

Dr. Magdalena Bus, The ISFG Short Term Fellowship in the Institute of Legal Medicine (GMI), Medical University of Innsbruck (11 – 17/12/2017).

In the project, human remains from a mass grave discovered in Sweden were subjected to mitochondrial DNA analysis. The grave was dated back to the Viking Age and osteoarchaeological analysis assigned the remains to at least 19 individuals: 13 men, five women, and one child, aged from approximately 7 to 55 years. DNA was extracted from bones and teeth. PCR amplification and Sanger sequencing of short mtDNA hypervariable regions HVS-I and HVS-II were performed covering the nucleotide positions 16128 to 16348, and 45 to 287, respectively. Mitotypes were obtained for most samples, which allowed re-association of the remains and revealed the possible maternal relationship among some individuals. However, problems with haplogroup determination for a few samples appeared. Therefore, information from additional mtDNA positions would be helpful to perform reliable haplogroup determination adding further support to the possible maternal relationships of some individuals. A subset of DNA samples was subjected to whole mitogenome sequencing with the Precision ID mtDNA Whole Genome Panel and the Ion S5 system (Thermo Fisher Scientific). This part of the project was performed in collaboration with the scientists from the Institute of Legal Medicine (GMI), Medical University of Innsbruck. Haplogroup determination was performed using the EMPOP database.

Based on the combined information from Sanger sequencing and whole mitogenome sequencing, all individuals were assigned to West Eurasian haplogroups (i.e., H, U, J, T, X, V, R). Most individuals from the grave were maternally unrelated. Several samples that presumably belonged to a single skeleton were assigned to different individuals. In one case, remains apparently representing different individuals were finally re-associated as belonging to a single individual. For three samples, Sanger sequencing data showed that these individuals might be maternally related. However, the additional information obtained after whole mitogenome sequencing facilitated discrimination of these individuals by assigning them to three different mitotypes. Most haplogroups determined based on Sanger sequencing data did not change after the additional information from the entire mitogenome. In a few cases, however, the mitogenome data indicated a different haplogroup status, which could be a result of the absence of control region patterns. We conclude that a minimum of 20 persons were buried in the grave and possible maternal relationships were observed for two pairs of individuals. Although the remains displayed an advanced level of DNA degradation, the combined use of Sanger sequencing and MPS with the Precision ID mtDNA Whole Genome Panel revealed at least partial mtDNA data for all samples.

The ISFG Short Term Fellowship allowed me to finalize the project and establish a fruitful and continuing collaboration with the scientists from the group in Innsbruck. The data from the project was disseminated in the form of the publication entitled “Mitochondrial DNA analysis of a Viking age mass grave in Sweden.”

Magdalena M. Buś, Maria Lembring, Anna Kjellstrom, Christina Strobl, Bettina Zimmermann, Walther Parson, Marie Allen. Mitochondrial DNA analysis of a Viking age mass grave in Sweden. *Forensic Science International: Genetics*. 2019, 42:268-274.