A122 Effects of Relatedness on Likelihood Ratio Calculations for DNA Mixtures

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After attending this presentation, attendees will understand how relatedness among contributors to forensic DNA mixtures can affect likelihood ratio calculations when unknown contributors are modeled as unrelated, also understanding the related contributors as known in the model can nullify some of these effects.

This presentation will impact the forensic science community by exposing some of the strengths and limitations of likelihood ratios for forensic mixture analysis. Most laboratories wrestle with complex mixture analysis and relatedness among contributors and suspects can further create additional complications.

A likelihood ratio (LR) can be used to assign a statistical weight to a comparison between a DNA mixture obtained from an item of evidence and the DNA profile of a known individual, such as a suspect. An LR is a ratio of two probabilities. In forensic DNA analysis, these are typically the probability of the DNA mixture conditional on a prosecution hypothesis (H_p), often a scenario that includes a suspect, and the probability of the mixture conditional on a defense hypothesis (H_d), where the suspect is replaced by an unknown person. There may be one or more additional unknown persons in either or both scenarios. These unknown persons are most often assumed to be unrelated to one another and to the suspect.

If contributors to a mixture are related to one another or to the suspect and this is not considered in the formulation of the LR, the LR may be conservative or anti-conservative. As a consequence of relatedness, a mixture may appear to be composed of fewer than its true number of contributors, due to allele sharing. If this happens, the scenarios selected for the LR may be incorrect. As a consequence of relatedness between mixture contributor(s) and a non-contributing suspect, the suspect's alleles may appear in the mixture by chance. To explore these two possibilities and their effects on the LR, DNA profiles of related and unrelated individuals were simulated and theoretical mixtures were created.

Suspect profiles and six different types of three-person mixtures were simulated such that the suspect was not a contributor, but one or more of the suspect's relatives were contributors. Mixtures included: (1) two of the suspect's siblings and an unrelated person; (2) one of the suspect's siblings and two unrelated persons; (3) two of the suspect's half-siblings and an unrelated person; (4) One of the suspect's half-siblings and two unrelated persons; (5) The suspect's sibling, parent and an unrelated person; and, (6) two of the suspect's cousins and an unrelated person. Mixtures were also simulated including the suspect as a contributor and without allelic drop-out and drop-in.

Likelihood ratios were computed using the Forensic Statistical Tool (FST), developed and used for mixture analysis in casework by The Office of Chief Medical Examiner (OCME) of the City of New York. FST employs empirically determined drop-out and drop-in rates, so the contributors in the prosecution and defense scenarios need not fully explain the alleles in the mixture. For each mixture, H_p and H_d were formulated with and without the suspect's relatives and the unrelated persons as known contributors to the mixtures. After testing with the suspect, LRs were also computed for the same scenarios using a set of other non-contributors as the "suspect." This demonstrated the range of LRs expected for unrelated non-contributors and was used to determine whether the related suspect's LR was artificially inflated.

Analysis of the simulated mixtures showed that a non-contributing suspect's LR can sometimes be inflated when one or more of the suspect's relatives contributed to the mixture, particularly when the mixture included two of the suspect's siblings. However, this inflation can be mediated by inclusion of the true contributors as knowns in the LR. Therefore, it is important to attempt to obtain elimination samples from individuals related to the suspect if they may be part of the mixture. If it is not possible to obtain the elimination samples, the LR may be computed without known contributors, but it should be emphasized that the current model treats unknown contributors as unrelated. Ultimately, it may be necessary to develop LR calculation software that can account for relatedness through appropriate algorithms.

Likelihood Ratio, DNA Mixtures, Relatedness