B136 Evaluation and Optimization of DNA Recovery From Bullet Cartridge Cases

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After attending this presentation, attendees will be aware of optimized methods for the recovery of nuclear DNA from spent cartridge cases.

This presentation will impact the forensic science community by examining the ability forensic biologists have to obtain useful DNA profiles from cartridge cases through the evaluation and optimization of collection and extraction techniques.

Firearms were used in 69.3% of homicides, 41% of robberies, and 21.8% of aggravated assaults in the United States in 2012. Accordingly, both fired and unfired cartridge cases are commonly encountered at crime scenes; however, despite the prevalence of this sample type, DNA testing is not often sought as it frequently fails to produce an interpretable profile. A common explanation for this is poor/minimal "touch type" DNA transfer to non-porous surfaces. Another explanation is possible damage to DNA by the heat generated during the firing process. This degradation would lead to preferential amplification of those loci with shorter base pair lengths and the loss of amplifiable alleles at larger loci. It has also been hypothesized that co-eluting reactive metal ion species from Gun Shot Residue (GSR) or from the cartridge case itself can result in either inhibition and/or the accelerated degradation of DNA.

In order to optimize DNA recovery, different collection and extraction techniques were evaluated with cartridge cases of various metal compositions. Two collection techniques, double-swab and sonication, were evaluated by sampling sixty .22LR caliber cartridge cases. Additionally, two extraction techniques, a robotic extraction technique utilizing Qiagen®'s EZ1® Advanced XL system and a manual phenol:chloroform extraction protocol, were assessed by sampling 200 .45 caliber rounds. All samples were quantified using real-time quantitative PCR with Life Technologies® Quantifiler® Human DNA Quantification kit, amplified using Promega's® PowerPlex® 16HS amplification kit, and analyzed using an Applied Biosystems® 3130 Genetic Analyzer with ABI's® GeneMapper® software.

It was determined that the use of sonication for collection along with a phenol:chloroform extraction method results in significantly greater DNA recovery than using a double-swab collection technique or a robotic extraction technique. Sonication recovered an average of 50% of DNA compared to an average 11% recovered with a double-swab technique. Although the robotic extraction technique produced more consistent results, the average DNA recovery was significantly lower as compared to the phenol:chloroform extraction method. The robotic extraction technique resulted in an average DNA recovery of 3.65pg/µL with a standard deviation of 1.9, while the phenol:chloroform extraction technique allowed an average DNA recovery of 7.65pg/µL with a standard deviation of 10.6.

In order to assess the role GSR has on observed differences in the recovery of DNA from the various extraction methods used, a suspension of GSR was created using internal barrel swabs of recently fired guns. Increasing volumes of this suspension (1µL, 5µL, 7.5µL, and 10µL) were added to eight samples of 2800M positive-control DNA. These samples were then extracted using either the EZ1® protocol or the phenol:chloroform protocol. The EZ1® extraction protocol resulted in DNA profiles with significant variability and poor inter-locus signal balance. Several of the samples extracted using the EZ1® protocol demonstrated preferential amplification or peak height suppression. Samples which were extracted using the phenol:chloroform protocol produced DNA profiles with consistently high and well-balanced allelic peaks across all loci.

In order to assess the role which the extraction method plays in samples from handguns, 18 swabs were prepared under controlled laboratory conditions from the slide serrations of handguns known to contain multiple contributors. Half of each sample was extracted using the robotic protocol and the remaining half was extracted with a phenol:chloroform protocol. The EZ1® extraction protocol resulted in DNA profiles with an average RFU value of 60. Samples which were extracted using the phenol:chloroform protocol produced full DNA profiles with an average RFU value of 2,000.

This research offers an optimized method for DNA recovery from cartridge cases and demonstrates that the adverse impacts on DNA profiles associated with samples originating from handguns could be due to the inability of commonly employed robotic extraction methods to remove co-eluting species which have been demonstrated to affect downstream analysis.

Cartridge Cases, STR Typing, Touch DNA