DETECTION OF DELETION/INSERTION POLYMORPHISMS FROM EVIDENCE SAMPLES

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Analysis of short tandem repeats (STRs) is currently the most commonly used method for human identification. However, DNA extracted from evidence samples exposed to environmental insults does not always yield complete STR profiles. Forensic scientists, in an attempt to obtain complete DNA profiles from compromised samples, use more sensitive extraction procedures and modify amplification conditions. Analysis of bi-allelic insertion/deletion polymorphisms can be useful in supplementing data obtained with STR profiles.

The current study focuses on the detection of insertion/deletion polymorphisms from challenged samples using the Investigator DIPplex® kit from Qiagen. Unlike the PCR amplification kits currently available in the forensic community that amplify 15 or more STR loci, the DIPplex® kit allows for multiplex amplification of 30 bi-allelic areas of known insertions and deletions (InDels) plus the Amelogenin locus. This PCR amplification kit uses reduced amplicon sizes (maximum of 150 bp), similar to SNPs, improving the amplification of degraded samples. The combination of current STR analysis procedures and small amplicon sizes makes InDels suitable for pristine as well as degraded DNA evidence samples.

This study included analyzing different types of body fluids from humans, as well as pristine, degraded, inhibited, and mixture samples. Another goal of this research was to assess the DIPplex® kit's capacity for samples that closely resemble forensic casework evidence. For the purpose of validating the kit, samples from various animals were also included.

It was possible to obtain InDel profiles from samples exposed to environmental insults, washed bloodstains, membranes used for detecting body fluids by immunochromatographic assays, and other types of samples such as objects used by consumers on their lips. Complete profiles were obtained from as low as 0.1 ng/ul of DNA. This work indicates that the DIPplex® kit provides reproducible and sensitive results, and is suitable for use in conjunction with STR profiles when small amounts of degraded DNA are present in evidence samples. ⌘