DNA TYPING ANALYSIS FROM CHEMICALLY PROCESSED FINGERPRINTS

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STR and mitochondrial DNA profiles can be obtained from chemically processed fingerprints. 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. Methods for collecting the cells, purifying the DNA, amplification of the loci, and interpretation of mtDNA sequencing and STR analysis from chemically processed fingerprints will be presented.

A. STR analysis results:
Using the PowerPlex® 16 STR typing kit, STR results have been obtained from fingerprints collected from porous and nonporous substrates processed with the following methods: Ninhydrin, DFO plus Ninhydrin, Magnetic Powder, and Cyanoacrylate. Three methods were compared for collecting epithelial cells from the processed prints: dry swabbing, moist swabbing, or direct lysis. All three-collection methods resulted in STR profiles. The Qiagen QiaAmp DNA mini-kit was used for purification and extraction of the DNA. Inhibition studies confirmed the removal of potential PCR inhibitors. Standard protocols were used to amplify the Promega PowerPlex® 16 loci. Full 16 locus profiles were obtained from DNA purified from the aforementioned fingerprints processes; however, some fingerprint samples resulted in partial profiles. 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 two years) collected from various substrates were performed. Interpretation of STR results regarding peak height ratios, mixture ratios, and peak height thresholds will be presented.

B. Mitochondrial DNA Analysis
Fingerprints collected on porous and nonporous substrates were treated with the following processes: Ninhydrin solution, Physical Developer, Magnetic Powder, DFO, Genetian Violet, Sudan Black, Cyano-acrylate, and RAM. Genomic DNA was extracted from these fingerprints using the Qiagen QiaAmp DNA Blood Mini Kit. MtDNA corresponding to the hypervariable region was amplified and sequenced. Direct sequencing of the amplified products produced interpretable DNA sequence for each of the tested processed fingerprints. The method was further validated by testing processed fingerprints that had been processed with a variety of different methods processed from a time period of several days to several years.