

Short report – ISFG short-term fellowship



Applicant

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Purpose

Japan's Ministry of Health, Labor and Welfare started a project of identifying victims of World War II by DNA typing in 2003. In this project, forensic scientists extract DNA from old tooth or bone (post mortem interval: over 70 years) and examine autosomal short tandem repeat (STR), Y-STR, and mitochondrial DNA. Final decision of identity is performed by kinship analysis. However, because extracted DNA is low in quantity and quality, obtained profiles are sometimes partial and their interpretation is difficult. To improve these problems, I visited University of North Texas center for human identification (UNTCHI) from September 2 to September 29, 2018. The main purposes of my visit were to get information about DNA typing techniques from challenged remains and consider a method for kinship determination in multiple comparison.

Outcome

UNTCHI has several specialized sections such as Missing Persons and Forensic Unit. Among them, Research and Development Lab conducts advanced researches about various topics. I learned their DNA extraction protocol of challenged skeletal remains and observed their experimental instruments. They take account of contamination prevention by careful washing and UV-crosslink. I'm going to apply their protocol to challenged remains and evaluate the power of detection. I also learned the experimental method and data analysis of massively parallel sequencing (MPS). MPS can examine many markers and samples simultaneously and detect sequencing variation in STR allele. On the other hand, the method of data analysis depends on panel, sequencer, and condition of samples. Therefore, we must validate the capability of the system and set appropriate method of data analysis prior to actual casework. During the stay, I attended lab meetings and received advices about my research. We plan to do collaborative research about efficiency of X-STR in familial searching.

In addition, I visited Missing Persons, Forensic, and CODIS Unit to learn practical casework of human identification in the center. Thresholds for data interpretation (e.g. analytical and stochastic threshold) were set by internal validation according to the purpose. CODIS has multiple different databases and can search candidates by using autosomal STR, Y-STR, and mtDNA. I also heard about National Missing and Unidentified Persons System (NamUs) managed by UNTCHI. NamUs provides various information (e.g. DNA profiles, fingerprints, and dental records) about missing persons and unidentified remains. I found that comprehensive database and searching tool such as CODIS or NamUs are needed for effective screening of unidentified remains.

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