B107 Massively Parallel Sequencing (MPS) and Short Tandem Repeat (STR) Analysis of Human DNA From Partial Bloody Fingerprints Enhanced With Columnar Thin Films (CTF)

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Learning Overview: After attending this presentation, attendees will understand how CTF development is conducted using the Conformal-Evaporated-Film-By-Rotation (CEFR) method on partial bloody fingerprints. STR analysis completed on these types of samples will demonstrate to the audience, that certain evaporant materials do not inhibit Polymerase Chain Reaction (PCR) or capillary electrophoresis. Additionally, presentation of the data from Single Nucleotide Polymorphism (SNP) genotypes will inform the audience on new technologies that can be implemented in crime laboratories.

Impact on the Forensic Science Community: This presentation will impact the forensic science community by focusing on new DNA analysis methods and the non-traditional enhancement of fingerprints.

Fingerprints are commonplace on various substrates at crime scenes. Traditional methods of enhancing latent fingerprints include cyanoacrylate fuming and dusting with carbon-based, fluorescent, magnetic, or other powders. Enhancement of partial bloody fingerprints is challenging because the latent and the patent components require different methods that may be difficult to cascade. Deposition of a columnar thin film (CTF) on partial bloody fingerprints has been shown to be effective for some types of forensically relevant substrates. CTF deposition requires the use of the conformal-evaporated-film-by-rotation (CEFR) method, allowing for conformal growth of CTFs from the fingerprint. Prior research with deposition of CTFs of Alq_3 on partial bloody fingerprints on brass has established that CTF deposition preserves DNA for short tandem repeat (STR) DNA analysis.

Recent advances in massively parallel sequencing (MPS) have made sequencing more economical and faster compared to earlier technologies. Single nucleotide polymorphisms (SNPs) are advantageous for use with low-quality samples because their amplicon size is smaller than that of STRs. MPS technology, in combination with SNPs, can be helpful in identifying DNA profiles from low-quality samples such as fingerprints. The primary goal of this research is to combine fingerprint enhancement with CTFs, and DNA analysis with MPS allowing for dual identification of an individual, thereby strengthening evidentiary value. Additionally, MPS libraries may be prepared manually or through automation. A secondary goal of this research was to compare sequencing data between the two library preparation methods.

Partial bloody fingerprints collected on glass, brass, cherry wood, black garbage bags, and clear sandwich bags were used in this project. CTFs of Alq_3, gold, $Eu(tta)_3phen$, or GeSbSe chalcogenide glass, as appropriate, were deposited on the samples. DNA was extracted from undeveloped as well as CTF-developed fingerprints. Quantification using qPCR was performed to determine the degradation index of every sample. In addition to STR testing, DNA extracts were also sequenced on the Ion S5™ to determine SNP genotypes. The Precision ID Identity Panel contains primers for 124 SNPs and consists of 90 autosomal and 34 Y-clade SNPs. The Ion Chef™ was used to prepare the libraries via automation, as well as to template the libraries onto the semi-conducting chip for sequencing. This study demonstrated that CTF nanotechnology can be used to individualize humans using both STR and MPS techniques. It was determined that the use of gold, chalcogenide glass, and $Eu(tta)_3phen$ as evaporant materials were not inhibitory to STR analysis. It was concluded that automated and manual library preparations have different advantages, and laboratory throughput may influence which method is implemented.

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Massively Parallel Sequencing, Columnar Thin Films, Partial Bloody Fingerprints