B100 Defining the Limits of Forensic DNA Profile Interpretation: An Assessment of the Information Content Inherent in Complex Mixtures

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After attending this presentation, attendees will gain a clearer understanding of the information content in complex forensic DNA profiles. Attendees will learn to support a decision to interpret or not interpret a sample and will be able to base their decision on whether the profile supports a clear separation between a true contributor and a non-contributor.

This presentation will impact the forensic science community by providing more accurate information about forensic DNA profiles that may reliably be interpreted and those that should not be interpreted. This will provide useful information to the legal and judicial system as well as assisting laboratories in efficiently allocating resources and communicating results to their clients.

With the increasing sensitivity of DNA typing methodologies and the increasing awareness by law enforcement of the perceived capabilities of DNA typing, complex mixtures consisting of DNA from two or more contributors are increasingly being encountered; however, it remains to be shown whether it is possible to distinguish a true contributor from a non-contributor in these complex samples. In order to assess this, sets of six Caucasian genotype profiles were simulated and used to create mixtures containing two to five contributors. Each experiment was run 10,000 times. This simulation experiment was intended to illustrate the best-case scenario in which all alleles from the true contributors were detected in the simulated evidence samples. Therefore, the possibility of drop-out was not modeled for this experiment. The computer program DNAMIX was then used to compute Likelihood Ratios (LRs) for both True Contributors (TC) and Known Non-Contributors (KNC), assuming varying numbers of unknown individuals in the mixtures. These complex mixture simulations show that, even when all alleles are detected (no drop-out), true contributors can generate LRs less than one across a 15-locus profile; however, this outcome was rare (seven of 14,000 replicates (0.05%)) and associated only with mixtures comprising five contributors in which the numerator hypothesis includes one or more unknown contributors. For KNCs, LRs were found to be greater than one in a small number of replicates (75 of 14,000 replicates (0.4%)). These replicates were limited to four- and five-person mixtures with one or more unknown in the numerator. Only five of these 75 replicates yielded a LR greater than 1,000.

The informative metric for LRs is not the absolute value, but rather the separation between TCs and KNCs. By plotting the distribution of LRs, it can be seen that the ability to distinguish TCs from KNCs in mixtures containing up to five contributors is remarkably good. This is true even when multiple unknown contributors are required. Overall, these results imply that the strength of evidence that can be derived from complex mixtures containing up to five contributors, under a scenario in which no drop-out is required to explain any of the contributors, is remarkably high. Therefore, such mixtures are worth the time and effort required to perform the statistical analysis required to estimate the weight of evidence.

Mixture Interpretation, Complex Mixture, Likelihood Ratio