E5 Assessing the Implications for Close Relatives in the Event of Similar But Non-Matching DNA Profiles

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After attending this presentation, attendees will understand the application of objective criteria to determine if a relative of an individual with a similar but non-matching DNA profile may have been the contributor of that similar sample.

This presentation will impact the forensic community by demonstrating a significant potential for increase in the number of investigations solved as a result of database searches.

One of the principle advantages of using STR genotypes for the purposes of human identification is their amenability to archiving in searchable databases such as the Combined DNA Index System (CODIS). More than two million complete, 13 locus STR-DNA profiles of convicted offenders have already been entered into the CODIS database in the United States and similar databases are maintained by European countries and Australia. These databases were created as investigative tools for law enforcement agencies tasked with identifying suspects in cases where a perpetrator has left biological material at the scene of a crime but few or no additional leads are available.

A perfect match between the STR DNA profile of an evidence sample and an individual whose genotype is maintained in a database of convicted offenders has clear utility as an investigative tool. Lack of concordance between the alleles of an evidence sample and an individual's DNA profile is also commonly used as an investigative tool in that the individual can be excluded as a source of the biological material in the evidence sample.

However, since the alleles associated with STR loci are inherited in a strictly Mendelian fashion, it is possible that the most likely explanation for a nearly perfect match is that the source of an evidence sample is a close relative of the individual whose DNA profile is available for comparison. While this information may prove to be very useful to law enforcement investigators, relatively little has been done to establish what level and kind of similarity between evidence and non- matching database profiles are sufficient to justify investigation of an individual's relatives.

Policies regarding familial searches within the United States vary widely. Using both the number and rarity of matching alleles, a general framework for determining the relative likelihood that an individual's close relative (e.g. a sibling, parent, or child) is the source of an imperfectly matching DNA profile is described. Also described are the results of simulations that provide statistical boundaries on both the number and rarity of the alleles shared between an evidence sample and an excluded suspect necessary to determine if a significant shadow of suspicion is cast upon the excluded suspect's relatives. It is not possible to arrive at a single metric such as "number of shared alleles" that is independent of allele frequencies, the number of initial suspects considered and the number of potential alternative suspects for the purposes of determining that the investigation of a sibling is warranted. Two important parameters, the size of the reasonable alternative suspect pool and the tolerance for false positives/negatives, are beyond the scope of forensic scientists and are left to be determined on a jurisdictional (and even case-by-case) basis.

Familial Search, DNA, Partial Match

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