A143 Performance of Statistical Approaches to Measure the Strength of DNA Evidence Exhibiting Possible Stochastic Effects

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After attending this presentation, attendees will appreciate how statistical approaches to assess the weight of DNA evidence perform when applied to samples exhibiting possible stochastic effects manifest as allelic drop-out. These conditions are frequently found in low-template samples or low-template components of mixed samples. Attendees will understand the conditions under which certain statistical approaches can, for example, over-state the strength of the evidence or lead to a false exclusion.

This presentation will impact the forensic science community by objectively exploring how commonly used simplistic approaches for interpreting challenging DNA samples perform in comparison to more rigorous approaches. The work presented provides a means to increase the accuracy and objectivity in interpreting DNA profiles.

Many biological samples recovered from crime scenes contain a limited amount of DNA. Because such samples contain relatively few copies of each locus, the random sampling of DNA molecules during the typing process may result in the failure to observe some alleles that are actually present. This phenomenon is known as allelic drop-out. The possibility of allelic drop-out can severely complicate the interpretation of forensic DNA profiles—even those obtained using the standard number of PCR cycles.

Several statistical approaches exist to assess the weight of DNA evidence for samples exhibiting stochastic effects. One strategy used, when only a single peak is observed at a locus, is to multiply the probability of sampling the observed allele from the population by two. This is called the “2p rule” and assumes that any other allele could be paired with the observed allele, but that this other allele has dropped out. A second strategy uses the standard random match probability, but omits those loci where allelic drop-out may be possible. In practice, loci containing any peaks below a pre-set stochastic threshold are excluded from the calculation. A third approach assesses the strength of the evidence using a likelihood ratio (LR). Extensions of the LR approach allow it to explicitly model and account for allelic drop-out in single- source and mixed samples.

While most published studies and a majority of statisticians favor the LR approach, many forensic laboratories in the United States still use one of the other two approaches described above when allelic drop-out is possible, presumably for the sake of simplicity. However, because no objective study has compared the performance of the three approaches on the same evidentiary profiles, it is unclear how much valuable information is discarded when using the simpler approaches and how often the simplistic approaches might be misleading. This study seeks to fill that void by comparing statistics calculated using each of the three approaches for low-template DNA profiles in mock evidence for which the contributors are known.

For mock evidentiary profiles, this study used 60 single-source DNA profiles generated using the IdentiFiler system by Dr. John Butler’s group at NIST. This dataset contains profiles obtained by amplifying 100 pg, 30 pg, and 10 pg of DNA from each of two individuals. For each of these 60 DNA profiles, LRs were calculated using each of the three previously described statistical approaches when the mock evidentiary profile originates from the person who contributed the reference sample. A good statistical approach to assess the weight of DNA evidence should produce a large LR under this situation. LRs were also calculated using each of the three statistical approaches when the mock evidentiary profile originated from a person other than the suspected contributor. Here the profile for the reference sample of the suspected contributor was simulated from a population frequency database. For a high-quality single-source profile, a good statistical approach should produce a small LR in this situation, ideally substantially less than one, indicating that the evidence supports an exclusion.

This presentation will include a comparison of the performance of each of the three statistical methods to quantify the strength of low- template DNA evidence. Situations where these methods have the potential to dramatically mis-state the strength of the evidence will be highlighted. For example, omitting loci containing peaks below a stochastic threshold frequently understates the strength of the evidence against the true contributor by many orders of magnitude relative to the approach that models allelic drop-out in a LR framework. However, the 2p rule performs similarly to the aforementioned LR approach when the suspected contributor was the true contributor.

DNA Interpretation, Allelic Drop-Out, Likelihood Ratio

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