B136 Working With Challenging Samples: An Independent Assessment of the Relative Performance of the Promega® Fusion™ and InnoGenomics® InnoTyper™ Kit With Probative Samples

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After attending this presentation, attendees will better understand the relative merits of the InnoGenomics® InnoTyper™ and Promega® Fusion™ kits for the analysis of challenging forensic samples.

This presentation will impact the forensic science community by providing information on gaining the most information from challenging forensic samples.

Traditional analysis of challenging forensic samples often relies on mitochondrial markers, due to their relative stability and high copy number; however, there are considerable drawbacks to this approach including the lack or recombination and the absence of paternal contribution. Therefore, the generation of reliable nuclear profiles from degraded samples continues to be increasingly important for forensic testing.

Recently, based in part on the recommendations from the Federal Bureau of Investigation (FBI), kit manufacturers have released multiplexes with heightened sensitivity and robustness when compared to standard genomic marker systems. These systems have been optimized for improved performance with challenging samples. The Promega® Fusion™ system interrogates 22 autosomal Short Tandem Repeats (STR), the amelogenin locus for gender identification, and a gender confirmatory marker on the Y chromosome. Eight of the STR markers produce alleles less than 200 base pairs in length, increasing the likelihood of producing results from compromised forensic samples and the chance of obtaining probative data from forensic evidence. The development of markers based on Retrotransposable Insertion Polymorphisms (RIPs) enables additional information to be retrieved from the most highly degraded and inhibited samples, including bone and hair shafts. Innogenomics® InnoTyper™ 21 system utilizes small amplicon DNA typing of repetitive Alu sequences from 20 loci and amelogenin in which each locus is scored for the presence of a stable heritable insertion. This biallelic system has been reported to produce interpretable genetic profiles with as little as 60 picograms of input DNA from compromised and challenging samples. This study assesses the sensitivity and amount of probative data obtained using the Promega® Fusion™ kit and the Innogenomics® InnoTyper™ 21 kit on low-yielding, highly degraded, and challenging forensic samples, including bone of varying age and condition, hair shafts, and touch samples.

InnoTyper™, Fusion™, STR

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