A153 Suspect-Centric Combined Probability of Inclusion: A Means of Attaching Objective Statistical Weights to Mixed DNA Profiles Where Dropout May Have Occurred

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After attending this presentation, attendees will have a better understanding of the difficulties associated with assigning a statistical weight to a mixed Short Tandem Repeat (STR) DNA profile where allelic dropout may have occurred. A solution to the problem that generates a suspect-centric combined probability of inclusion that can be empirically evaluated will be described.

This presentation will impact the forensic science community by providing a means by which statistical weights can be attached to mixed samples where allelic dropout may have occurred. A suspect-centric combined probability of inclusion can be evaluated by comparing the result of using the suspect's profile to results obtained from similar analyses with the profiles of a large population of individuals who could not have contributed to the mixture.

Attaching statistical weight to samples with contributions from more than one individual where allelic dropout may have occurred is one of the greatest difficulties facing forensic DNA profiling. Despite effort by numerous parties, there is still no generally accepted means of attaching a reliable statistical weight to such a result.

Generally speaking, there simply may not be enough information present within an STR DNA profile to allow a reasonable inference to be made regarding the likelihood of allelic dropout. At the very least, determination of allelic dropout rates from features of evidence samples themselves (such as relative peak positions and heights) is challenging and can lead to a range of estimates that dramatically impact the final statistical weight attached to a sample. The lower precision of quantitation results for low-level samples and difficulties determining the relative contributions and even the number of different contributors pose problems for alternative means of determining allelic dropout rates. Some testing laboratories opt, in error, to generate statistical weights for mixed profiles where allelic dropout may have occurred by simply disregarding information from loci where not all of a possible contributor's alleles are detected. Such a suspect-centric approach is biased and fails to take into consideration information that might support alternative theories of a case. As a result, work to develop a means to attach statistical weights to mixed samples where allelic dropout may have occurred has consciously endeavored to minimize the impact of allelic dropout and avoid using information from a possible contributor's reference profile to resolve ambiguities associated with evidence samples.

Somewhat paradoxically, a suspect-centric approach that liberally invokes allelic dropout in a fashion that is heavily biased so as to include an individual as a possible contributor may offer an easily implemented and readily understood means of attaching a statistical weight to mixtures where allelic dropout may have occurred. Such an approach could be used to generate a "Suspect-Centric Combined Probability of Inclusion", or "SCCPI", using the standard CPI calculation for a mixed-evidence sample — but only for loci where all of a possible contributor's alleles are observed. The resulting statistic can then be directly compared to values similarly calculated for a large population (either real or simulated) that only contains individuals who could not have been a contributor to the mixed sample. If, for example, a given suspect is found to have a smaller SCCPI statistic than that found for any of 1,000,000 individuals from a relevant reference population, then that observation can be used to objectively support the proposition that the subject of the investigation is very likely to be a contributor to a mixture even when numerous instances of allelic dropout need to be invoked. In contrast, if a large fraction of 1,000,000 individuals from a reference population are found to have smaller SCCPI values than a possible contributor, then the possible contributor's similarity to a mixed DNA profile could be shown to be relatively unremarkable.

The nature of the distribution of SCCPI values for simulated individuals in large reference populations changes for different types of mixed DNA profiles. Evaluation of the distribution of reference SCCPI values for a mixed STR DNA profile even in the absence of reference samples from possible contributors may by itself provide a useful means of characterizing a sample's potential probative value in a way that could assist in prioritizing the further analysis of evidence samples.

Mixed, DNA, Dropout

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