



## B66 Development of A Male-Specific, 12-Locus Fluorescent Multiplex

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The goal of this presentation is to present a new assay for analysis of Y-STR markers to the DNA typing community.

Short Tandem Repeat (STR) analysis has become the leading technology for genetic human identification. Frequently, autosomal markers are used for forensic, paternity and anthropological studies. However, some cases can benefit from the analysis of sex-specific Y-STR markers. Y-STR markers consist of polymorphic regions found on the non-recombining region of the Y chromosome. Amplification of these haploid markers occurs only in males and alleles are inherited only through the paternal line. These qualities simplify interpretation of complex male/female mixtures and male kinship studies by removing the female contribution.

Several web-based databases of observed Y-STR haplotypes have been initiated (http://www.ystr.org/). These databases include the so-called "Y-STR minimal haplotype," which consists of nine loci: DYS19, DYS385I/II, DYS389I/II, DYS390, DYS391, DYS392, DYS393. A commercially available, single-amplification assay for these loci has yet to be offered. To this end, a fluorescent multiplex has been developed to include the

Y-STR minimal haplotype plus DYS437, DYS438 and DYS439. This new PowerPlex<sup>®</sup> System uses four-color chemistry allowing analysis on the ABI PRISM<sup>®</sup> 377 DNA Sequencer. ABI PRISM<sup>®</sup> 310 Genetic Analyzer and

ABI PRISM<sup>®</sup> 3100 Genetic Analyzer. Amplified samples are labeled with fluorescein, 6-carboxy4',5'-dichloro-2',7'-dimethoxy-fluorescein (JOE) and carboxy-tetramethylrhodamine (TMR). Fragment sizing is provided by an internal size standard labeled with carboxy-X-rhodamine (CXR). Color deconvolution can be performed with color matrix kits currently available from Promega Corporation. Allelic ladders have been created, following ISFG recommendations<sup>(1)</sup>, to increase confidence in allele designation. A PowerTyper<sup>™</sup> macro, operating within

the Genotyper<sup>®</sup> software, has been designed to automatically label fragments from GeneScan<sup>®</sup> data using the supplied allelic ladder and size standard. Primers have been designed to yield amplification products that are less then 350 bp in length. System sensitivity, specificity, robustness and concordance with previously described primer sets will be discussed.

<sup>1</sup>Gill, et al. DNA Commission of the International Society of Forensic Genetics: recommendations on forensic analysis using Y-chromosome STRs. Int J Legal Med (2001) 114:305-309.

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