## B109 An Evaluation of the Quality of Short Tandem Repeat (STR) Profiles Generated by Rapid DNA Instruments

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After attending this presentation, attendees will understand the performance of the Rapid DNA instruments and whether the Rapid DNA instruments can be applied for casework samples.

This presentation will impact the forensic science community by reporting on the quality and characteristics of STR profiles produced by two different Rapid DNA instruments.

The Rapid DNA instruments are optimized to produce STR profiles from reference buccal swabs without human review. The applicability of the Rapid DNA instruments to disaster victim identification and casework samples is also of great interest to the forensic community.

In this study, the quality and the characteristics of STR profiles produced by the DNAscan™ 6C Rapid DNA Analysis System using the High DNA Content (HDC) Flexplex™ chemistry and the Low DNA Content (LDC) Flexplex™ chemistry, and the RapidHIT™ System using the GlobalFiler® Express chemistry were evaluated. High DNA content samples, such as reference buccal swabs, mock casework, bloodstain, and saliva stain samples were analyzed. Buccal swab samples were collected from volunteers. Blood dried on the glass slide and saliva on water bottles were collected by wiping using the swabs moistened with sterile distilled water. Cotton swabs manufactured for the DNAscan™ 6C Rapid DNA Analysis System were used. A full DNA profile without an incorrect allele calling and low-quality flag issued by the Rapid DNA expert systems was counted as a success. A profile with an allelic dropout at any loci caused by consumables or instrument defective was counted as a failure. A profile with a labeled non-allelic peak, such as a dye blob and spectral pull-up as an allele, was also counted as failure. The .fsa files were exported from both systems. Human review data analysis using the GeneMapper® ID-X Software was performed after the peak detection threshold for each system had been established using an electropherogram obtained from clean blank swabs.

The success rates for buccal samples for both Rapid DNA systems were approximately 80%, as reported by other publications. It was found that the success rate for mock casework samples was less than 50% due to low-quality flags that indicate the presence of non-allelic peak and/or the substantial variability in peak height and/or inter-loci balance, was more frequently issued by the Rapid DNA expert systems than buccal samples. No indications of carryover and cross contamination were observed in any of the blank samples by the Rapid DNA expert system and the GeneMapper® ID-X Software analysis. It was shown that the success rate can be improved significantly when .fsa files were analyzed by GeneMapper® ID-X Software.

An allelic ladder is run concomitantly with samples in each cassette. When the allelic ladder fails to meet the quality parameters of the Rapid DNA expert systems, the pre-loaded virtual allelic ladder implemented in each of the Rapid DNA instruments is employed to designate the sample alleles; however, it was found that some incorrect alleles were called by the Rapid DNA instruments in such cases. Therefore, it was considered that the success of the allelic ladder run was important for the correct allele calling.

**Rapid DNA, Data Analysis, Allelic Ladder**