B51 Recovery of DNA From Surfaces of Handguns: Targeting Relevant Sampling Areas

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Learning Overview: After attending this presentation, attendees will be familiar with collecting DNA samples from individual areas of handguns, a process that may help preserve evidence and minimize the generation of artificially mixed DNA profiles.

Impact on the Forensic Science Community: This presentation will impact the forensic science community by informing practitioners as to which specific area(s) of a handgun may be best suited for the recovery of DNA that generates useful results for probabilistic genotyping.

Because many factors potentially influence the transfer of DNA onto a firearm, such as the frequency of handling by one or multiple individuals, the frequency of cleaning, and how and with what the weapon is cleaned, designing an experiment that accounts for all variables is nearly impossible. To provide guidance on sample collection from firearms to assist in criminal investigations, testing many complex, interrelated variables must include a comprehensive understanding of DNA transfer mechanisms.

This study was designed to systematically test whether there is a detectable difference in the quality and quantity of DNA detected on four specific areas of the firearm: grip, trigger, slide, and magazine. Eleven handguns owned by 11 different law enforcement personnel were used in this study. A questionnaire was completed by each participant that ascertained length of ownership, length of daily contact, frequency of cleaning, time since last fired, and accessibility by other individuals. All weapons were Glocks® of varying calibers. Gun ownership ranged from less than a year to 25 years. Participants reported that service weapons were kept on their person 8+ hours per day and fired within the last 12-month period. Regular cleaning was reported to occur every two weeks, monthly, or bi-annually. Seven officers reported that no one else had access to their service weapon while four officers reported that a significant other had access.

Samples from the four designated areas of the firearm were collected separately using a single-swab technique. Each swab was moistened with 100µl of sterile Phosphate Buffered Saline (PBS). A total of 44 samples were extracted utilizing the QIAamp® DNA Mini Kit per manufacturer's instructions. Extracted DNA was amplified with the GlobalFiler™ Polymerase Chain Reaction (PCR) Amplification Kit and analyzed on an AB SCIEX™ 3130xl genetic analyzer. STRmix™ v 2.6.1 was utilized to aid in interpretation. Deconvolution of any mixtures was completed before comparisons to known reference samples from the owners. The National Institute of Standards and Technology (NIST) 1036 database was used to calculate Likelihood Ratios (LRs). The Scientific Working Group on DNA Analysis Methods (SWGDAM) scale of verbal qualifiers was used to express the degree of support for a specified proposition (H_1—owner of gun is a contributor) relative to an alternative proposition (H_2—unknown, unrelated individual is a contributor).[1]

Data was obtained from all 44 samples. The amount of DNA recovered varied from area to area and from gun to gun. On average, more DNA was obtained from the slides and magazines and less DNA was obtained from the triggers and grips. Single-source DNA profiles (9% grip, 27% trigger, 36% slide, 27% magazine) and mixed DNA profiles of two or three contributors (91% grip, 91% trigger, 64% slide, 73% magazine) were observed. There was no discernable pattern as to Number Of Contributors (NOC) based on area. Interestingly, mixtures of two to three contributors were obtained from weapons that were reported to be accessible only by the officer.

The LRs for all grip, slide, and magazine samples provided very strong support (i.e., LR ≥ 1,000,000) in favor of H_1. Varying LRs were obtained from the trigger samples. For the majority of the trigger samples, the LRs provided very strong support in favor of H_1. In one instance, the LR provided moderate support (i.e., 100 ≤ LR ≥ 9,999) in favor of H_1. In this sample, data was only detected at 29% of the GlobalFiler™ loci. Interestingly, the LR (i.e., 2 ≤ LR ≥ 99) for one trigger sample provided limited support in favor of H_2. In this sample, data was detected at 54% of the GlobalFiler™ loci.

This study has demonstrated that useful DNA profiles can be obtained by single swabbing certain parts of a handgun. Based on the results, the slide and magazine samples appear to provide the best results. Although the amount of DNA on average obtained from the grip samples was less, useful results were still obtained from this area of the weapon. Trigger samples appear to provide the least impressive results.

Reference(s):

1. Recommendations of the SWGDAM Ad Hoc Working Group on Genotyping Results Reported as Likelihood Ratios. Accessed September 2020. https://www.swgdam.org/publications.

Transfer DNA, Handguns, Probabilistic Genotyping

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