B68 DNA Extraction of Archived Palm Prints: Implications for Cold Case Evidence

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Attendees will learn how DNA can be extracted from archived palm prints, allowing for the genereation of CODIS compatible PCR DNA profiles. DNA considerations for the collection of palm print evidence.

This presentation will impact the forensic community and/or humanity by showing how archived palm prints, which may be too smudged or incomplete for traditional fingerprint identification, can be used for PCR DNA typing. This method could allow for the examination of cold cases in which this type of evidence is present. Obtaining a CODIS profile could allow for another way to identify a suspect.

The goalof this presentation is to improve the recovery of DNA and the production of PCR DNA profiles from palm prints that have been dusted with soot based fingerprint powder, and archived by tape lifting.

Archived latent prints are often the only probative evidence in many unsolved cases. Employing protocols previously developed for Low Copy Number (LCN) DNA samples by the High Sensitivity Team in the laboratory of the OCME, the DNA recovered from tape lifts of fingerprints was often insufficient to produce DNA profiles that could be compared to the national database, CODIS. Therefore the extraction method was optimized and applied to archived palm print evidence, in order to maximize DNA recovery.

Samples were collected from ten different subjects on two types of surface (Linoleum tiles and Plastic). Subjects, at least one hour after washing their hands, were asked to press both of their palms onto each surface for five seconds. The prints were then dusted using both black and dual-use fingerprint powders. Following enhancement, the prints were lifted from the surface using a clear adhesive tape and stored on a standard fingerprint lift card. In order to diminish the adhesive properties of the tape, the cards were stored in the freezer at -20° C for at least four hours prior to extraction.

The tape was then removed from the card to allow the digestion buffer, 5 mls of 0.01% SDS and Proteinase K, access to the epithelial cells attached to the tape. Thirty minutes was sufficient to digest the cells, yet still preserve the DNA. Samples were purified and concentrated with a centriplus 100 (Millipore) followed by a microcon 100 (Millipore) with the addition of Poly A RNA to prevent loss of DNA. DNA recovery was measured with SYBR Green I and real time amplification of an ALU sequence. All samples containing at least 6 pg of DNA were amplified for 35 cycles with PowerPlex® 16 (Promega) PCR reagents with a halved reaction volume and a doubled extension time. 4 µL of each PCR product was injected at 3 kV for 20 seconds on the ABI 3100 Genetic Prism® Analyzer. Data is expressed as the percentage of correctly determined alleles out of the possible thirty-two alleles amplified.

Twenty eight palm prints were collected and archived from six different subjects. At least 6 pg of DNA was recovered from 64.3% of these samples. This DNA was amplified to produce allelic determinations that were 57.4% correct. However, many of these samples were multi-component mixtures. Since extraction of the tape alone produced DNA alleles, the source of this contamination could be due to prior handling of the adhesive edges of the rolls of tape. Therefore, the middle of the tape containing the print was excised and extracted. Control pieces from the center of the tape did not contain extraneous sources of DNA.

Consequently, fifty more palm prints were processed with two methodologies to accommodate contamination from the tape. Half of the prints were collected as described above, but only the middle portions of the tape lifts were digested. Alternatively, the remaining prints were collected on tape that was UV treated prior to sample collection. Similar to the previous study, 65% of these samples contained at least 6 pg of DNA. However, these experiments demonstrated a significant decrease in the number of drop-ins. The non UV-treated tape averaged 46.34% correct alleles with 5.3 spurious alleles called, and the UV-treated tape produced on average 52.2% correct alleles with 15.2 spurious alleles. Furthermore, in order to generate reliable profiles, samples were amplified twice, and alleles were assigned only if they were occurred in both amplifications. Employing only concurrent correct allelic determinations, usable database eligible profiles were apparent, on average, in thirty percent of the samples
examined.

These studies suggest that archived palm and likely fingerprints may provide DNA evidence. In order to avoid sources of contamination, collection tape could be treated with UV and the DNA analyst should only process the center of the tape. Regarding archived prints from cold cases, the latter strategy is feasible, but depending on collection precautions, mixtures should be anticipated.

Low Copy Number DNA, Tape Lifts, Finger/Palm Prints

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