B185 A Comparison of the Deconvolution and Likelihood Ratios (LRs) Produced Using a Continuous Probabilistic Software From Low-Level Samples When Amplifying the Entire Extract or Splitting the Extract

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After attending this presentation, attendees will understand the potential benefits and differences of information gained from either a single analysis of a low-template sample versus splitting and combining replicate testing of the samples using a continuous probabilistic genotyping software.

This presentation will impact the forensic science community by demonstrating the range of LRs generated analyzing a single DNA profile versus splitting, then jointly analyzing, replicates of the DNA template.

Touch DNA samples typically contain much less than 1ng of total DNA. Strategies to maximize the genetic information from low-level samples is to: (1) concentrate the entire extract down to 10uL, then amplify the entire extract volume; or, (2) split the extract into multiple amplification reactions, then develop a consensus profile for interpretation.[1,2] Some laboratories may be hesitant to implement enhanced detection methods to increase the sensitivity of the amplification or analysis (e.g., increased cycle number, increased injection time/voltage, post-amplification de-salting, etc.) due to the potential for an increased detection of allele drop-in. Therefore, more information may be gained through replicate amplifications using standard protocols. Probabilistic genotyping software using continuous models of interpretation has the ability of analyzing replicates of the same DNA sample to produce a combined deconvolution and LR. This option poses the question, which analysis will produce a more informative result — amplifying and analyzing the entire DNA extract or splitting the extract and conducting a joint analysis? By splitting the DNA extract, the total DNA template used for the amplification is halved, but the replicate analysis may provide additional information for the statistical analysis.

In this study, DNA profiles were generated from a range of single source and two- and three-person mixed DNA samples in which the template DNA was amplified: (1) once with a determined quantity of template DNA; and, (2) in duplicate using one-half of the original quantity of template DNA in each amplification. All samples were amplified using the standard Polymerase Chain Reaction (PCR) amplification conditions and analyzed using capillary electrophoresis. The DNA profiles were then processed using a continuous probabilistic genotyping software. The duplicate DNA profiles generated from the split DNA extract were analyzed together, resulting in a single combined deconvolution and LR result. The information from deconvolved genotypes and the range of LR values for a single analysis compared to a joint analysis using replicate profiles will be presented.

Reference(s):

1. Gill P., Whitaker J., Flaxman C., Brown N., Buckleton J. (2000) An investigation of the rigor of interpretation rules for STRs derived from less than 100 pg of DNA. *Forensic Sci Int.* 112(1): 17-40.
2. Grisedale K.S., van Daal A. (2012) Comparison of STR profiling from low template DNA extracts with and without the consensus profiling method. *Investig Genet.* 3(1): 14.

Low-Template DNA, Likelihood Ratio, Probabilistic Genotyping