A120 Analysis of Allelic Drop-Out Using the Identifiler® and PowerPlex® 16 Forensic STR Typing Systems I: Estimation of Drop-Out Probabilities

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After attending this presentation, attendees will learn how empirically derived drop-out probabilities can be obtained using low-template DNA profiles that were run as part of their laboratory's internal validation studies, and how these probabilities perform well when used on model evidentiary samples. They will then discover how the calculation of dropout probabilities can be incorporated into a likelihood ratio that assesses the strength of the DNA evidence under competing hypotheses.

This presentation will impact the forensic science community by providing a means of assessing the weight of low-template DNA evidence that requires consideration of allelic drop-out, also providing a means to increase accuracy and objectivity in interpreting DNA profiles.

Low-template (LT) DNA profiles continue to present interpretational challenges to the forensic community. Whether the LT contribution comprises the main profile, or whether it is present as the minor component of a mixture, ambiguity arises from the possibility that alleles present in the biological sample may not be detected in the resulting DNA profile. This phenomenon is known as allelic drop-out. This ambiguity complicates both the assessment of the potential number of contributors as well as an estimation of the weight of the DNA evidence for or against specific propositions. One possible solution to estimating the weight of the evidence is to use a likelihood ratio (LR) that incorporates the probability of allelic drop-out $P(D_O)$. Such methods can be improved by including an estimate of the drop-out probability for the specific evidence sample. However, while a vast repository of data exists from which dropout probabilities might be calculated, few empirical studies to determine such probabilities have been performed to date. Here patterns of allelic drop-out are characterized using the Identifiler® and PowerPlex® forensic STR multiplexes in single-source samples generated by the National Institute of Standards and Technology (NIST). Briefly, DNA was adjusted to amplify 100pg, 30pg, or 10pg from each of two individuals. Each of the six samples (three concentrations of each of the two individuals) was amplified 10 times with both the Identifiler® and PowerPlex® 16 kits using the standard number of PCR cycles suggested by the manufacturer. Thus, a total of 60 profiles were produced for each kit.

Crucial to the determination of dropout probabilities is the selection of an appropriate detection threshold. A threshold derived from analytical chemistry, designed to properly balance signal and noise, was used to evaluate the samples, as well as thresholds commonly used in forensic DNA laboratories. The effect of these different allelic detection thresholds on observed patterns of drop-out were then evaluated. Drop-out was defined to be the situation where a particular peak known to exist in the sample does not rise above the allelic detection threshold, and, as a result, is not detected in the profile. Not surprisingly, fewer instances of apparent drop-out were found when using a lower detection threshold.

Logistic regression to model the fraction of alleles that dropped out of a profile as a function of the average height of the detected peaks was used. The equation derived from the logistic regression model allowed the authors to estimate the expected drop-out probability for a model evidentiary sample based on the average peak height of the profile. The correlation of the proportion of allele drop-out from a profile with the average peak heights within a particular profile supports using logistic regression to model the relationship between these two variables. In several cases, the parameters of the logistic regression models differed significantly between typing systems, different allelic detection thresholds, and samples. Finally, a positive correlation exists between allele drop-out and allele length; longer alleles tend to drop-out more frequently than shorter alleles, even in good quality samples. These results provide an initial foundation for empirically estimating drop-out probabilities that can be incorporated into LR calculations to assess the weight of complex DNA evidence including LT components.

Dropout Probabilties, Logistic Regression, Likelihood Ratios

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