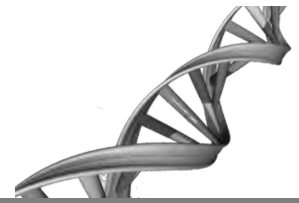


Hungarian
Biochemical
Society



MAGE

Hungarian Genetics Society



O-26

Genetic history and life of Bronze Age communities in Western Hungary

Dániel Gerber^{1,2}, Bea Szeifert^{1,2}, Balázs Egyed², Ágnes Kustár³, Szilvia Fábán³, Balázs Gusztáv Mende¹, Eszter Ari^{2,5,6}, Viktória Kiss⁴, Anna Szécsényi-Nagy^{1,2}

¹*Institute of Archaeogenomics, Research Centre for the Humanities, Eötvös Loránd Research Network (ELKH); Budapest, Hungary*

²*Department of Genetics, Faculty of Science, ELTE Eötvös Loránd University; Budapest, Hungary*

³*Hungarian National Museum; Budapest, Hungary*

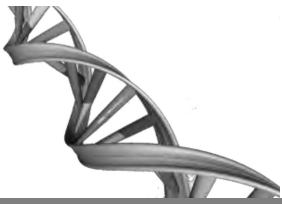
⁴*Institute of Archaeology, Research Centre for the Humanities, Eötvös Loránd Research Network (ELKH); Budapest, Hungary*

⁵*HCEMM-BRC Metabolic Systems Biology Lab; Szeged, Hungary*

⁶*Synthetic and Systems Biology Unit, Institute of Biochemistry, Biological Research Centre, Eötvös Loránd Research Network (ELKH); Szeged, Hungary*

Bronze Age Europe was home to a number of well documented and shifting communities, when today's genetic makeup was formulated. Nevertheless, regional demographic and population genetic histories are yet to be described. Here we provide 20 newly sequenced human genomes at an average ~0.1x coverage from three archaeological horizons of previously understudied archaeological periods from the excavation site of Balatonkeresztúr, Western Hungary, dated between ~2400-1650 BCE. Our results indicate a population turnover from first to second horizon around ~2200 BCE with a group of high (~42%) Hunter-Gatherer component previously unknown from the period, which during the transition from the second to third horizon subsequently blended into the prevailing genetic pool of surrounding populations through female-biased admixture. The origin of this particular Hunter-Gatherer ancestry likely comes from unsampled regions of Eastern Europe, and contributed to various populations to some extent, while becoming most prominent in the Baltic region from the middle of the second millennium BCE. Kinship network and uniparental genetic makeup revealed patrilineal social structure in line with previous results of Bronze Age Europe. We also made inferences on health qualities by using an extended set of (~3800) SNP variants of clinical significance. Our results indicate prevalence of highly pathogenic variants, e.g. SNP-s for LHON, Lig4 syndrome, Coffin-Siris syndrome and MRT53, although these are hard to be associated with actual manifestation, even in the presence of skeletal malformations. In the future, we aim to explore further possibilities for pathogenic variant screening, in order to provide new prospects for archaeogenetic studies.

Keywords: *archaeogenetics, population genomics, clinical variants*



O-27

Chapters from Carpathian Basin's Early Medieval genetic history

Bea Szeifert^{1,2}, Balázs Gyuris^{1,2}, Dániel Gerber^{1,2}, Veronika Csáky¹, Attila Türk^{3,4}, Béla Miklós Szőke⁵, Sándor Évinger⁶, Balázs Egyed², Balázs Gusztáv Mende¹, Anna Szécsényi-Nagy¹

¹*Institute of Archaeogenomics, Research Centre for the Humanities, Eötvös Loránd Research Network (ELKH), Budapest, Hungary*

²*Department of Genetics, ELTE Eötvös Loránd University, Budapest, Hungary*

³*Department of Archaeology, Faculty of Humanities and Social Sciences, Pázmány Péter Catholic University, Budapest, Hungary*

⁴*Hungarian Prehistory Researchgroup, Research Centre for the Humanities, Eötvös Loránd Research Network (ELKH), Budapest, Hungary*

⁵*Institute of Archaeology, Research Centre for the Humanities, Eötvös Loránd Research Network (ELKH), Budapest, Hungary*

⁶*Department of Anthropology, Hungarian Natural History Museum, Budapest, Hungary*

The archeological transformation in the Hungarian Conquest Period of the Carpathian Basin is intensively investigated, while there is not much genetic data from this period. The impact of the arrival of the Hungarians could be measured by monitoring the genetic continuity in this region.

For this purpose, we have included archeologically well-described burials ($n > 100$) from the 9-12th centuries Transdanubia (Zalavár, Himód). This way we could resolve questions about biological continuity after the Migration Period, impact of the Conquerors and detect possible connections with Hungarians associated populations from the Ural-Volga region. Here we also present ancient DNA data from 6-14th centuries AD burials ($n > 120$) from the Volga-Ural region, which all have either archaeological, chronological and/or geographical connections with the early Hungarians in the Carpathian Basin and with each other. This research supplements the results of Csáky et al 2020, in which we reported data from the Trans and Cis-Ural regions from sites that can also be related to the early Hungarians.

Based on uniparental markers (whole mitogenomes and Y-chromosome STR profiles) we can see that the genetic compositions of the groups related to the Hungarians were heterogeneous even in the Volga-Ural region. We detected phylogenetically close connections between individuals associated with the same and other cultures/sites. We identified uniparental markers that connect the Volga-Ural region with the Carpathian Basin (e.g. maternal A12a, N1a1a, paternal N1a-Z1936). The examined sites from the Carpathian Basin show a typical European genetic picture, but also contain elements of East-Eurasian origin that could be evidence of late Avar continuity or possible immigrant Conquerors.

The preliminary results of whole genome analysis show corresponding results. Individuals from the 9-12th century Carpathian Basin are similar to other European groups with exception of a few outlier samples showing yet undescribed Eastern-Eurasian genetic affinities. Interestingly, some of our Hungarian Conqueror samples show a highly similar genetic profile to these outliers. Our results are significant steps towards the understanding of the Early Medieval population genetic history of the Carpathian Basin, including also the ethnogenesis of the Hungarians.

Keywords: *archaeogenetics, population genetics, Carpathian Basin, Hungarian Conquest*



P-109

Towards building the genetic map of the Carpathian Basin

Noémi Borbély¹, Dániel Gerber^{1,3}, Bea Szeifert^{1,3}, Horolma Pamjav²,
Balázs Gusztáv Mende¹, Balázs Egyed³, Anna Szécsényi-Nagy¹

¹*Institute of Archaeogenomics, Research Centre for the Humanities, Budapest, Hungary*

²*Department of Reference Samples Analysis, Institute of Forensic Genetics, Hungarian Institute for Forensic Sciences (HIFS),
Budapest, Hungary*

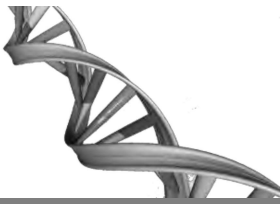
³*Department of Genetics, Eötvös Loránd University, Budapest, Hungary*

Our research was aimed at mapping the genetic structure and paternal gene pool of the early 20th/late 19th-century population of the Carpathian Basin, as part of which we performed full mtDNA-based and Y-chromosomal genotyping of samples collected from present-day Hungarian-speaking villages located in Transylvania, Drávaszög in Croatia and Zobor-region in Slovakia. Our basic assumption was that we reconstruct the uniparental gene pool of the Hungarian speaking populations that existed 100-150 years ago by finding elderly sample donors living in isolated villages and documenting their genealogies carefully. The aim of the research was to monitor any regional genetic structure discrepancies of the Hungarian speaking population and to confirm preliminary uniparental genetic studies that revealed an increased number of Eastern Eurasian lineages in isolated populations, compared to populations of larger cities.

Our partial results from the Sekler population indicate a mainly West-Eurasian uniparental makeup that also points to limited admixture with neighboring populations. European mtDNA haplogroups characterize the majority of the population, but differently from the Hungarian-speaking population in Hungary, as there is a perceptibly higher proportion of Eastern Asian haplotypes. Phylogenetic analyses confirmed the presumed eastern origin of certain maternal lineages and in some particular cases, they can also be linked to ancient DNA data of early Hungarians.

So far we have examined 286 newly sequenced whole mitochondrial genomes and Y chromosome STR and SNP profiles of 214 men from the three regions. Our follow-up plan is to generate whole-genome data to receive more detailed inferences on the origin and connection of ancient and modern-day Hungarian-speaking populations.

Keywords: *population genetics, Hungarian-speaking minorities, Transylvania, mitogenome, Y-chromosome*



P-110

Similar or a little different? Two Hungarian-speaking populations in the Hungarian-Slavic contact zone

Horolma Pamjav¹, Ábel Fóthi^{2,3}, Dániel Dudás¹, Erzsébet Fóthi²

¹*Hungarian Institute for Forensic Sciences, Institute of Forensic Genetics, Budapest, Hungary*

²*Institute of Archaeogenomics, Research Centre for the Humanities, Budapest, Hungary*

³*Institute of Enzymology, Research Centre for Natural Sciences, Budapest, Hungary*

Distribution of Y chromosomal haplotypes and haplogroups of two recent Hungarian-speaking populations were analysed: one from the Rétköz region of Hungary and another from Vág Valley of Slovakia, both live in the Hungarian-Slavic contact zone. The common feature of the two regions is that many cemeteries from the time of the Hungarian conquest were unearthed on both territories. We analysed twentythree male-specific Y-STR markers and more than 30 Y-SNPs on 106 independent male lineages from Rétköz and 48 from the Vág Valley.

Y-STR analysis of Rétköz population gave evidence of heterogeneous Y chromosomal composition with ten haplogroups. Mainly European lineages are represented by the following seven haplogroups: E1b1-M78 (7.5%); G2a-L156 (6.6%); I1-M253 (4.7%); I2a and I2b (8.5%); J2a and J2b (3.8%); R1a-Z280, -M458 and -Z93 (38.7%); R1b-312, -P25 and -U106 (23.6%). Three Eurasian haplogroups occurred in the dataset (H1a-M82 0.9%, N-Tat 2.8%, Q-M242 2.8%). Three males have an N-Tat Y-STR haplotype (2.8%): one by one N1c-L1034, N1c-Z1936, N1c-VL29.

In contrast to the population of Rétköz, that of Vág Valley proved to be less heterogeneous, with only seven haplogroups covering 100% of the studied Y chromosomal variability. The three Eurasian haplogroups found in Rétköz are completely absent in the Vág Valley. The complete lack of N-Tat, Q-M242 and R1a-Z93 markers, which are probably related to the Hungarian conquering population, is particularly striking.

Based on Fst genetic distances a multidimensional scaling (MDS) plot constructed with 76 modern populations shows all Hungarian groups close to each other. The population of Rétköz is most similar to the population of Bodrogek, which is geographically closest to it. The Vág Valley group is a little further away from them.

The history of the two Hungarian-speaking populations living in the Hungarian-Slavic contact zone seems to be slightly different. It seems very probable that the vast majority of both Hungarian-speaking populations are descendants of the Neolithic and Bronze Ages peoples, as well as the Eastern and Western Slavs. However, almost 10% of the present-day Rétköz population comes from the ancient Hungarians, while the Hungarians living in the Vág Valley lack this stratum.

As a preliminary study, Median Joining (MJ) networks analyses were constructed with haplotypes of 183 E1b1-M78, 179 N1c-Tat, 166 Q-M242, 121 R1a-Z93 haplogroups to gain deeper insight into the origin of the studied populations.

This study was supported by Ministry of Innovation and Technology TKP2019 (No. 690024) and TKP2020-NKA-20.