B167 Patterns of Allele Sharing in 13-Locus DNA Profiles of Siblings and Other Relatives

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After attending the presentation, the participants will gain an understanding of the usefulness and limitations of assessing whether similar DNA profiles may come from related individuals. Determining such relationships can be a valuable tool in conducting criminal investigations.

This presentation will impact the forensic community and/or humanity by demonstrating Identifying the likelihood that DNA profiles are from close relatives can be of great value to criminal investigations. This can aid investigators in identifying new suspects, and may result in faster apprehension of perpetrators of serious crime.

In criminal investigations involving DNA evidence, it can be useful to know if DNA profiles may have come from related individuals. Previous studies have shown that the profiles of siblings match at six of the thirteen CODIS loci, on average. Since matches at five or six loci are not uncommon in unrelated individuals, the authors would like to assess whether two similar profiles are the result of coincidence or biological relationship. Profiles from over one hundred sets of siblings were compared, along with other first and second-degree relatives. The average number of identical loci (both alleles shared) in full siblings was 4.7, with a range of 1 – 9. The average number of non-matching loci (neither allele shared) was 1.5, with a range of 0-5. These results were compared with a database of several hundred unrelated individuals, with primary focus on those unrelated profiles with were identical at four or more loci. The average number of non-matching loci in these pairs was approximately 4, with a range of 1-9. Thus, the number of non-matching loci is the best predictor of whether two similar profiles are more likely from siblings than from unrelated individuals. However, because there is substantial overlap in the ranges, caution should be used when assessing the possible biological relationship of persons with similar DNA profiles. Another factor that should be considered is the overall expected frequency of the 13-locus profile. One individual in the database showed a high degree of similarity with a large number of unrelated profiles, matching at seven loci in two separate instances. The overall expected frequency of this profile is approximately 1 in 1 trillion (FBI Popstats). While this exceeds the threshhold for declaring identity, it is considerably more common than the frequencies observed for most 13-locus profiles.

The results of this study have proved useful in several cases in the authors' jurisdiction. In one such case, a bottle was obtained from the trash of a possible suspect in a series of sexual assaults. A 9-locus DNA profile obtained from the bottle matched the semen profile at six loci and shared one allele at the three other loci, a strong indication that the DNA on the bottle came from a sibling of the perpetrator (the suspect shared the house with two brothers). Based on this information, surveillance was increased on the suspect and a DNA sample was obtained when the suspect blew his nose and discarded the tissue on the sidewalk. This sample matched the semen profile from the sexual assaults, leading to the arrest and conviction of the rapist.

DNA, STRs, Siblings

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