# DNA MIXTURE INTERPRETATION STUDY: INTER- & INTRA-LABORATORY VARIABILITY

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Forensic laboratories currently deconvolute DNA mixtures utilizing STR analysis to generate DNA profiles for contributors present in the sample. As the complexity of a sample increases, so does the range of genotype interpretations generated by an examiner. Factors affecting sample complexity include low-copy template or degraded DNA, increased numbers of contributors to the sample, and the ratios of each contributor to the mixture. In addition to the variations within a given sample, various forensic laboratories utilize their own 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. This study attempts to quantify the variation at the inter- and intra-laboratory levels in local, state, and federal DNA forensic laboratories using a genotype interpretation metric (GIM) system developed at the Defense Forensic Science Center (DFSC). Six mixtures comprised of two- or three-person contributors and 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. It 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 dropout. The resultant six mixture *.fsa* files were submitted to DNA examiners at local, state, and federal laboratories, and the generated genotype interpretations were analyzed for variation at the intra- and inter-laboratory levels. Interpretations were submitted from laboratories using CPI, RMP, and LR statistics. Examiner GIM scores were generated and analyzed at each mixture and then compared to other examiner GIM scores within their laboratory and outside their laboratory. The presence or absence of genoptype variation among the examiners could help improve the understanding of the current limitations of mixture interpretation at varying laboratories. Also, the GIM score provides a quantifiable measurement of variability that helps determine whether examiners are interpreting in a similar manner within a laboratory. 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 inter- and intra-laboratory variations.