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The official deadline of present grant expired in Augustus 2021, when I submitted a work report, which can be regarded as a terminal report, because the project had been finished by that time. As far as the scientific fulfilment is concerned, here I can just repeat what has been described in my last report (Aug. 2021), which I copied below. The only advance what I can add to these, is that in addition another publication has been submitted to Current Biology, entitled "Whole genome analysis sheds light on the genetic origin of Huns, Avars and conquering Hungarians" , which is now under review https://papers.ssrn.com/sol3/papers.cfm?abstract_id=4020523. Besides, we presented our results at several additional conferences.

Last year, when we have completed our project, published the mitogenome results, which appeared last year in the GENES journal (2021, 12(3), 460; https://doi.org/10.3390/genes12030460) under the title "Maternal lineages from 10-11th century commoner cemeteries of the Carpathian Basin".

As indicated in my previous report, another paper was published in Scientific Reports in 2019, (https://doi.org/10.1038/s41598-019-53105-5) under the title: "Y-chromosome haplogroups from Hun, Avar and conquering Hungarian period nomadic people of the Carpathian Basin" and a third paper one year before in PLOSone (2018) (https://doi.org/10.1371/journal.pone.0205920) under the title "Mitogenomic data indicate admixture components of Central-Inner Asian and Srubnaya origin in the conquering Hungarians".

As I indicated in my previous reports, we also we sequenced 30 whole genomes at the expense of present NKFI grant, which was supplemented with 230 other genomes from additional financial sources. We planned to publish the genome results earlyer, but but while working on the genome project, several papers appeared in the literature, publishing hundreds of relevant new Bronze Age – Iron Age genomes from Kazakhstan, Mongolia, Russia and China. Thus we had to reanalyze our genomes in the light of these new results. The re-analysis has been completed now, and we have submitted the publication to Current Biology. In short, the following outstanding results were found:

a) Hun period: In spite of our low European Hun sample size, we were able to identify practically the whole genetic spectrum present in late Xiongus; Scytho-Siberian, East Asian, Han Chinese and Sarmatian providing evidence for the long debated Xiongnu affinity of European Huns.

b) Avar period: We identified an "Avar Asia core" population predominantly from elite graves, which unambiguously originated from present day Mongolia. These genomes preserved 7-8 thousand years old Early-Neolithic Siberian features. Other Avar samples were genetic compounds of the "Avar Asia core" and Scytho Siberians, or the "Avar Asia core" and people from the Caucasus region. A significant proportion of the Avars had no Asian roots, but had pure Caucasus origin.

c) conquering Hungarians: We could also identify a "Conqueror Asia core" population mostly derived from elite graves, certainly representing the immigrant elite without local roots. We have shown that "Conqueror Asia core" had common origin with modern Nganasan, Mansi, Enets and Selkup people, each speaking languages belonging to the Uralic family, indicating Nganasan (Samoyedic) origin of the Siberian component in Conquerors. The "Conqueror Asia core" genome could be modelled as 50% modern Mansi, 30% Early Sarmatian, 20% late Xiongnu, inferring a shared genome history with Mansis till the end of the Bronze Age and subsequent Sarmatian admixture during the Iron Age, then a severe impact from late Xiongnus during Antiquity. Thus our genomic data corroborated linguistic results, verifying that Uralic languages did not spread independent of people (genes), including Hungarians. Furthermore, our results confined the geographic range of this ancient Bronze Age relation to the Northern Kazakhstan region settling the long debated origin of Hungarians. Besides, these data also reveal that ancestors of the Hungarians had been part of the organized steppe nomadic societies at least since the late Bronze Age, and were later associated with Asian Huns, settling another long debated question of Hungarian prehistory.

The results were presented last year on several conferences, as listed below:

- Szegedi Tudományegyetem - Sófi József Ösztöndíj konferencia (online): 2021. február 11.
- Új Nemzeti Kiválósági Program (ÚNKP) ösztöndíj konferencia (online): 2021. június 21.
- Kőrösi Csoma Sándor – Az idők arcai című tudományos konferencia, Kovászna: 2021. júl. 1-3.
- 27th Annual Meeting of the European Association of Archaeologists, Kiel (online): 2021 szeptember 6-11.
- XX. “Genetikai Műhelyek Magyarországon” Minikonferencia 2021. szeptember 24.
- Magyar Humángenetikai és Genomikai Társaság XIII. kongresszusa 2021 Szept. 2-4
- Archeogenetikai adatok a hunokról: A világhódító hunok Ázsiában és Európában MKI Konferencia 2021 okt 27-28.
- Hungarian Molecular Life Science Conference, Population genomic characterization of migration period populations in the Carpathian Basin Magyar Genetikai Társaság és Magyar Biokémiai Társaság konferenciája, 2021 nov. 5-7
- Hadak útján - népvándorlás kori konferencia, Mit tudtunk meg a honfoglalók teljes genom adataiból? Laczkó Dezső Múzeum, Veszprém 2021 nov. 25.
- Magyar Biológiai Társaság Szeged, Populáció-genomikai eredmények a hunok, avarok és honfoglalók származásáról Szeged 2021 nov. 18