DIPPLEX: MULTIPLEX ANALYSIS OF DELETION INSERTION POLYMORPHISMS FOR HUMAN IDENTIFICATION

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Often compromised samples are the sole available source for retrieving genetic information for identification of persons. Nuclear DNA that can be obtained from these kinds of samples is typically of low concentration and strongly degraded due to adverse environmental conditions. Because of their high discrimitory power, short tandem repeats (STRs) have become the favourite type of genetic marker for human identification. However, STR loci require quite large fragments of genomic DNA to be amplified and drop out of markers are frequently observed with degraded DNA. Introducing “mini-STRs” by reducing amplicon length of STRs as much as possible has been used as a strategy to deal with this limitation.

We made use of an alternative approach to cope with degraded DNA by choosing short Deletion Insertion Polymorphisms (known as DIPs or Indels) to build up a multiplex assay that has a maximum of app. 150bp amplicon size. The Investigator DIPplex Kit combines amplification of 30 biallelic DIP markers and amelogenin in a single PCR reaction. The assay follows the same workflow as STR assays and thus can be performed by any forensic lab without a need for new instrumentation. A freely available software tool can be used for convenient interpretation of data. Selected DIP markers are distributed over 19 chromosomes and each one is at least 10Mbp away from any commonly used STR marker. The assay provides a discriminatory power of 2.83×10^{-13} (Combined probability of identity) based on a Caucasian population.

The DIPplex assay is highly sensitive and full profiles can be robustly obtained from only 63pg of DNA. Artificially degraded DNA as well as real life samples have been used to validate performance on compromised samples. Results show that the DIPplex assay returns more genetic information from samples like old bones compared to a common STR assay.