B67 STR Profiles From Chemically Processed Fingerprints

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The goal of this presentation is to present to the audience a method for obtaining STR profiles from processed fingerprints that are complete, partial, or smudged. Attendees will understand the use of processed fingerprints for identification beyond standard fingerprint analysis. STR profiles can be obtained from a processed fingerprint and are useful for DNA typing and identification. Modified extraction, amplification and analysis protocols used to obtain the STR profiles will be presented.

Fingerprints are often used in the forensic community to associate an individual with a crime scene. Fingerprints that are smudged or contain partial fingerprint profiles that are non-interpretable cannot be used for fingerprint analysis, however; DNA profiles can be analyzed from these types of fingerprints and provide valuable information for crime scene analysis or for investigative leads. Modified extraction, amplification, and analysis protocols were used to obtain STR profiles from processed fingerprints.

Using the Powerplex 16 STR typing kit, STR results have been obtained from fingerprints. Fingerprints were collected from both porous and nonporous substrates to include photocopy paper, polyethylene trash bags and polyvinyl chloride material. Fingerprints were processed with a variety of chemicals including the following processes: Ninhydrin, DFO plus Ninhydrin, Magnetic Powder, and Cyanoacrylate. For collecting epithelial cells from the processed prints, 3 methods were compared: dry swabbing, moist swabbing, or direct lysis. All 3 collection methods resulted in STR profiles. DNA from processed fingerprints was purified using the Qiagen QIAamp DNA Mini Kit and further concentrated with a Microcon 100 membrane. The amount of DNA obtained from a processed fingerprint corresponds to approximately 0.25 nanograms of genomic DNA. Current quantification methods for measuring DNA below 0.25 nanograms are inconsistent. Additionally, using the whole volume of purified DNA from the processed print is necessary to obtain maximum amplification yield. Therefore, quantification was not performed prior to amplification. Modified amplification protocols were used to amplify the Promega Powerplex 16 loci. Amplified product was electrophoresed on the ABI 3100 and analyzed using ABI Genescan and Genotyper software.

Full 16 locus profiles were obtained from DNA purified from the aforementioned fingerprint processes; however, some fingerprint samples resulted in partial profiles. Inhibition studies with human and non-human target DNA indicated the removal of potential PCR inhibitors. Results also indicate that the partial profiles were due to the variation in the number of cells associated with individual fingerprint samples, not the presence of PCR inhibitors associated with chemical processed fingerprints. Validation studies of STR methods using fresh and aged prints (up to 2 years old) collected from various substrates were performed. Fingerprints used in the validation studies were processed with a variety of chemicals including the processes listed above. Results from the validation study will be presented. Interpretation of STR results regarding peak height ratios, peak height thresholds, and mixture ratios will be also presented.

STRs, Processed Fingerprints, DNA Extraction

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