B80 Analysis of California's Unidentified Remains – Lessons From the Lab

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After attending this presentation, attendees will learn how some of the obstacles presented by challenging human remains samples have been overcome with the implementation of the herein described techniques and how these time-saving techniques have allowed for the analysis of large numbers of samples.

Identifying human remains using DNA is an important and yet often very difficult and time-consuming task. After analysis of hundreds of remains, new techniques have been learned through the California Department of Justice Missing Persons DNA Program that will be useful to the forensic science community, whether in dealing with day-to-day cases or mass disasters. This presentation will impact the forensic community and/or humanity by sharing these techniques which will provide a signif- icant contribution will be made to the critically important task of returning unidentified remains to their families.

Analysis of remains that have been burned, buried or submerged in water for a number of years, treated with lime (calcium hydroxide) or for- malin-fixed and paraffin-embedded can be extremely challenging. The analysis of such samples is very time consuming and often results in only a partial STR DNA profile, making conclusive identifications difficult if not impossible. After analysis of hundreds of unidentified remains as part of the California Department of Justice Missing Persons DNA Program, new techniques have been developed and implemented to improve effi- ciency and increase the number of overall STR profiles obtained from unidentified human remains. Such improvements offer the additional benefit of ready preparedness for large numbers of samples in the event of a mass disaster.

New techniques such as an in-house developed and validated quanti- tative polymerase chain reaction (PCR) assay have decreased the time taken for quantification of the DNA from remains. This qPCR assay is a duplex amplification allowing for simultaneous quantitation of human-spe- cific mitochondrial and nuclear DNA. This assists in assessing upfront the best approach for sample processing. Furthermore, determining whether a sample is degraded or inhibited is often critical in assessing the next step in a difficult case analysis, especially when DNA quantity is limited. An in- house degradation assay allows for the assessment of the relative sizes of nuclear target and the possible presence of inhibitors by incorporating an internal positive control. The assays will be briefly presented along with case examples illustrating their application.

A modified amplification technique has allowed for a more efficient amplification of samples containing PCR inhibitors. Introduction of both additional Bovine Serum Albumin Fraction V (BSA) and AmpliTaq Gold™ DNA polymerase to nuclear DNA amplifications has been shown to have synergistic effects on overcoming inhibition. Enhanced PCR yield has been observed in varying samples and thus the technique is applicable to a variety of sample types (*e.g.*, bone, samples deposited in soil, etc.). Application of this technique to cases allowed for the identification of remains where initially no STR profile was obtained. Case examples will be presented.

Finally, in some jurisdictions all that remains of unidentified bodies from some of the older cases are formalin-fixed and paraffin-embedded tissues. Methods for enhancing extraction efficiency from these types of tissues have been explored and will be discussed.

Enhanced Amplification, Quantitative PCR, Human Remains

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