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КОЧЕВЫЕ ИМПЕРИИ ЕВРАЗИИ В СВЕТЕ АРХЕОЛОГИЧЕСКИХ И МЕЖДИСЦИПЛИНАРНЫХ ИССЛЕДОВАНИЙ

**IV международный конгресс
средневековой археологии евразийских степей,
посвященный 100-летию российской
академической археологии**

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**NOMADIC EMPIRES OF EURASIA IN ARCHAEOLOGICAL
AND INTERDISCIPLINARY STUDIES**

**IV International Congress of Medieval Archeology
of the Eurasian Steppes, dedicated to the 100th anniversary
of the Russian academic archeology**

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Кочевые империи Евразии в свете археологических и междисциплинарных исследований: сб. науч. ст. IV международного конгресса средневековой археологии евразийских степей, посвященного 100-летию российской академической археологии (Улан-Удэ, 16–21 сентября 2019 г.). В 2 кн. Кн. 2 / отв. ред. Б. В. Базаров, Н. Н. Крадин. – Улан-Удэ: Изд-во БНЦ СО РАН, 2019. – 182 с.

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В сборник включены доклады участников IV международного конгресса средневековой археологии евразийских степей «Кочевые империи Евразии в свете археологических и междисциплинарных исследований». Статьи посвящены городской культуре степной Евразии, погребальным и ритуально-культовым памятникам кочевников Евразии, духовной и художественной культуре народов Евразии по археологическим и письменным источникам.

Книга предназначена для археологов и историков, специализирующихся в области средневековой истории и археологии Евразии, а также преподавателей, аспирантов и студентов исторических специальностей.

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Volume is included the papers of the participants of the IV International Congress of Medieval Archeology of the Eurasian Steppes «Nomadic Empires of Eurasia in Archaeological and Interdisciplinary Studies». Articles examines issues of urban culture of the steppe Eurasia, funerary, ritual, and cult monuments of nomads of Eurasia, spiritual and artistic culture of the peoples of Eurasia in archaeological and written sources.

The book will be interesting for Eurasian archaeologists and historians, as well for lecturers, and graduate students.

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EASTERN GENETIC CONNECTIONS OF TWO NOMADIC POPULATIONS IN THE EARLY MEDIEVAL CARPATHIAN BASIN

The Carpathian Basin in Central Europe was settled by various nomadic populations from Asia in several migration waves during the Early Middle Ages. Here we present medieval ancient DNA from Avars and Hungarian Conquerors from the Carpathian Basin, as well as some ancient individuals from the Volga-Ural region and Western Siberia. We describe here their maternal genetic composition and highlight their connections to populations of Northeast and Central-Asia. We focus on the phylogeny of selected Asian mitochondrial lineages, belonging to haplogroups A12a, D4j and Y1a, which were detected in the aforementioned ancient populations.

Keywords: migration; Avars; Hungarian Conquerors; Carpathian Basin; Ural region; ancient mitochondrial DNA.

Archaeological and historical introduction. After the fall of the Roman Empire, the Carpathian Basin was under the rule of barbarian peoples for a long period. Until the end of the Migration Period, up to the arrival of the ancient Hungarians – i.e. Magyars (895 AD), nomadic or semi-nomadic groups (e.g. Huns, Avars, Magyars) arrived from the Eurasian Steppe at this final destination and conquered the local population (Romanised population in *Pannonia*, Sarmatians at the Great Hungarian Plain, Germanic tribes and Slavs).

The Avars settled down in the Carpathian Basin after 568 AD and founded their empire, the Avar Qaganate, which united under the Qagan's rule the inhabitants of the region. About 80,000 graves of the Avar Age have been excavated in the Carpathian Basin, and about a third of these burials can be dated to the Early Avar Age (568–700 AD). The fall of the Avar Qaganate was the result of the attack of the Frankish and the inner civil war at the beginning of the 8th c.

The assumed Asian origin of Avar people appeared in the 18th c. Since then several archaeological studies have hypothesized different regions as their homeland (e.g. Inner Asia, Central Asia). This debate is still unsolved, however the historical evidences (eg. Avar ruler's title the 'Qagan') are increasing in favour of the Inner Asian origin (Golden 2013: 43–46; Pohl 2018: 567–822).

With the Avars, new archaeological elements appeared in the Carpathian Basin (Bálint 1989; Csiky 2015; Vida 2018) that shared common characteristics with Eurasian nomadic cultures. These phenomena are even more emphasised in the burials of the Avar period elite group composed of only a dozen graves located in the central part of the Carpathian Basin (Danube-Tisza Interfluve) and dated to the middle of the 7th c. These burials might be linked to leaders of the early Avar polity and the Qagan's military retinue (Bálint 1989; Csiky 2015).

Ancient Hungarians had their Homeland probably in the southern Trans-Ural region (Bakal and Kushnarenkovo culture, 4–6th c. AD). They first moved to the Cis-Ural region most likely in the mid-6th c. AD, and part of the population

crossed the Volga River and settled in the Dnieper-Dniester region in the first half of the 9th c. (based on written sources and archaeological data). They lived there during the middle and second half of the 9th c. (Subbotsy archaeological horizon) until the Hungarian Conquest of the Carpathian Basin in 895 AD (Иванов 1999; Комар 2018; Türk 2012), although nowadays it seems that a few Hungarian graves first appeared there as early as 870–880 AD (Türk-Lőrinczy 2015).

The Hungarians occupied in successive campaigns the central territories of the Carpathian Basin until 907 AD. The occupation policy of Avar and ancient Hungarian tribes were similar due to similar steppe-type husbandry and management of space and power. The Hungarian tribal alliance had also a mixed ethnic composition with attached folk elements/ethnic groups that joint along the way westwards from the Ural region through the Middle-Volga region and eastern European steppe (along the border of the Khazar Qaganate). The Eurasian Avars and Hungarians were among the peoples who determined the fate of Europe during the Antiquity-Middle Ages transition.

Review of the archaeogenetic results. Two papers have been published including data on the genetic composition of the Avar period population of the Carpathian Basin. One describes a local Avar group from the south-eastern Great Hungarian Plain (Csősz et al. 2016) based on hypervariable region (HVR) I profile of the mitochondrial DNA (mtDNA), whereas another study investigates samples of aforementioned Avar elite group mostly from Danube-Tisza Interfluve (Csáky et al. 2019a). The Avar elite group presented a wide range of Eurasian lineages with dominance of the Asian mtDNA haplogroups (69.5%). Despite the limited number of available ancient whole mitogenome sequences from Central-Asia, the genetic affinities of the Avar elite individuals to Central and East-Central Asian ancient populations are appreciable (Csáky et al. 2019a). Further DNA data from East and Central Asia are needed to specify the ancient genetic connections, especially from the 4th–5th c. of Mongolia, which would be an important region in the study of the origin of Avars (Kradin 2005: 149–169).

Concerning the Hungarian Conquerors, several cemeteries from the different part of today's Hungary have been intensively studied recently. Csősz et al. (2016) describes maternal gene pool of 76 individuals from Hungarian conquest period as a mixture of West-, Central- and North Eurasian elements. They suggest that Central-Asian influxes (beside Uralic/Finno-Ugric and Turkic inflows) had possible but limited genetic imprint in the genetic composition of Hungarian Conquerors. On the other hand, Neparáczki et al. (2018) published 102 whole mitochondrial genomes from early Hungarian Conqueror cemeteries with an East Eurasian component of 30.4%. They suggest that steppe nomads (Central Asian Scythians) and Eastern European Srubnaya culture's population could have been the basis of Conquerors' mixed maternal genetic makeup, among other genetically unknown candidates. It is important to note, that the majority of their investigated Hungarian sample set comes from a small region, from today's northeast Hungary, therefore not obviously represents the whole Conqueror population. Furthermore, the Srubnaya culture existed more than 2000 years before the appearance of the first traces of archaeological heritage of ancient Hungarians, and direct link between Scythians and Hungarians also doesn't conceivable. Additionally, they claim that the results support the Hunnic-Hungarian genetic connection too (Neparáczki et al. 2018), although the Xiongnu genetic dataset is bare from Eurasia and Huns' genetic heritage is also unknown. Here we highlight four individuals from the Hungarian Conqueror population (10th c. AD) investigated by Neparáczki et al. (2018), who belong to Asian haplogroups A12a, D4j2 and Y1a1.

The hypothetical ancient homeland of Hungarians was on the east side of the Ural Mountains (i.e. Trans-Ural region), where also the Uyelgi cemetery (fig. 1) has been excavated since 2010 (Грудочко and Боталов 2013). The cemetery, where also several kurgans (burial mounds) were erected, belongs to the late Kushnarenkovo culture. Three chronological horizons (i.e. phases) could be separated on the site: 1) end of 8th and 9th c., 2) 9–10th c. and 3) 10–11th c. Whereas the all phases show continuity of maternal lineages, new elements of probably eastern origin appeared in the third phase, with a mtDNA A12a lineage among them (Csáky et al. 2019b). At the other investigated site – in the western foothills of the Ural Mountains (i.e. Cis-Ural region) in the Kama-Valley, 4th–9th c. sites are ordered to the Nevolino culture, whose end was probably connected to the migration of ancient Hungarians. Brody cemetery belongs to the early Nevolino culture (5th c. AD), where one individual with mitochondrial haplogroup D4j2 was investigated by our team (Csáky et al. 2019b). The next cemetery close to the Volga River in the territory of the Karayakupovo culture (9–10th c.) is Bolshie Tigani, probably belonged to ancient Hungarians of “Magna Hungaria”, where an A12a mtDNA haplogroup was detected by our team. Because the Hungarian language belongs to the Ugric branch of the Uralic linguistic family (Abondolo 1998) and evolved probably in the Trans-Ural region, two linguistically related ancient Khanty/Mansi people from Western Siberia were investigated as well, who are dated to the 10–13th c. AD, and assigned to proto Ob-Ugric cultures.

Discussion of three detected mitochondrial haplogroups with Asian origin. We performed three Neighbour Joining phylogenetic trees in program PHYLIP (Felsenstein 1989) using all published ancient and modern mitogenome sequences assigned to the given mtDNA haplogroups.

On the phylogenetic tree of subhaplogroup A12 (fig. 2a) four individuals from Uyelgi cemetery (10–11th c.), Bolshie Tigani cemetery (9–10th c.), Hungarian Conqueror Harta-Freifelt site (10th c. Carpathian Basin) and modern-day Hungary are clustering together, where they are showing identity (in case of Harta and Bolshie Tigani) or close proximity to each other, hence supposing tight connections between them. A modern-day Mansi and an ancient Khanty/Ugor individual from Vikulovo site (Tyumen Oblast) are also showing relatively close proximity to this subcluster on a basal position, which may indicate some relationship between them. One previously described Hungarian Conqueror sample from Karos III. clusters together with a Buryat sample as it was described in Neparáczki et al. (2018). However, new Conqueror sample from Harta shows the heterogeneity of Asian lineages in the conqueror population, and also that apparent “East-Inner Asian” connections become reshaped by new ancient data from Volga-Ural region.



Fig. 1. Location of the discussed cemeteries in the Carpathian Basin and in Ural region
 Рис. 1. Расположение исследованных могильников в Карпатском бассейне и на Урале

The phylogenetic tree of subhaplogroup Y1a1 (fig. 2b) consist of various North and East-Central Asian lineages, where an Avar period individual from Kecskemét-Sallai út is in basal position compared to the other modern samples from China and Far Eastern Russia. Furthermore, a Hungarian Conqueror from Karos I. is also represented, closest to a modern Uygur Y1a1 lineage. Due to the small number of available Y1a1 lineages along with their defined relative geographical proximity, but considering the fact, that they are separated by many mutation points, only a common geographical origin can be considered for the presented Y1a1 lineages.

The phylogenetic tree of D4j (fig. 3) covers a wide geographic range, where many of our samples are represented. Interestingly, one Avar period elite individual from Békésszentandrás and two Hungarian Conquerors from Karos I. show relative proximity to each other, surrounded by lineages from various origins. The second Avar elite individual from Kunpeszér clusters with modern individuals from Pamir region signaling the origin of their maternal ancestor. The Hungarian and Avar lineages could have an East-Central Asian origin based on the here presented phylogenetic tree. The lineage found in Brody is clustered strictly together with East European samples, whereas other Northwest Asian lineages can be observed at relatively close proximity probably representing a remaining or backflowing branch to Northwest Asia. The ancient Mansi lineage from Panovo (Omsk Oblast) is clustered with modern North-Asian Nganasan, Even and Evenk individuals.

Conclusion. The Carpathian Basin witnessed certain level of new genetic influxes from Eastern Eurasia at the time of the Avar and Hungarian Conquests. Localizing the origin of these Eastern elements is powered by our phylogenetic analyses. Avar lineages seems to more concentrate to East-Central and North-East Asia (Csáky et al. 2019a). The Hungarian Conquerors however had a very variable genetic composition. Avar and Hungarian lineages coincide on some haplogroup trees, such as on the here presented A12, D4j and Y1a1 trees. New mitochondrial lineages from the Ural and Volga region, studied by our team, ad a new perspective to the analyses of genetic origin of nomadic tribes settled in the Carpathian Basin. Neparáczi et al. (2018) connected some Hungarian Conqueror lineages ultimately to Central and Inner Asia, based on their phylogenetic connections to modern individuals. However, the increasing number of ancient samples from geographically closer populations restructure the phylogenetic trees of some haplogroups and change the apparent connections (such as in fig. 2a). The A12 tree also demonstrates the importance of full mitogenome analyses in order to reveal deeper structures and lineage clustering behind identical haplogroup labels. With the here presented examples we encourage all researchers who are interested in maternal genetic composition of populations or genealogical questions to analyse entire mitogenome sequences instead of hypervariable regions or certain SNPs of the mtDNA.

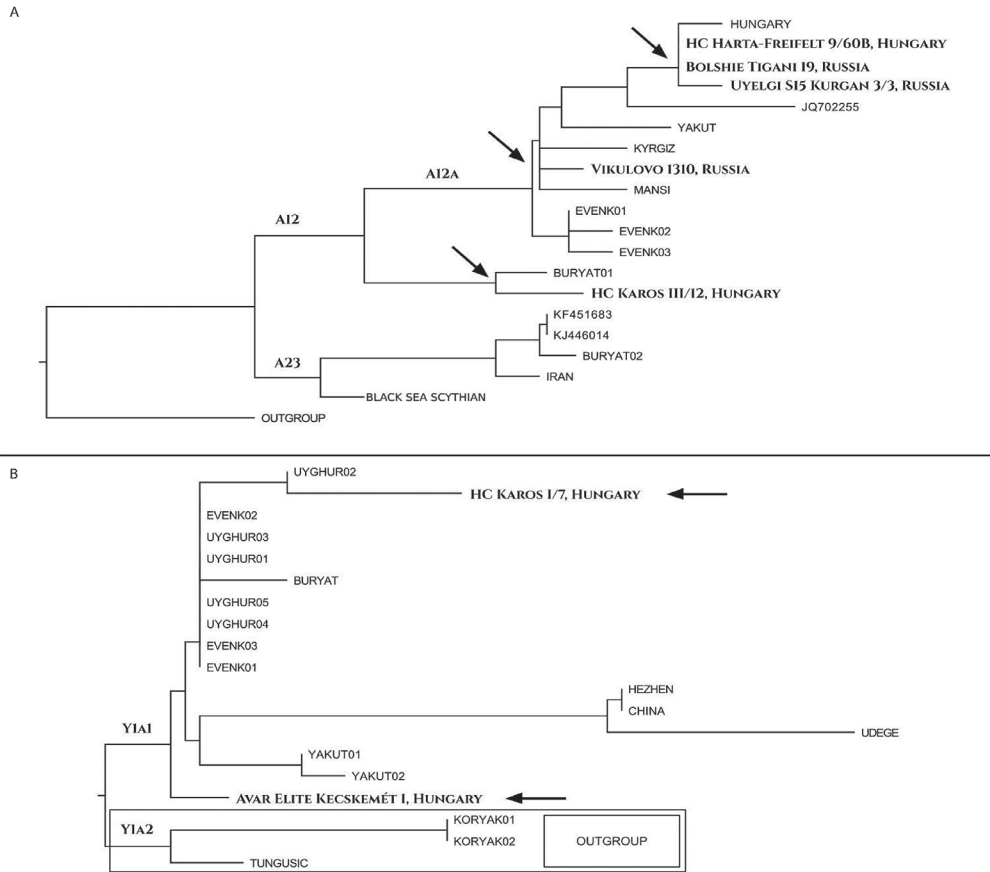


Fig. 2a. Neighbour Joining phylogenetic tree of mitochondrial haplogroup A12
 Рис. 2a. Соседство, соединяющее филогенетическое дерево митохондриальной гаплогруппы A12
 Fig. 2b. Neighbour Joining phylogenetic tree of mitochondrial haplogroup Y1a1
 Рис. 2б. Соседство, соединяющее филогенетическое дерево митохондриальной гаплогруппы Y1a1

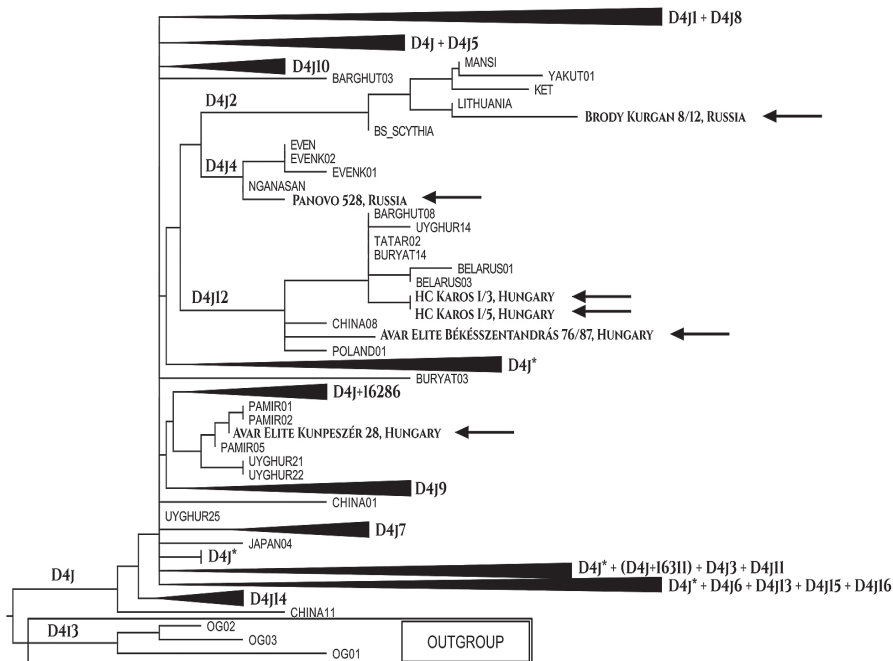


Fig. 3. Neighbour Joining phylogenetic tree of mitochondrial haplogroup D4j
 Рис. 3. Соседство, соединяющее филогенетическое дерево митохондриальной гаплогруппы D4j

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