B4 Concordance Study of STR Results Using Multiple ABI PRISM® Genetic Analysis Instruments, AmpF*l*STR® Kits, and ABI PRISM® Analysis Software

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The goals of this presentation are to present a concordant study using multiple ABI PRISM® genetic analysis instruments, AmpFLSTR® kits, and ABI PRISM® analysis software to demonstrate that accurate STR profiles are obtained.

Significant advances in the combination of reagents, instruments, and software have increased throughput capabilities for the profiling of casework samples and database samples in the human forensic and parentage communities. Multiplex assays amplifying greater than ten (10) STR loci, combined with higher-throughput instrumentation and higher-performance software have been developed by Applied Biosystems (Foster City, CA, USA) that allow laboratories to better address the demands of casework and databasing needs. Concordance studies are important to perform when evaluating a new assay, instrument, or software package.

The authors have conducted a comprehensive concordance study of STR profiles generated with six (6) different AmpFLSTR® PCR Amplification kits, analyzed on three (3) ABI PRISM® genetic analysis instruments, and using various ABI PRISM® software packages for both data collection and data analysis. This study presents an evaluation of STR profiles generated with different combinations of kits, instruments, and software (described as "systems" in this abstract) and illustrates: (1) verification of software packages; (2) comparison of instrument platforms with identical PCR products; and, (3) concordance in genotyping.

Six AmpFLSTR® PCR Amplification kits (Identifiler®, Profiler Plus™ ID, Profiler Plus™, COfiler®, SGM Plus®, and SEfiler™ kits) were used in evaluating a panel of forensic-simulated samples (e.g., stains, mixtures, degraded DNA). The AmpFLSTR® kits combine STR loci that meet CODIS, ENFSI, GITAD, and GEDNAP standards. All kits are multiplex assays that co-amplify six (6) to fifteen (15) tetranucleotide repeat loci and the Amelogenin gender-determining marker. For example, the Identifiler® kit amplifies all 13 loci required for CODIS, and the loci D2S1338 and D19S433. The combination of these 15 loci meets the requirements of several worldwide database recommendations. Furthermore, the SGM Plus® kit co-amplifies ten (10) tetranucleotide loci consistent with the Identifiler® kit (D2S1338, D3S1358, D8S1179, D16S539, D18S51, D19S433, D21S11, FGA, TH01, and vWA). Concordant genotype results are achieved regardless of the system used by various counties, states, or countries. These concordant results can support the forensic investigation of blind hits across jurisdictional lines, even internationally. This study demonstrates that interjurisdiction and even international database matching is possible worldwide with different system configurations.

Selected samples were processed on the ABI PRISM® 310 Genetic Analyzer (for both Macintosh® and Windows NT® operating systems), 377 DNA Sequencer (for both Macintosh® and Windows NT® operating systems), and 3100 Genetic Analyzer. All samples were then analyzed using both GeneScan® software and Genotyper® software, or GeneMapper™ ID software. Data were analyzed with GeneScan® software version 3.7.1 and Genotyper® software version 3.7, for use with Windows NT® OS; GeneScan® software version 3.1.2 and Genotyper® software version 2.5.2, for use with Macintosh® OS; and GeneMapper™ ID software in the following modes: Basic, Classic, or Advanced.

The presentation will include a comparison of the profiles generated from these samples and kits on the different systems listed above. Enhanced features of each system will be presented to demonstrate ease-of-use and throughput capabilities. Generated electropherograms and genotype profiles will be presented. The data support that these systems, regardless of the instrument, kit, or software, will produce accurate genotype profiles for comparative analyses. These analyses can then be used by databasing laboratories, criminal casework laboratories, identification laboratories, and parentage laboratories to report accurate genotypes.

Concordance Study, AmpFLSTR® Kits, Genotype

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