

## High Throughput Automated Forensic Genetic Analysis

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The implementation of the Combined DNA Index System (CODIS) will significantly impact law enforcement in this country. Currently, the backlog of convicted offender samples which exist in some states may continue to grow as a result of a lack of processing facilities and the anticipated broadening of sample collection mandates. The delay in processing these convicted offender samples may therefore prove to be the greatest impediment to the realization of the potential benefits afforded by CODIS.

Unlike crime-scene samples, the convicted offender samples are uniform and lend themselves to processing by automated and high throughput techniques. Attributes can be designed into highly automated platforms which present key advantages in processing this sample type. Herein, the automated platform employed at Myriad Genetic Laboratories for clinical cancer predispositional testing has been modified to process offender samples. This system is highly developed and incorporates the advanced sample tracking and biochemical processes which have been proven in Myriad's clinical laboratory. These aspects are combined with proprietary data analysis software initially developed for positional cloning projects which generate  $2.5 \times 10^6$  genotypes annually.

In this system, database interactive sample tracking is maintained from accessioning through data analysis by bar-coding all samples and assay plates. All sample associations that are required during processing are made through software to database interaction and do not require operator intervention. Confirmation that reagent aliquots are released by the QC department for production is also determined prior to all biochemistry through a database-barcode interaction. All liquid handling and sample transfers occur on robotic pipetting stations which are controlled by the informatics system. Proprietary applications that reside on the computers controlling the sequencers automatically generate sample sheets from barcodes on the gel loading plates, thus maintaining sample confidence during cross platform operations. Following electrophoresis, the informatics system automatically transfers completed gel files from the sequencers' computers to Unix-based workstations for data analysis. Fully automated gel-tracking and processing, and allele-calling software greatly improves genotyping accuracy compared with commercially available programs. During data analysis, algorithms evaluate signal strength, signal to noise, gel resolution, and the mobility of internal standards, control samples and allelic ladders. This quantitative analysis permits minimum quality thresholds to be set for each critical aspect of the genotyping process.

This system has unique advantages with respect to sample tracking, biochemistry, data analysis and accuracy. A comprehensive bioinformatics system administers the platform and affords detailed and extensive process control. Also, a variety of proprietary algorithms are applied to the raw data to yield unprecedented quantitative measures of quality control and quality assurance.