# MASSIVELY PARALLEL SEQUENCING AND SHORT TANDEM REPEAT ANALYSIS OF DNA FROM PARTIAL BLOODY FINGERPRINTS DEVELOPED WITH NANOTECHNOLOGY

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Fingerprints are commonplace on various substrates at crime scenes. Traditional methods of enhancing latent fingerprints include cyanoacrylate fuming and dusting with carbon-based, fluorescent and magnetic, or other powders. Enhancement of partial bloody fingerprints is challenging because the latent and the patent parts 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. 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 to use for 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. Combining fingerprint enhancement with CTFs and DNA analysis with MPS allows for dual identification of an individual, thereby strengthening evidentiary value.

Partial bloody fingerprints collected on glass, brass, cherry wood, black garbage bags, and clear sandwich bags were considered in this project. CTFs of $Alq_3$, gold, $Eu(tta)_3$phen, 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.