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DISSERTATION SUMMARY

# Genetic polymorphism in Cumanian population determined by analysis of ancient bone samples

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In the Hungarian village of Csengele, on the borders of what is still called Kiskunsag, an archaeological excavation in 1975 revealed the ruins of a mediaeval church with 38 burials. Supported by historical data archaeologists have established that the buried persons belonged to the Cumanian ethnic group. In 1999, the grave of a high-status Cumanian was discovered, about 50 meters from the church of Csengele, which could prove the ethnic identity of the former excavated remains.

The ethnic origins of the Cumanians are uncertain, although their anthropological characteristics suggest that their geographical origin might be in Inner-Asia, South-Siberia. According to historical data after the ravage of Hungary by Tartar hordes, the Cumanians settled down on the partially uninhabited area of the early Hungary. So far these ethnic groups both genetically and culturally completely assimilated into Hungarians. In order to study the genetic origin and relationships of an ethnic group in such cases, analyses of ancient DNA (aDNA), obtained from archaeological bones of very early settlers of that particular ethnic group, could be the only reliable solution.

Mitochondrial DNA (mtDNA) is commonly used in aDNA studies because of its high copy number and the lack of recombination due to its exclusively maternal inheritance (Giles et al. 1980). The hypervariable region 1 (HVR-1) of the mitochondrial control region is routinely used in human phylogeographic studies, because it evolves 10 times faster than the protein coding-region of mtDNA (Richards and Macaulay 2001; Vigilant et al. 1991). Human mtDNA HVR-1 mutations have accumulated sequentially along radiating maternal lineages, during and after the process of human colonization of different geographical regions of the world (Marjoram and Donnelly 1994). Hence, haplogroups (groups of mitochondrial DNA types) often show geographic specificity (Torroni and Wallace 1995). Analysis of mtDNA in populations therefore allows reconstruction of their maternal lineages, makes it possible to study the genetic traces of migration and admixture of different human communities, and helps to estimate the degree of relationships within and between populations.

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To determine the genetic background of ancient Cumanian population, DNA was extracted from 11 bone samples. The nucleotide sequences of the mitochondrial HVR-1 were determined. To define the haplotypes and the haplogroups, where the Cumanian samples belong to, the HVR-1 polymorphic sites and in problematic cases the haplogroup–associated SNPs in the mitochondrial protein coding-region were determined. A database was set up from previously published mtDNA HVR-1 sequences, representing 7,099 persons from 153 different worldwide populations. Median-joining networks were created to assign the relationships between Cumanians and the components of our database. The maternal origin of the Cumanian samples examined was determined through these phylogenetic networks.

A genetic method based on X and Y chromosome specific alphoid satellite markers (Lin et al. 1995) was applied to determine the gender of the bone material from an infant and a juvenile individual and for confirming the anthropological sex identification of four adult individuals.

It was established that the Cumanian population derived from the excavation was not genetically homogenous. According to our results the Cumanians could be originated from Central-East Asia. As a result of genetic admixture those Cumanians, who settled down 800-900 years ago in Hungary, contained several European genetic elements.

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