

## EVALUATION OF INVESTIGATOR® STR GO! LYSIS BUFFER FOR FAST DNA EXTRACTION FROM COTTON SWABS

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**Background:** The solutions provided for fast extraction of known samples have greatly improved over the last few years with each system being faster than the last. DNA database labs have bypassed this step altogether with the release of direct amplification kits that are now commonly used with FTA punches. However, for labs that routinely receive a variety of sample types, alternate methods are needed that efficiently reduce overall processing time.

Qiagen has developed the Investigator® STR GO! Lysis Buffer which provides a direct amplification solution for reference samples by creating a crude lysate in just 5 minutes. This solution significantly reduces the sample preparation time when compared to other lysis methods that require a longer incubation period.

**Objective:** The objectives of this study were to: 1) evaluate the performance of the Investigator® STR GO! Lysis Buffer with known swab reference samples, 2) compare the Investigator® STR Lysis Buffer method to another lysis method that is currently in use, and 3) scale the Qiagen procedure to a high throughput, 96 well plate based method.

**Methods:** Samples were prepared by using sterile Puritan Cotton Swabs. Buccal cells were orally collected by swabbing the insides of both cheeks several times. Samples were air dried prior to DNA processing. Approximately ¼ of the cotton swab tip was cut and placed into a well on a 96 well plate. One hundred microliters of the Investigator® STR GO! Lysis Buffer was added to each well. The 96 well plate was placed on a heat block for 5 minutes at 95°C. After incubation, the swab lysate was mixed using an 8-channel pipette. Two microliters of the lysate were added to the Investigator® 24plex GO! reaction mix. Samples were amplified according to manufacturer's protocol for 26 cycles and genotyped using the ABI 3500xL Genetic Analyzer with GeneMapper® IDX v1.4 (Life Technologies).

**Results and Discussion:** The profiles generated with this extraction method were acceptable with great inter-locus and intra-color balance. Peak height balances were greater than 70% and there were few occurrences of off-scale data. The data quality of this method was comparable to the method currently used at the USACIL DNA Database; however, with the Investigator® STR GO! Lysis Buffer method the extraction time and reagent cost were less. Further study is needed to test this method using non-probative database-type samples. This preliminary evaluation supports that this processes is acceptable for high throughput analysis. This method could also be employed in DNA casework labs where quantification of reference samples is not required.