EVALUATION OF METHODS TO PROCESS BONE EVIDENCE FOR FORENSIC DNA ANALYSIS

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After attending this presentation, attendees will be familiar with the research that has been conducted for processing bone evidence for forensic investigations. This study has the potential to make a significant impact on the processing of skeletal evidence for the forensic community and law enforcement agencies. Forensic analysis of DNA from bone can be important in investigating a variety of cases involving violent crimes and missing person cases. However, bone is difficult to process for isolating DNA. To remove the potential presence of co-mingled remains and to eliminate contamination by environment-borne inhibitors, and bacterial growths that interfere with forensic DNA analysis, the outer surface of the bone fragment must be cleaned, which is a labor-intensive and a time-consuming step. Thus, a simple and reliable processing method is highly desired. This study is to address this issue and evaluate two methods for processing bone specimens prior to DNA isolation. Mechanical sanding and trypsin enzymatic processing methods were compared in this study. The effects of these methods on the yield of DNA isolated and the quality of DNA analysis were studied.

The effects of cleaning methods on the yield and the quality of DNA isolated were compared side-by-side:

1) DNA extracts of the sanding method, and,
2) DNA extracts of the trypsin method.

It was revealed that comparable values of DNA yields between the two methods were observed. Additionally, to evaluate the capabilities of the cleaning effect of the bone processing methods, the presence of environment-borne inhibitors in the DNA extracts was monitored using IPC. In this study, similar IPC C_t values were observed as the DNA extracts of the trypsin method compared with that of the sanding method. This suggests that the cleaning effect of the trypsin method was consistent with that of the sanding method. The characterization of the effects of the trypsin treatment on the quality of DNA profiling was carried out. To evaluate the integrity of the genomic DNA isolated, the percentage of allele calls of STR profiles and the rfu values of STR alleles were compared between the two methods. To evaluate the quality of mtDNA isolated, the amplified mitochondrial DNA at the HVI and HVII regions were quantified and compared. Comparable levels of amplification success of STR and mtDNA fragments were observed between the two methods. Paired-sample t-tests revealed no significant difference between the two methods in most of these experiments. This study suggests that the trypsin method can be used as an alternative to mechanical cleaning method for human bone samples. ⌘