B95 A Large-Scale DNA Mixture Interpretation Study of DNA Examiners: Inter- and Intra-Laboratory Variability

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After attending this presentation, attendees will understand the inter- and intra-laboratory variation of genotype interpretations that occur during the DNA deconvolution process. This large-scale study attempted to quantify the variability that exists in the DNA interpretation process and was able to gather participation from a large number of DNA examiners from local, state, federal, and international forensic laboratories.

This presentation will impact the forensic science community by serving to explain the current limitations of DNA mixture interpretation, to quantify the genotype variations in the mixtures utilized in the study, and could be used to help train new DNA examiners and guide DNA interpretation protocols.

Forensic laboratories generally deconvolute DNA samples to identify DNA profiles for contributors present in the mixture sample. As the complexity of a sample increases, so does the range of genotype interpretations generated by an examiner. The interpretations may be affected by sample complexity including low template or degraded DNA, increased numbers of contributors in the sample, and the ratios and allelic overlap between each contributor in the mixture. In addition to the genotype interpretation variation generated with a given sample, various forensic laboratories utilize distinct DNA mixture interpretation guidelines and protocols that influence their interpretation of a sample. In some cases, this will determine if a sample is analyzed or deemed inconclusive; however, the degree of variation between examiners within and outside a laboratory has not been quantified.

This study attempts to quantify the variation within and between local, state, federal, and international DNA forensic laboratories using a Genotype Interpretation Metric (GIM) system developed at the Defense Forensic Science Center (DFSC). The GIM establishes a gradient to incorporate the multitude of potential genotype interpretations, converting the genotype interpretation into a quantifiable metric. Six mixtures comprised of two- or three-person contributors with varying contributor ratios were generated at DFSC using Identifiler® Plus and PowerPlex® 16 amplification kits. To establish a variation baseline, a two-person mixture was generated with a clear major and minor contributor ratio that displayed all alleles present at each locus and did not exhibit dropout at any of the loci in the electropherogram. The other five mixtures were more complex and included variations such as number of contributors, contributor ratios, and varying degrees of dropout. The resultant six mixture .fsa files were submitted to more than 275 DNA examiners at more than 50 local, state, federal, and international laboratories and the genotype interpretations were analyzed for variation at the intra- and inter-laboratory levels prior to technical review. Participants varied in their use of Combined Probability Of Inclusion/Exclusion (CPI/E), Random Match Probability (RMP), and Likelihood Ratio (LR) in their mixture interpretations; a smaller subset of examiners utilized probabilistic modeling software systems. GIM scores and an accompanying survey form were generated and analyzed for each mixture, then compared to other examiner GIM scores within and outside their laboratory. The presence or absence of genotype variation among the examiners will contribute to the overall understanding of mixture interpretation, its current limitation, and the variety of interpretational methods. The results of this study can help shed light on sources of variation seen with DNA mixture interpretation. These findings may also inform training programs for DNA examiners with the goal of reducing variation.

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