B174 Mixture Interpretation and Statistics Town Hall Meeting

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After attending this presentation, attendees will have a greater understanding of the impact that biological phenomena, amplification artifacts, and making assumptions can have on the conclusions that are drawn from DNA mixture profiles.

This presentation will impact the forensic science community by providing an open forum for discussing key factors in DNA profile interpretation.

The primary objective of this session is to share opinions and experiences regarding mixture interpretation. Forensic DNA interpretation is in a period of transition or, to use the theme of the 2016 meeting, a period of “transformation.” It is clear that a “cookbook” approach to analyzing mixtures is not feasible and that a static set of rules cannot be applied to the interpretation of every DNA profile; however, it may be possible to generate a list of technological and biological phenomena for analysts to consider throughout the analysis and interpretation process. Likelihood Ratios (LR) are now considered to be the more appropriate statistical method for the majority of mixture conclusions. In addition, sophisticated modeling algorithms (probabilistic genotyping) are being employed to account for the behavior of DNA during Polymerase Chain Reaction (PCR) amplification. There is a great deal of uncertainty in how to apply probabilistic genotyping and LRs, particularly concerning what assumptions to make and what factors to incorporate for allele sharing, relatedness, stochastic events, PCR artifacts, and other casework scenarios. Furthermore, how should these assumptions and conclusions be documented, reported, and presented in court?

Rather than holding individual presentations on this topic, this Special Session of the Criminalistics Forensic Biology Scientific Session is intended to be an interactive discussion. This will not be a series of demonstrations of various software programs or theoretical explanations of the mathematical formulas. Instead, six panelists from diverse backgrounds (practitioners, researchers, mathematicians, and legal consultants) will be on hand to share their perspectives on the proper thought process for arriving at scientifically valid conclusions during mixture interpretation. The session will be driven primarily by questions solicited from DNA analysts ahead of time, from selected examples of complex mixtures, and from questions generated during the Special Session. The goals at the end of the session are for the audience to feel more confident in their approach to mixture interpretation based on the advice and experience provided by the panel and to be aware of the options available for statistical modeling of PCR-based DNA data. As a result, the forensic DNA community may grow or “transform” to keep in step with the complex types of mixtures that are becoming more prevalent in routine casework.

Mixture Interpretation, Probabilistic Genotyping, Statistics