

Continuous Evolution of DNA Typing Systems for Forensic Casework and High Throughput Databanks

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The ideal DNA typing system is one that is optimized for maximum performance on difficult forensic case work samples, and is also amenable to high throughput automated analysis for DNA databank purposes. Meeting both of these requirements has driven the development of an integrated system that encompasses the AmpF/STR™ reagent kits, ABI Prism® instrument platforms and Gene Scan® Genotyper® and DataBank STR™ software. Continuous advancements in each of these areas promise to provide DNA typing systems of ever higher performance and throughput.

All AmpF/STR™ reagent kits have been designed, optimized and thoroughly validated for forensic casework analysis. Forensic validation includes all studies outlined in the TWGDAM guidelines. Furthermore, the AmpF/STR™ Profiler Plus™ and Cofiler™ kits together amplify the 13 STR loci selected for the CODIS database. Thus, these AmpF/STR™ kits that are used for high throughput database analysis are exactly the same as the kits, primers and protocols that are optimized and used for forensic casework. This approach provides 100 percent compatibility between database and casework results without compromise to the robust performance that is critical with forensic casework samples. The recent development of Data Collection instrumentation software for five dyes provides a foundation for the possible future expansion and enhancement of these multiplex systems.

Recent advances in high throughput instrumentation include hardware and software upgrades to the ABI Prism® 377 platform for 96 gel lane analysis. Multi-channel loaders are available that are specifically designed to load these gels. Also, "neural-net" lane tracking has been developed to provide further levels of automation. A new ultra-high throughput instrument under development, the ABI Prism® 3700, will also be described. The ABI Prism 3700 is a multi-capillary instrument capable of fully automated operation. Software applications are also being developed to accommodate the management of the large amounts of data that can be generated by these instruments.

Alternative DNA typing methods, such as the analysis of SNP (Single Nucleotide Polymorphism) loci in micro-formats, will be considered in light of the continuous developments and momentum that accompany the analysis of STR loci. The implications of bi-allelic (SNP) vs. multi-allelic (STR) loci for casework interpretation of mixtures will also be considered.