AN INDEPENDENT ASSESSMENT OF THE RELATIVE PERFORMANCE OF THE PROMEGA POWERPLEX® FUSION AND INNOGENOMICS INNOTYPER™ 21 KITS FOR USE WITH CHALLENGING SAMPLES

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The generation of reliable nuclear profiles from challenging samples has become increasingly important for forensic and relationship testing. Often the most severely degraded and low quantity samples have required mitochondrial sequencing; however, there are a number of drawbacks to this approach, in terms of cost, complexity and reduced discrimination power. The increase in sensitivity and robustness of standard genomic marker systems has increased their utility for challenging samples, while the development of unique markers based on Retrotransposable Insertion Polymorphisms (RIPs) has added another tool to the investigators tool box. Promega's PowerPlex® Fusion System interrogates 22 autosomal short tandem repeats (STR), the amelogenin locus for gender identification, and a gender confirmatory marker on the Y chromosome. The optimized performance of this system and the fact that 8 of the STR markers produce alleles less than 200 base pairs in length increases the likelihood of producing results from compromised forensic samples. InnoGenomics' InnoTyper™ 21 kit is a small amplicon (~60-125 bp) DNA typing system containing 20 RIP markers and amelogenin in which each locus is scored for the presence of a stable heritable insertion. This bi-allelic system, which is compatible with commonly used PCR and capillary electrophoresis platforms, has been reported to produce interpretable genetic profiles from extremely degraded and/or low-level forensic samples, including bone fragments and rootless hair shafts that typically yield minimal results with other systems. This study assessed the relative performance of the Promega Fusion System and the InnoGenomics InnoTyper™ 21 kit in comparison to Promega's PowerPlex® 16 kit on low yield, highly degraded, and challenging forensic samples. Results indicate that both systems provide advantages when compared to older technologies, and may provide resolution of difficult forensic cases that previously would have yielded limited nuclear DNA results.