## E25    Resolution of Forensic DNA Mixtures

*Dan E. Krane, PhD\*, Wright State University, 3640 Colonel Glenn Highway, Biology, Dayton, OH 45435*

The goal of this presentation is to present an objective means of resolving individualities between the DNA profiles of distinct contributors to two-person mixed DNA profiles.

This presentation will impact the forensic community by demonstrating that the statistical weight of a single source sample is far greater than that of a mixed DNA sample. The approach described here will allow analysts to resolve various types of mixtures into pairs of single source samples.

Samples containing DNA from two or more individuals can be difficult to interpret. The striking difference in the weight of the DNA evidence associated with single source and mixed evidentiary samples has motivated the development of approaches that attempt to elucidate the genotypes of the individual contributors from mixed evidentiary samples. The reality of mixed STR DNA profiles is that some loci cannot be resolved into two single genotypes because the observed electropherogram data provides equivalent or very similar support for two or more of the competing alternative hypotheses of genotype combinations that could account for all the detected alleles.

This study describes and tests a novel methodology that provably determines which alternative hypotheses of genotype combinations are mathematically feasible (in light of peak height balance and additivity expectations) and which should be eliminated from consideration due to its failure to satisfy one or more objective rules. The approach rests primarily on the same two principal assumptions of existing resolution methods: (1) that the number of contributors is known (or explicitly hypothesized) and (2) that alleles from the same individual will be present at approximately the same intensity ("in balance" within a specified margin of error). Each locus is considered separately. When only a single combination of genotypes is supported by the underlying data, random match probability calculations can be used to describe the rarity of those individual genotypes. In instances where some but not all alternative hypotheses of contributor genotypes can be eliminated from consideration, a combined-probability-of-inclusion-with-constrained- hypotheses value for a mixed DNA profile can be calculated.

This approach is demonstrably objective as only information from the evidentiary sample is required for resolution. Eight two-person nine- locus mixture ratios ranging from 5:1 to 1:28 were examined to validate this approach. Every mixture had at least six loci that were either fully or partially resolved. The approach is robust enough to demonstrably handle situations of allelic dropout. Failures observed in the method were due to low DNA concentrations with the presence of technical artifacts. The method is also amenable to both computer automation and can be customized with constraints that have been validated by a given testing laboratory.

**DNA, Mixture, Random Match Probability**