

B65 The Optimization of DNA Extraction From Buccal Samples Collected With the CollectEject[™] Oral Swab for High-Throughput Testing

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Learning Overview: After attending this presentation, attendees will be informed of a new collection product that can be utilized for collection of reference samples, Gentueri's CollectEjectTM Oral Swab. Attendees will also learn two optimized extraction procedures to produce maximum yield from the CollectEjectTM Swabs and how it compares to other common collection devices.

Impact on the Forensic Science Community: This presentation will impact the forensic science community by providing insight into various collection devices that can be used to streamline processing of reference DNA samples as well as two optimized extraction techniques that maximize DNA yield with the CollectEject[™] Oral Swabs for a high-throughput workflow.

As the submission of casework samples to be processed for DNA increases, and a newer panel of testing options becomes available for law enforcement (e.g., Rapid DNA or genetic genealogy), crime scene processors and laboratories look for ways to streamline collection and testing procedures to keep up with this demand. Collection techniques and devices continue to evolve to allow samples to be collected more efficiently without compromising integrity or contamination of the sample. Gentueri has recently released a product line of swabs, CollectEject[™], that allows for a quick and efficient collection process. The swab is attached to an applicator that ejects the tip of the swab straight into a tube with no cutting necessary. The swab design also allows for increased surface area for DNA collection and retention. Newer technologies and workflows rely on high first-pass success, like Rapid DNA devices, or newer investigative lead processes like genetic genealogy or phenotyping that require higher quality and quantity DNA for investigative leads. The collection techniques utilized for these processes should be quick and of high quality.

This research evaluated the CollectEject^M swab for collection of reference samples. The first study focused on optimizing the yield of DNA extracted from the CollectEject^M swab following two different DNA extraction protocols, PrepFiler[®] Express using the AutoMate Express^M System and the Promega[®] Maxwell extraction. Various incubation times and temperatures were analyzed and compared by quantitation of total DNA extracted. A statistical analysis was performed on the yield of DNA recovered through each variable, and the optimal parameters for each extraction process was determined. The second phase of the study compares the CollectEject^M swab to the Whatman[®] Omni Swab. Reference swabs were collected using each device and stored in Gentueri's SwabSaver^M. The SwabSaver^M allows for samples to be stored at room temperature for a prolonged periods of time and the initial extraction stage can be performed directly in the SwabSaver^M tube. Samples were then extracted following the optimized Automate extraction procedure and quantified for comparison. A select number of samples will be carried through to amplification to ensure there is no effect on the quality of DNA profile generated.

Quantitation results of the first study were separated and analyzed by extraction type. For the Automate ExpressTM extraction, the 80-minute incubation mixed at 850RPM at 70 °C was found to yield significantly higher total DNA compared to other parameters tested. The 80-minute extraction yielded an average of 7,261pg of DNA and the remaining variables ranged from 963 to 2,230pg total DNA. All other variables tested generated no significant differences. The Maxwell extraction yielded no significant difference between incubation temperatures (56–70°C) and incubation times (30 minutes–12 hours). A higher sample size and DNA profile generation will be completed to further examine compare these devices.

DNA Collection, CollectEject[™], STR Profiling