B106 Validation and Applications of the ABI 3130 Genetic Analyzer for Forensic Casework Analysis

Alan B. Dixon, MSFS, and Kaajal Patel, MS, Georgia Bureau of Investigation, 3121 Panthersville Road, Decatur, GA 30034; Kristen O. Fripp, MS, Georgia Bureau of Investigation, 925-A Mohawk Street, Savannah, GA 31419; and Ted R. Staples, MS, Georgia Bureau of Investigation, 3121 Panthersville Road, Decatur, GA 30034*

After attending this presentation, attendees will understand the internal validation for forensic casework of a new genetic analyzer platform can be daunting. It is the goal of this presentation to demonstrate possible methods and studies that can be used to validate a multi-capillary instrument such as the ABI 3130 Genetic Analyzer for forensic casework. It is also intended to present some practical considerations related to the instrument.

This presentation will impact the forensic community and/or humanity by demonstrating how the internal validation of methods and instruments is a critical aspect to any forensic laboratory's quality program. The ABI 3130 is a powerful tool for use in forensic DNA casework but is useless without proper validation. Once properly evaluated, the 3130 genetic analyzer will be invaluable in producing quality results in approximately a quarter of the time of the ABI 310 instrument.

The anticipated use for the ABI 3130 will be to decrease the backlog of no-suspect DNA cases. Typically, these cases are processed at the request of submitting agencies with suspect-DNA cases receiving higher priority. With the dedication of the ABI 3130 to the backlog of nearly 350 no-suspect DNA cases, the anticipated increase in productivity will be approximately 12-fold.

The internal validation for forensic casework of a new genetic analyzer platform can be daunting. It is the goal of this presentation to demonstrate possible methods and studies that can be used to validate a multi-capillary instrument such as the ABI 3130 Genetic Analyzer for forensic casework. It is also intended to present some practical considerations related to the instrument.

With ever-increasing caseloads and backlogs in state crime labs, the need for rapid and efficient genetic analysis has become critical. High throughput instruments such as the Applied Biosystems 3130 Genetic Analyzer have been developed to meet this need for both fragment and sequencing analysis. Along with its four capillary arrays, the 3130 Genetic Analyzer has an Automated Polymer Delivery System enabling reduced analysis time and instrument maintenance. Before the ABI 3130 Genetic Analyzer could be operational in a forensic casework setting at the Georgia Bureau of Investigation headquarters laboratory, the instrument had to be internally validated. Utilizing the QAS document, ISO 17025 guidelines, ASCLD-LAB guidelines and Georgia Bureau of Investigation quality documents, a validation study was developed and performed to demonstrate the instrument's ability to produce reliable and accurate results for forensic casework analysis. This study included analyzing known and non-probative samples as well as precision, reproducibility, mixture, and sensitivity studies. Other aspects of the 3130 instrument including capillary to capillary sensitivity, injection times, contamination, amplicon load, and software (data collection and genotyping) settings had to be evaluated. All samples were amplified using the AmpF*l*STR® Identifiler® Kit (*Applied Biosystems*) and genotyped with GeneMapper ID v3.2 software (*Applied Biosystems*) with a relative fluorescence unit (RFU) threshold of 150.

Known samples consisting of blood, saliva, and semen as well as non-probative evidence samples consisting of epithelial portions from differential extractions all produced the correct genotypes when compared with Profiler Plus and COfiler genotypes. The 3130 instrument produced quality results in regards to precision, reproducibility, and sensitivity, although the 310 platform (*Applied Biosystems*) produced slightly better results in precision and sensitivity studies. Precision data exhibited standard deviations well below the +/- 0.5 base pair sizing standard with higher standard deviations observed at larger loci. Sensitivity data revealed a recommended range of 0.5 to 4 nanogram starting template DNA. However, it should be noted that the 0.25 nanogram template produced partial profiles that may, in certain instances, provide valuable information. Secondary donor profiles could be determined in mixture samples at dilutions of 1:10, 1:3, and 1:1. The 1:20 dilution showed little to no secondary donor alleles that were not considered stutter. Contamination was not detected during the course of the validation experiment even in the presence of overloaded samples. Although peak height differences were evident between capillaries, overall sensitivity was nearly identical between capillaries.

Internal validation of methods and instruments is a critical aspect to any forensic laboratory's quality program. The ABI 3130 is a powerful tool for use in forensic DNA casework but is useless without proper validation. Once properly evaluated, the 3130 genetic analyzer will be invaluable in producing quality results in approximately a quarter of the time of the 310 instrument.

The anticipated use for the ABI 3130 will be to decrease the backlog of no-suspect DNA cases. Typically, these cases are processed at the request of submitting agencies with suspect-DNA cases receiving higher priority. With the dedication of the ABI 3130 to the backlog of nearly 350 no-suspect DNA cases, the anticipated increase in productivity will be approximately 12-fold.

ABI 3130, Validation, Multi-Capillary

 ** Presenting Author*