

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 complete-

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