LOW-TEMPLATE DNA: PERFORM A SINGLE DNA ANALYSIS OR TWO REPLICATES?

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The interpretation of low-template DNA (LT-DNA) typing results is challenging because of the increased influence of stochastic effects. One approach for dealing with the uncertainty produced by these stochastic effects is to perform replicate analyses to obtain several EPGs for the sample. Another approach, which is contradictory to the previous one, is to concentrate all of the DNA into the same tube and obtain a single EPG for the sample. The reasoning behind the former is to produce more data for making inferences about the donor's genotype. The idea behind the latter is that the template quantity in this tube will be slightly greater and this might lead to less allele and locus drop-outs. This presentation addresses the decision of performing a single DNA analysis or performing two replicate analyses for LT-DNA samples.

This research models this decision problem using decision theory, and applies this model to LT-DNA data obtained for a range of very small quantities of DNA. The methodology consists of three parts: (i) DNA typing of the LT-DNA samples, (ii) probabilistic analyses of the results to obtain the probabilities required for the decision analysis, and (iii) decision-theoretic analyses of the results. For the first part, single-source dilution samples were prepared for a range of DNA concentrations that led to electropherograms having no allele or locus drop-outs to having all loci dropping out (for an analytical threshold of 10rfu). For the second part, genotype probabilities were assigned using a semi-continuous approach. For the third part, the expected net gain (ENG) of each approach was assessed for a plausible range of utility functions. The results indicate that performing two replicates produces a greater ENG than performing a single DNA analysis for profiles where the average observed peak height of an allele is greater than 43rfu.

These results support the position that two replicates increase the information content for LT-DNA profiles with an average allelic peak height greater than 43rfu. With these results, this study also illustrates how a decision-theoretic model can be applied to a decision problem encountered by forensic DNA analysts.