The Validation of a PCR Based Evidence Analysis Program Using AmpF*l*STR™ Profiler Plus™ and AmpF*l*STR™ Cofiler™ for the Identification of Short Tandem Repeats (STRs) Using the ABI Prism® 310 Genetic Analyzer

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The purpose of this research was to enable the Northern Illinois Police Crime Laboratory (NIPCL), through validation studies, to establish a DNA analysis program employing Polymerase Chain Reaction (PCR) and capillary electrophoresis (CE) technologies. The use of this type of analysis will assist in the examination of probative biological evidence and will greatly enhance criminal investigations by identifying or exonerating possible suspects involved in these criminal acts. The funding of these studies were made available through the DNA Identification Act of 1994 [Public Law 103-322] Forensic DNA Laboratory Improvement Program, Phase 3.

NIPCL undertook a careful and comprehensive review of the forensic DNA analysis techniques that were available and in use at the current time. The techniques and instrumentation selected needed to be safe, have short analysis times and have the ability to provide a profile that is of significant statistical relevance. In order to generate allelic frequency probabilities that provided identification to a reasonable degree of scientific certainty, it was necessary to identify multiple polymorphic short tandem repeat (STR) sequences. To this end, NIPCL decided to pursue analysis techniques based on the Polymerase Chain Reaction (PCR) and capillary electrophoresis (CE) using the ABI Prism® 310 Genetic Analyzer. To ensure that the results of the PCR-based genetic analysis were significant, NIPCL employed multiple systems of analysis through the use of the AmpF*l*STR™ Profiler Plus™ and AmpF*l*STR™ Cofiler™ kits.

NIPCL conducted experiments on the ABI Prism® 310 Genetic Analyzer with miscellaneous substrates, miscellaneous biological fluids from a single subject, environmental insults, miscellaneous species, mixed stain samples, and both internal and external proficiency tests. The precision and sensitivity of the system was also established. After running the above samples the data was collected and a basis for interpretation was identified.