B69 Maximizing DNA Recovery and Short Tandem Repeat (STR) Data From Spent Cartridge Casings

Ashley M. Mottar, MS, 560 Baker Hall, East Lansing, MI 48824; and David R. Foran, PhD, Michigan State University, Forensic Science Program, 560 Baker Hall, East Lansing, MI 48824*

After attending this presentation, attendees will understand the highly improved performance of optimized methods for touch DNA recovery and analysis from spent cartridge casings, which are commonly retrieved from shooting incidents.

This presentation will impact the forensic science community by providing improved procedures for recovering and amplifying DNA from spent cartridge casings in order to increase DNA yields and STR data. The findings have the potential to influence the techniques scientists utilize when analyzing DNA from spent casings, ultimately connecting an individual to a crime based on the presence of their genetic material on casing evidence.

Firearms, particularly pistols, are commonly used in violent crimes, though the weapon is rarely recovered. Nevertheless, spent cartridge casings ejected during firing are often recovered by law enforcement and may contain DNA deposited by the loader of the firearm, who could potentially be identified via STR analysis. DNA recovered from spent casings; however, is often degraded and present in low copy numbers. Owing to this, crime laboratories have had limited STR typing success from casings; thus, it is essential that effective methods for DNA recovery and analysis are determined.

Previous research in this study's laboratory examined multiple variables in cell/DNA isolation to improve DNA yields and typing results from spent casings, including swabbing versus soaking casings, the duration of digestion, shaking during digestion, etc. Based on the results, in the current study, DNA yields were examined and STR profiles were generated using five optimized methods: swabbing or soaking with an organic extraction, swabbing or soaking with a silica-based extraction (QIAamp® DNA Investigator Kit), or swabbing with a non-binding DNA extraction (Fingerprint DNA Finder® Kit). Volunteers loaded uncleaned cartridges into the magazine of a pistol, the cartridges were fired, and the casings were collected. The first method consisted of swabbing casings with a wetted swab followed by a dry swab. The second method involved fully submerging casings in digestion buffer for 30 minutes, transferring the buffer to microcentrifuge tubes, then swabbing the casings with a dry swab, and incubating the tubes containing the soaking solution and swabs at 85°C for ten minutes. Proteinase K was added to all samples, which were digested for one hour with concurrent shaking at 900rpm. Organic or QIAamp® extractions were then conducted, with the former followed by purification using an Amicon® column pre-treated with yeast RNA. FDF® processing followed the manufacturer's instructions. DNAs were quantified and amplified with AmpFlSTR® MiniFiler™ and/or PowerPlex® Fusion kits. Statistical analysis of DNA yields, the percent of loaders' STR profiles recovered, and allelic consistency with the loader were performed.

Significantly more loader alleles were amplified using Fusion than MiniFiler™, while the average number of non-loader alleles did not differ. Therefore, Fusion was used for subsequent analyses. Overall, organic extractions of swabbings or soakings yielded significantly more DNA than QIAamp® or FDF®. Further, double swabbing and organic extraction resulted in significantly higher DNA yields than the other four methods and generated, on average, 30% of loaders' profiles (~12 alleles), including some full 24 locus profiles. Organic extraction of soaked samples produced the second-highest amount of DNA, and an average of 10 loader alleles. QIAamp® purification of swabbed or soaked samples recovered significantly less DNA and resulted in fewer STR alleles than those organically extracted. The non-binding DNA extraction, which was specifically designed for touch samples, generated minimal or no loader alleles (an average of only 2.7% loaders' profiles); however, the method that produced the most DNA (double swabbing and organic extraction) also resulted in the most non-loader/drop-in alleles, although their prevalence was concentrated in a small percentage of samples and were generally of undeterminable origin. Taken together, these findings indicate that genetic analysis can become a viable tool for identifying the loader of a firearm, increasing the probative value of this type of evidence.

Cartridge Casings, DNA From Touched Objects, STR Analysis