



Criminalistics Section - 2016

B143 Complex Mixtures and the Minimum Number of Contributors: A Case Study

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After attending this presentation, attendees will better understand the challenges associated with estimating the number of contributors in a complex DNA mixture and the importance of making accurate assessments before attempting probabilistic genotyping to ascertain likelihood ratios. Results from an empirical analysis of simulated mixtures using real genotypes will be described.

This presentation will impact the forensic science community by: (1) illustrating the difficulties of assessing the number of contributors to a mixed sample; (2) presenting an exploration of novel empirical mixture analyses; and, (3) showing the impact these analyses have had on recent investigations involving probabilistic genotyping.

The scenario considered for this simulation study consists of a case in which a forensic DNA testing laboratory developed genotypes from three injections of DNA extracted from a swabbing of the grip area of a firearm found to be associated with a crime. The testing laboratory performed probabilistic genotyping analyses on the multiple injections, resulting in a single Likelihood Ratio (LR) reported for the swab of the grip area.

The calculation of LRs in forensic DNA statistics requires an explicit assumption of a number of contributors in both the numerator and denominator. Despite the observation of seven unique peaks at a single locus, the testing laboratory generated LRs under the assumption that only three individuals contributed to the observed DNA profile, suggesting that the single observation of a seventh peak at one locus across three injections was an artifact rather than an indication of a real allele and a fourth contributor. The final reported LR supported the data under H1 (Hp; Defendant + two unknowns) as being 4,190 times more probable than under H2 (Hd; three unknowns). The probabilistic genotyping system used for these analyses has not been validated for analyzing samples containing DNA from more than three individuals (as of June 2015). As a result, the testing laboratory was unable to evaluate the alternative hypotheses that four or more individuals contributed to the mixture.

An empirical analysis of 361 Caucasian genotypes published by the National Institute of Standards and Technology (NIST) indicates that of the 15 genetic loci genotyped by the commercially available Identifiler® test kit, approximately half of simulated, known, four-person mixtures ($N=695,946,630$) would have no more than six unique alleles observed at any locus. When disregarding the single locus with the highest count of unique alleles (as is the practice of the testing laboratory for this case) approximately 90% of all four-person mixtures would have no more than six unique alleles observed across the remaining loci. The results of this analysis indicate that the use of maximum allele counts for assessing the number of contributors is frequently inaccurate, especially for three or more contributors, and that an abundance of caution should be exercised when evaluating LRs in such instances.

The testing laboratory suggested that it was “more cautious” to consider the evidence sample to be a mixture of at least three individuals (presuming that allelic drop-in was likely to have occurred) rather than a mixture of at least four without providing any LR or level of confidence to that assertion. When confronted with these results and their implications, the testing laboratory and prosecution chose to withdraw their conclusions regarding DNA testing in this case prior to a judge’s ruling in an admissibility hearing in a federal court.

Complex Mixtures, Number of Contributors, Likelihood Ratios