Recent trends in sample processing for databasing and paternity purposes have moved towards direct amplification systems. DNA samples can be collected and stored on non-treated matrices, such as the Bode Buccal DNA Collector™, until sample processing is required. Qiagen’s recently released direct amplification kit encompasses the CODIS core loci, the European standard set markers, and additional loci including a Y-STR and quality sensors.

This presentation will describe the studies performed with the Investigator® 24plex GO! Kit to obtain optimal results from samples collected utilizing the Bode Buccal DNA Collector™, a non-treated matrix, at varying reaction volumes. The amplification reaction volumes analyzed in this experiment were 20µl (Full Reaction), 10µl (Half Reaction), and 5µl (Quarter Reaction). A total of one hundred (n=100) self-collected samples, approximately 1.5 years old at time of testing, were utilized in this experiment. These one hundred samples were stored in a controlled microenvironment (~20-25˚C and <10% humidity). Slightly aged samples were chosen as they may be more representative of a routine databasing sample rather than a fresh sample collected a few days prior to testing.

This presentation will display the optimized procedures for cell lysis, reaction mix components, thermal cycling parameters, and 3500xL injection conditions. The manufacturer’s recommended procedure for “other papers” or non-treated matrices did not include a cell lysis step. A modified and optimized procedure was developed in order to perform a direct amplification procedure with a 1.2mm punch from a non-treated matrix.

Capillary electrophoresis setup and run parameters were optimized to achieve consistent, reliable, and reproducible results. Optimization parameters, including the use of additional ILS and a standard amplification product dilution, will be discussed during the presentation. Direct amplification of reference samples utilizing Qiagen’s Investigator® 24plex GO! Kit can provide a time efficient method for obtaining complete genetic profiles with a high first pass success rate. This presentation will demonstrate methods to increase direct amplification feasibility by decreasing overall costs per sample through the use of reduced volume reactions.