## A161 Mitochondrial DNA Recovery and Analysis From Spent Cartridge Casings

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After attending this presentation, attendees will learn about the utility of mitochondrial DNA (mtDNA) analysis of epithelial cells from spent cartridge casings and the optimal DNA recovery method from such evidence.

This presentation will impact the forensic science community by detailing a highly sensitive DNA analysis method that allows for the identification of a weapon's handler using mtDNA recovered from spent cartridge casings.

It is not uncommon that the only evidence remaining at the scene of a shooting is spent cartridge casings. Because cartridges are usually loaded into a firearm by hand, forensic scientists have long attempted obtaining fingerprints from spent cartridge casings, but these efforts are almost never successful. An alternative method for identifying the person who loaded bullets into a clip or chamber of a firearm comes from the epithelial cells that may be deposited onto handled cartridges. Previously, scientists have examined the feasibility of STR typing of DNA from spent cartridge casings, but have had limited success, most likely due to a combination of low copy number DNA, DNA degradation caused by temperatures reaching 1800°C during firing, and PCR inhibition resulting from the metal and/or primers in the gunshot residue.

While obtaining even a partial STR profile from spent cartridge casings can be beneficial, in most cases not enough DNA data is recovered to link a suspect to the scene. In this regard, there is a greater likelihood of obtaining DNA typing results by focusing on mtDNA due to its higher copy number and protection in the mitochondrion. In spite of this, however, researchers have not looked into the inherently promising mtDNA analysis as a tool for identifying the handler of cartridges.

In this study, volunteers loaded ten 40-caliber cartridges each into the magazine of a gun. The cartridges were then fired and DNA was recovered from five of the ten fired casings individually using a double swab method—a wet swab followed by a dry swab—for each casing. For the remaining five casings, one pair of swabs was used to swab them all, resulting in a "cumulative swab." A standard organic extraction, followed by the use of spin columns for removal of PCR inhibitors, was used to purify the DNA. Yields were determined, and no statistical difference between the recovery methods was found.

Next, STR and mtDNA assays were investigated. STRs were amplified and the number of alleles consistent with the handler was compared among the double swab method, cumulative swab method, and a consensus profile method that considered the five STR results from the individual casings in combination, to help distinguish real peaks from drop-in. For mtDNA, amplification parameters were optimized, segments between 220 and 270 base pairs in hypervariable regions I and II (HVI and HVII) were amplified, and the products underwent Sanger (dideoxy) sequencing. The mtDNA haplotypes produced were compared to those of the handlers in order to determine the utility of mtDNA analysis, and processing the spent cartridge casings individually and cumulatively.

Almost all of the samples, regardless of the swabbing method, produced few or no STR alleles, which was consistent with previous studies. In contrast, mtDNA was successfully amplified and sequenced from the vast majority of both individually and cumulatively swabbed spent cartridges, including those for which STR testing was negative. Given the increased sensitivity of mtDNA testing, contamination represents a particular problem, and extreme care is required to avoid it during evidence collection and processing. In spite of this caveat; however, mtDNA analysis from spent cartridge casings was quite successful, proving to be a more viable technique than STR typing of these samples.

**Mitochondrial DNA, Cartridge Casings, DNA Collection**

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