B135 An Analysis of the Complex Biological Components of Touch DNA

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After attending this presentation, attendees will better understand the complex biological components of touch DNA and the ways in which this important forensic evidence can be collected and analyzed.

This presentation will impact the forensic science community by providing a description of the relationship between the basic and applied scientific aspects of touch DNA. A systematic evaluation of the components of fingerprints, as well as the optimization of their collection and analysis, could help advance touch DNA technology and ultimately provide the forensic scientist with expanded capabilities.

Touch DNA is a trace-level sample left by human physical contact with surfaces, such as countertops, weapons, or clothing, that results in the transfer of epithelial cells. With advances in knowledge and technology over the past decade, forensic scientists have been increasingly more successful in profiling the nuclear DNA found in these touch samples, providing valuable evidence in many cases. Fingerprints are a prime example of the touch sample, but they also contain other biological components, such as microbial signatures and cell-free DNA, that could play a role in individualization.

The experimental approach described here was two-pronged, as it is rooted in both the basic and applied sciences: (1) basic science — analysis of the biological components of a fingerprint using massively parallel sequencing technology and evaluation of the differences between individuals; and, (2) applied science — optimization of the collection and analysis techniques of DNA in fingerprints deposited on various substrates and development of a set of fingerprint-positive controls for co-analysis with questioned samples to increase confidence in both positive and negative results.

To attain the basic scientific goals of the project, massively parallel sequencing technology was used to analyze the cell-free DNA and the microbiome of fingerprints. Cell-free DNA was collected as the portion of nucleic acid contained in a sample supernatant. Various extraction techniques were evaluated, including protocols involving carrier DNA and sample concentration. Metagenomic analysis of the microorganisms in fingerprints was accomplished after careful optimization of DNA extraction techniques designed to minimize bias introduced in the sample by factors such as incomplete homogenization of the sample matrix or insufficient and incomplete cell lysis. Bioinformatic analysis of sequence data provided an estimate of variance between samples and identified sequences that may be common between individuals. Further work will confirm the results.

To meet the applied science objectives of the project, a "fingerprint solution" was developed by the proportional combination of the major chemical components of an eccrine fingerprint. Buccal epithelial cells were collected in suspension, treated to reduce clumping, and counted using a hemocytometer. This number was equated to the DNA content of a certain volume of the suspension; therefore, a known quantity of DNA could be added to the fingerprint solution. The mixture was deposited on a surface and collected in parallel with true fingerprints, thus acting as a known positive control with the chemical characteristics of the fingerprint. The procedure has been tested and optimized for a number of surfaces and collection devices. The results of both the basic and applied experiments will be presented and discussed in the context of operational forensic science.

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Touch DNA, Microbiome, Cell-Free DNA

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