B135 Evaluation of the QIAGEN® Investigator 24Plex Polymerase Chain Reaction (PCR) Kit for Amplification of Forensic Samples

Clinton D. Buchanan, PhD, 4930 N 31st Street, Forest Park, GA 30297; and Joel D. Sutton, MSFS, 4930 N 31st Street, Forest Park, GA 30297-5205*

The goal of this presentation is to provide attendees with information regarding performance of the QIAGEN® Investigator 24plex PCR kit during assessment studies addressing sensitivity, reproducibility, precision, mixtures, contamination, concordance, and non-probative case-type samples.

This presentation will impact the forensic science community by providing insight to laboratories considering implementation of expanded core loci PCR kits for forensic casework applications.

The QIAGEN® Investigator 24plex QS kit is a recently National DNA Index System (NDIS) -approved Short Tandem Repeat (STR) amplification kit used for human identification applications. The kit allows for multiplex amplification of the Combined DNA Index System (CODIS) core loci, the European Standard Set (ESS) markers, SE33, DYS391, D2S1338, D19S433 and Amelogenin. Laboratory studies of the QIAGEN® Investigator 24plex QS were performed to determine the efficacy of the kit for amplification of forensic samples. DNA samples were amplified using the standard cycling protocol, and sample amplicons were processed on the Applied Biosystems® 3500xl genetic analyzer following steps outlined in the Investigator 24plex QS handbook (rev. 08/2014). GeneMapper ID-X_v1.2 panels, bins, and stutter files for the Investigator 24plex QS kit were provided by QIAGEN® (Investigator_TemplateFiles_GeneMapper_ID-X_v7). These default files were used for data analysis; however, default stutter ratios for some loci (provided in the Investigator Template GeneMapper ID-X _v7 files) were modified based on maximum stutter findings observed.

The experiments focused on sensitivity and mixtures prepared from DNA sourced commercially and via in-house extraction methods. Comprehensive mixture studies were conducted. Additional work included reproducibility, concordance, contamination assessment, non-probative case-type samples, precision, and qualifying samples (National Institute of Standards and Technology (NIST) standard reference material) studies. Artifacts observed throughout the course of testing included elevated baseline, spectral pull-up, elevated stutter, and occasional spikes. DNA template amounts ranging from 0.008ng to 1.25ng from multiple sources were included in sensitivity studies. Admittedly, elevated stutter is not unexpected in lower-level DNA samples; however, stutter values exceeding filter values provided in the Investigator Template GeneMapper ID-X _v7 files were observed in samples associated with DNA template amounts ≥0.125ng. In addition, allelic drop-in of a 14 allele at locus D8S1179 was observed in one 9948 sensitivity sample at 0.016ng; however, this is not unexpected when working with lower-level DNA samples. Heterozygous peak height ratios were generally ≥50% in sensitivity samples targeting ≥0.125ng of DNA, and complete profiles were generally observed in samples targeting ≥0.063ng of DNA. The data gathered and analyzed from the laboratory studies of the QIAGEN® Investigator 24plex QS kit supports the PCR kit as being a robust and reliable tool for obtaining STR results for the expanded CODIS core loci set.

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*Presenting Author