A121 Analysis of Allelic Drop-Out Using The Identifiler® And PowerPlex® Forensic STR Typing Systems II: Evaluation of Estimated Drop-Out Probabilities

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After attending this presentation, attendees will appreciate how empirically based drop-out probabilities can be obtained for low-template DNA profiles. Further, they will learn how a simulation approach can be used to determine the accuracy of the drop-out probabilities.

This presentation will impact the forensic science community by objectively exploring the performance of likelihood ratio approaches to assess the weight of low-template DNA evidence that require consideration of the allelic drop-out. The work presented provides a means to increase the accuracy and objectivity in interpreting DNA profiles.

One major challenge in the analysis of forensic DNA profiles concerns the analysis of low-template (LT) DNA samples. Due to the small number of DNA molecules analyzed, such samples may not yield the complete profile(s) of the contributor(s). It is difficult to correctly interpret such profiles because some of the information may be missing. Further, it is even more challenging to accurately assess the weight of such evidence.

To fill this void, patterns of allelic drop-out were recently characterized using the Identifiler® and the PowerPlex® forensic STR multiplexes in 60 LT single-source samples. Logistic regression was employed to model the relationship between the fraction of alleles that have dropped out of a profile as a function of the average height of the detected peaks. This model allowed the estimatation of the drop-out probability for a simulated low-template LT evidentiary sample based on the average peak height of the profile. These estimated drop-out probabilities could then be incorporated into a likelihood ratio (LR) to assess the strength of the LT DNA evidence.

However, one concern is that there were several statistically significant differences in the relationship between peak heights and drop-out between different samples and experimental conditions. The practical effect of these differences remained unclear. Thus, previous work was expanded and extensive simulation studies were performed to evaluate the accuracy and practical applicability of estimated drop-out probabilities.

Each of the LT DNA profiles, simulating an evidentiary profile, was compared with the profile of a suspected contributor. For each of these comparisons, two different LRs were computed. The first one used the estimated drop-out probability. The second LR used the true drop-out probability. If the estimated drop-out probabilities are accurate, then the LRs calculated using them should be similar to those calculated using the true drop-out probability.

Two different types of comparisons between LT profiles and suspected contributors to assess how well the drop-out estimator functions were analyzed. The first type of comparison evaluated the true contributor as the suspected contributor of the LT DNA evidence. The second type of comparison evaluated a true non-contributor as the suspected contributor of the LT DNA evidence. Here, the suspected contributor was a random individual simulated from a U.S. population database with European ancestry. For all comparisons, LRs were calculated using the Balding and Buckleton (2009) R program.

For both types of simulations, the LRs calculated using the estimated drop-out probabilities were similar to those calculated using the true drop-out probabilities, suggesting that the estimates of the drop-out probability are accurate and useful. This trend holds even when using the data from the PowerPlex® 16 typing system to estimate the drop-out probability for an Identifiler® profile and vice versa. Thus, even though some of the logistic regression model parameters differ significantly from each other across different experimental conditions, they are similar enough to have little practical effect on the final LRs calculated using these estimated drop-out probabilities. This research demonstrates that use of an LR that incorporates empirically estimated allelic drop-out probabilities provides a reliable means for extracting maximum information from LT forensic DNA profiles.

Low Template DNA, Drop-Out, Likelihood Ratio

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