B101 The Recovery of Mitochondrial and Nuclear Touch DNA From Spent Cartridge Casings

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After attending this presentation, attendees will understand the advantages and disadvantages of Short Tandem Repeat (STR) analysis and mitochondrial DNA (mtDNA) sequencing of touch DNA from spent cartridge casings for the identification of the loader of a firearm.

This presentation will impact the forensic science community by detailing how the recovery of touch DNA from spent cartridge casings is influenced by casing caliber and how the type of testing employed, either mitochondrial or nuclear, influences DNA typing success and the potential identification of the loader of a firearm.

Crimes involving firearms are common, yet the weapon itself is seldom recovered at a crime scene. In contrast, cartridge cases that are ejected during a shooting are regularly left behind by the shooter and are commonly submitted as forensic evidence in an attempt to identify the loader or shooter of the gun. Fingerprints may be deposited on cartridge cases by the loader; however, they are seldom recovered following a shooting. Due to the lack of fingerprints, DNA profiling may be attempted. This has had limited success from spent cartridge cases, most likely because the DNA is in trace amounts or highly degraded, possibly due to the intense heat generated or other aspects of the shooting process. Thus, mtDNA, which is present in hundreds of copies per cell encased inside the mitochondria, may be more advantageous for DNA testing from spent cases.

In the research presented, all testing had Michigan State University (MSU) Institutional Review Board (IRB) approval. Volunteers loaded magazines of firearms with 0.22 and 0.45 caliber cartridges. The volunteers also provided a buccal swab for reference. Firearm examiners at the Michigan State Police Lansing Forensic Laboratory subsequently fired the weapons. The ejected cartridge cases were collected and taken to the MSU Forensic Biology Laboratory for DNA analysis. DNA was isolated using an optimized double swabbing technique and organically extracted, followed by purification using pre-treated Amicon® filters. DNA was quantified via an Alu-assay using real-time Polymerase Chain Reaction (PCR). STR analysis was then performed using a PowerPlex® Fusion kit, and results were assessed based on the number of alleles consistent and inconsistent with the loader. MtDNA sequencing was also performed, and results were categorized as consistent or inconsistent with the loader or the presence of a mixture. The two analysis methods were then compared.

MtDNA haplotypes and STR profiles were typically in agreement with regard to the mtDNA classification and number of alleles consistent with the loader. Mitochondrial haplotypes consistent with the loader had a median of 11 loader alleles in STR profiles, while haplotypes inconsistent with the loader had a median of 7.5 loader alleles. Haplotypes displaying a mixture had a median of nine; however, the methods differed in terms of amplification success and identification of the loader. MtDNA sequencing proved to be more robust than STR analysis, as mtDNA was successfully amplified from all extracts, whereas complete STR profiles were rare. Alternatively, STR profiles that had numerous loci amplifications were more individualizing than mtDNA in that some volunteers shared haplotypes, while STR results were unique. Cartridge caliber also played a substantial role in DNA results. Significantly more DNA was recovered from 0.45 caliber cases than 0.22 caliber cases (p = 0.0023), with 0.45

caliber cases also producing a significantly higher median number of loader alleles ($p = 0.0062$) even though both calibers were loaded into magazines in the same manner. On the other hand, classification of mtDNA haplotypes did not differ significantly between case caliber ($p = 0.321$). Given these results, it is important to recognize that STR analysis and mtDNA sequencing generate different outcomes, each having distinct advantages and disadvantages. The results also demonstrate the value of the optimized DNA isolation methods, which were successful in obtaining DNA from spent cases, which is vital if DNA profiling of cases is to widely undertaken.

Cartridge Casings, Touch DNA, Mitochondrial and Nuclear DNA