B13 Trace DNA: Casework Experience

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The learning objective of this presentation is to familiarize forensic scientists with the concept and practical applications of trace DNA analysis.

This presentation adds to the developing trace DNA casework analysis body of knowledge. For those in the forensic science community not familiar with the advantages and disadvantages of trace DNA analysis, this presentation will introduce its conceptual and practical applications. Forensic scientists who routinely conduct trace DNA analysis can compare their findings to the data in this study. As this data accumulates, the best methods for analyzing trace DNA can be developed.

Trace DNA is defined as the minute quantities of DNA transferred through skin contact, which can be successfully analyzed and follow the general principles of trace evidence. Polymerase chain reaction (PCR) technology has made the analysis of short tandem repeats (STRs) possible on the most minute and degraded DNA samples, such as trace DNA samples. Trace DNA STR analysis is a relatively new field in forensic science. Similar to the general principles of trace evidence, this type of analysis involves analyzing areas of potential skin contact to determine if an STR DNA profile can be obtained from these areas.

At the time of this publication, the Acadiana Criminalistics Laboratory (ACL) had analyzed 105 potential DNA trace samples over an 11-month period. Typical samples analyzed include steering wheels, cloth and latex gloves, caps/hats, tools, firearms, clothing, latent print smudges, and commercial containers. Using previously validated STR analysis procedures and adhering to the ACL's STR interpretation guidelines, the lab was successful in obtaining DNA profiles from 71% of the samples. 34% of the samples had results at 14 loci (13 STR CODIS core loci and amelogenin) and 37% of the samples produced partial profiles of 13 or fewer loci. 29% of the samples produced no results. Of the samples that produced DNA profiles, 55% were mixtures, 41% appear to have originated from a single source, 3% of the profiles were not interpretable, and 1% was traced to a contaminating source. When compared to reference samples submitted for comparison to the potential trace DNA samples, the reference samples were excluded as the source of the DNA in 31% of the samples. The reference samples were included as a possible source of the DNA in 44% of the samples. No conclusion as to the source of origin of the DNA could be drawn in 23% of the samples. 1% of the samples had contamination that could be traced to a known source.

Specific collection techniques, analytical methods, STR interpretation guidelines, updated information, and case examples will be presented at the meeting.

Trace DNA, STRs, PCR

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