Y-CHROMOSOME ANALYSIS OF GOTHS FROM THE MASLOMECZ GROUP CEMETERIES IN SOUTHEASTERN POLAND

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The Goths were an important part of European history from the 1st to the 8th century AD. For many years, various hypotheses have emerged among researchers regarding their origin and dispersal. Unknown is also the scale of assimilation of the local people they encountered during their migrations across Europe. The aim of this study was to determine the origin and genetic structure of the male lineages of the Goths from the Masłomęcz group who inhabited the Hrubieszów Basin (southeastern Poland) from the 2nd -4th century AD using Y chromosome. The material for analysis consisted of skeletal fragments collected from 43 individuals. Samples with the highest endogenous DNA content were sequenced directly to low genome coverage. For the others, after sex determination, we performed targeted enrichment with a custom panel of 10k Y chromosome SNPs. This allowed us to determine the Y chromosome haplogroup of 18 individuals. A total of 14 individuals (78%) represents the Y chromosome haplogroups most closely related to the Scandinavian population. Thirteen individuals were classified into subclades of haplogroup I1, four to haplogroup R1a and one to haplogroup J2b. Haplogroup I1 currently occurs mainly among people living in Scandinavia. Ancient DNA analyses showed show that I1 has been present in the Scandinavian population since at least the Bronze Age. One of the individuals belonging to haplogroup R1a-Z284 belongs to a subclade found almost exclusively in the ancient and modern Scandinavians. The remaining four individuals belong to haplogroups R1a and J2b most probably represent the effect of assimilation of local people, met by Goths during their numerous war expeditions and settlement expansion.

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Keywords

ancient DNA, Goths, Y chromosome

Note/comment

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