High Through-Put Analysis of DNA Database Reference Samples using the PowerPlex™ STR System Performing Capillary Electrophoresis

Walther Parson[1], Alexandra Netzer[1], Ann M. Lins[2], Silvano Köchl[1], James W. Schumm[2]
[1]Institute of Legal Medicine, University of Innsbruck, Muellerstr. 44, Innsbruck, Austria
[2]Promega Corporation, 2800 Woods Hollow Road, Madison, WI 53711-5399 USA

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The forensic community is on the way towards establishment of DNA intelligence databases throughout many European countries. The idea is to match DNA profiles from casework samples with a database consisting of corresponding profiles from reference samples. The appropriate tool for generating such profiles is the analysis of Short Tandem Repeat (STR) loci, which proved to be both highly polymorphic within a given population and sensitive for the identification of minute quantity and/or low quality DNA. The simultaneous amplification of several STR loci - generally known as multiplexing - is an economical technique to generate STR profiles from a single PCR assay. Back in the beginning of this decade triplexes, quadruplexes and pentaplexes have been developed, offering matching probabilities in the range of 1 in 1000 to 1 in a million, which usually met the requirements for inclusion of a suspected person in casework analysis. During the past few years, not only the demand for more expressive multiplexes increased, but also the technical improvements in PCR technology led to the development of megaplexes including more than 6 STR loci in one reaction. These systems are now also commercially available, offering extremely high matching probabilities - in the range of more than one in a billion - from a single PCR assay.

We here present the application of the Powerplex™ (Promega) consisting of 8 STR loci in combination with the gender-specific marker Amelogenin for DNA databasing. The processing of the samples involves capillary electrophoresis (PE/ABD) and automated allele calling, taking advantage of the macro-assisted program Genotyper™ (PE/ABD).

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