B67 Population Study on 20 Intronal SNP's as a Guideline for Use in Forensics

Rijad Konjhodzic, BS, Jon M. Davoren, MS, Daniel Vanek, PhD, International Commission on Missing Persons, Alipashina 45a, Sarajevo, 71000, Bosnia and Herzegovina; Amina Kurtovic, BS, University Clinical Center, Alipashina 45a, Sarajevo, 71000, Bosnia and Herzegovina; Edwin F. Huffine, MS, International Commission on Missing Persons, Alipashina 45a, Sarajevo, 71000, Bosnia and Herzegovina*

The goal of this presentation is to discuss the results of a SNP population study using the Applied Biosystems Taqman® assay. This study is part of a larger project aimed at the development of a rapid and inexpensive SNP tests that provides enough discrimination to be useful as a tool in forensic casework.

This presentation will impact the forensic community and/or humanity by demonstrating the potential of using of SNPs in terms of identification of victims of mass diasters.

There are currently a number of methods available for SNP testing including Taqman®, Snapshot®, pyrosequencing, and GC-MS. Each of these techniques has been developed for different purposes and each has advantages and disadvantages for different uses. For forensic testing an ideal technique would ideally be inexpensive, robust, allow high throughput and have low requirements for DNA quantity and quality.

For some time, testing of Single Nucleotide Polymorphisms, or SNPs, have been used as a molecular biology method, mainly for medical research, although there have been implementations in forensics, with various degrees of success. However, the very nature of a SNP, as a potential single base difference, makes it attractive for forensic scientists, who in their work are forced to deal with not only very low quantities of DNA template, but also a degraded ones.

As a first step, the feasibility of the Taqman® assay was evaluated as a potential forensic testing method. Twenty tested SNP's, located in intronal sequences and with the a lesser allele having a frequency of above 40% were selected from the Applera SNP database. The 20 SNPs were genotyped by 5' nuclease reactions using TaqMan MGM probes. The amplification, which is very simple, and allows preparation of large numbers of samples in short periods of time. Amplifications were performed done on an Applied Biosystems 9700 master cyclers, and a post PCR read for allelic discrimination was performed done on an Applied Biosysytems SDS 7700.

SNPs, ICMP, DNA

 ** Presenting Author*