**Short Term Fellowships of the ISFG: a report**

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I have visited the Institute of Legal Medicine (GMI), Medical University of Innsbruck from April 02-30 2018. The collaboration between GMI and the Department of Forensic Genetics, Pomeranian Medical University in Szczecin includes a project of identification of human remains discovered at the death camp in Sobibor, Poland. Genetic testing on remains of a total of 10 individuals performed until April 2018 revealed that both mitochondrial haplogroups and individual haplotypes of all the individuals could be found among modern Ashkenazi Jews. Also, the initially estimated Y chromosomal haplogroups were the ones prevalent for Ashkenazim.

The aim of the visit was to extend the genetic testing of the discussed bone samples. Due to that a new extraction of the samples with the protocol introduced by GMI has been performed. One part of the visit was assigned to work confirming the Y haplogroup estimations based on available Y-STR data. In reference to the already published studies on modern Ashkenazim we have decided for the SNP markers characteristic for this population. All of them corresponded with the Y-SNPs suggested by the used online prediction tool, Nevgen. We have designed primer pairs for all the SNP sites and performed Sanger sequencing of the PCR products. The results were analyzed with Sequencher DNA Sequence Analysis Software. We managed to confirm all the estimations and to establish the final Y chromosomal haplogroups, which according to the studied papers are known to be prevalent for Ashkenazim. Additionally, we have extended the genetic testing of 4 individuals in order to perform the comparison of their Y-haplotypes to the published Cohen Modal Haplotype. We have observed that all of them belong to the same haplogroup, namely P58, which is known to be more frequent among Jewish priestly caste named Kohanim. The available Y-STR data didn't include two STRs from the CMH (DYS388 and DYS426) and those were then sequenced. The analysis of the results revealed that two of the studied individuals show a full match with the CMH in the range of 12 Y-STRs and the remaining two represent similar haplotypes.

The second part of the visit was used to extend the research by analyzing ancestry-informative markers. We have performed massively parallel sequencing using in-house kit including more than 200 global AIMs. For MPS we used ThermoFisher Ion S5 System. The genotypes were analyzed with the IGV software. The analysis is ongoing and the results will be used to estimate the ancestry of the studied individuals based on AISNPs.

The remaining DNA extracts will be used for further forensic analysis in order to establish more details of the studied remains. The findings of this collaboration are currently being summarized in a manuscript to be submitted for peer-reviewed publication.