JOURNAL OF FORENSIC SCIENCES

J Forensic Sci, July 2011, Vol. 56, No. 4
doi: 10.1111/j.1556-4029.2011.01766.x
Available online at: onlinelibrary.wiley.com

TECHNICAL NOTE

CRIMINALISTICS

Nicholas J. Richert,[1] *B.S.*

Swabbing Firearms for Handler's DNA

ABSTRACT: Obtaining quality DNA profiles from firearms can be instrumental in assisting criminal investigations. Typically, swabbings of firearms for handler's DNA are conducted on specific regions of the firearm prior to submission to the laboratory for analysis. This review examines and compares 32 cases whose gun swabbings were either analyzed individually according to the specific region which was swabbed, or analyzed collectively by combining the swabbings from all the individual areas. Those firearms whose swabs were analyzed separately exhibited lower DNA yields and consequently fewer loci exhibiting genotypes. Those cases whose swabs were analyzed collectively exhibited higher DNA yields and consequently greater numbers of loci exhibiting genotypes. These findings demonstrate that collective swabbings result in more complete profiles and lead to the recommendation that a firearm be swabbed in its entirety using no more than two swabs.

KEYWORDS: forensic science, firearm, handler's DNA, sample collection, trigger, grip, hammer

The Illinois State Police Forensic Science Center at Chicago has seen an increase in the number of requests for DNA analysis from firearms in recent years. Advances in forensic technology have made it possible for crime laboratories to draw associations between an individual and cellular material swabbed off a firearm containing handler's DNA (1).

The initial procedure utilized by a user agency of the Forensic Science Center at Chicago for collecting handler's DNA from firearms was to swab certain areas of a firearm (trigger, grips, hammer, etc.) individually. The DNA analyst would then analyze the swabs from each of these areas separately. In doing so, it was thought that the incidence of obtaining a mixed profile could be minimized, while at the same time associating a given profile or individual to a specific area on the firearm.

Unfortunately, swabbing and analyzing individual areas of a firearm often resulted in low level DNA extracts which yielded only partial DNA profiles or none at all. Since the primary goal of analyzing a firearm for DNA profiles is to either associate a given individual to that firearm or exclude an individual from it, it was decided that the swabs collected should be combined prior to extraction. The hypothesis was that by combining multiple swabs the overall DNA yield is optimized along with the opportunity to obtain the most complete DNA profile.

Materials and Methods

The data collected for this study was organized into two categories. The first category was denoted as the "Individual Swabbing Group." This group consisted of swabbings from individual regions on a firearm which were extracted and profiled separately. These regions included triggers, grips, hammers, cylinder releases, magazines, slides, straps, and front sites. At the discretion of the crime scene investigator, the number of individual regions swabbed on any given firearm ranged from two to six. A total of 53 swabbings collected from among 18 different firearms were represented in this group.

The second category was denoted as the "Combined Swabbing Group." This group consisted of samples created by combining the swabbings from individually swabbed regions on a firearm. The combined swabbings were extracted and profiled. Swabbings from a total of 59 individual regions taken from among 19 firearms were represented in this group. As was true for the first category, the number of swabbings collected from each firearm was left to the discretion of the crime scene investigator.

All swabbings were performed using sterile white cotton swabs prewetted with distilled water. The entire swab head was removed from the stick and utilized for extraction.

All DNA extractions were performed utilizing a standard phenol chloroform extraction protocol (2–6). The volume of TE used for recovery ranged from 24 to 100 μL at the discretion of the analyst.

Samples collected from 14 cases in 2003 and 2004 were quantified using the QuantiBlot® Human DNA Quantitation Kit (Applied Biosystems, Foster City, CA) (7–11). All samples collected from the remaining 18 cases in this study up through 2007 were quantified by real-time polymerase chain reaction (PCR) using the Applied Biosystems 7500 Real Time PCR System with the Quantifiler® Human DNA Quantitation Kit (Applied Biosystems) (12–17).

The amplification of DNA was performed using the AmpFℓSTR® Profiler Plus®/COfiler® amplification kits (Applied Biosystems) in a 50-μL reaction volume. The samples were amplified on a GeneAmp® PCR System 9700 (Applied Biosystems) or a PE Applied Biosystems model 480 thermal cycler (Applied Biosystems) using 28 cycles (18,19). The ideal target amplification amount using the QuantiBlot® Human DNA Quantitation Kit was 1.5 ng while the ideal target amount using the Quantifiler® Human DNA Quantitation Kit was 3.0 ng.

The preparation of amplified DNA samples for capillary electrophoresis was performed by preparing samples as prescribed by

[1]Illinois State Police, Forensic Science Center at Chicago, 1941 West Roosevelt Road, Chicago, IL 60608-1248.

Received 08 Mar. 2010; and in revised form 13 July 2010; accepted 16 July 2010.

Applied Biosystems for analysis on an ABI Prism 310 Genetic Analyzer (20).

A standard injection time of 5 sec was used for all samples. Additional injections at 10 sec were used on a discretionary basis. Genotyper® 2.1 and GeneMapper® ID v3.2 were used to complete the analysis of the data (21,22). A minimum peak height threshold of 150 RFUs was set for allele calls.

Results and Discussion

DNA Yields Obtained Between Groups Using Real-Time PCR

Table 1 is a summary of the DNA yields for the 16 combined swabbing samples and the 16 individual swabbing samples that were quantified using the Quantifiler® Human DNA Quantitation Kit. Only those samples that were quantified with the Quantifiler® Human DNA Quantitation Kit were used for the DNA yield comparison because it is a more sensitive quantitation technique than the QuantiBlot® Human DNA Quantitation Kit. The mean DNA yield for the combined swabbing group was 4.4 ng (range 0.3–20.6 ng), more than a two-fold increase over the value of 1.8 ng (range <0.02–14.4 ng) observed for the individual swabbing group. Similar individual swabbing DNA yield values were reported in a study conducted by Polley et al. (1).

Size of Profiles Detected Between Groups Comprising This Study

A complete DNA profile is defined as complete genotypes at all 14 loci (amelogenin plus the 13 standard CODIS STR loci). A partial profile is defined as one exhibiting less than 14 loci but complete genotypes at one or more of these loci. An incomplete profile is defined as one where alleles are detected at one or more loci but at no locus can it be conclusively determined to be a complete genotype.

Table 2 is a list of the number of loci observed in DNA profiles from the combined swabbings for each firearm and the mean number of loci obtained collectively from the individual swabbings for that particular firearm.

The mean number of loci identified in a DNA profile for the combined swabbings group was 8.0 (range 0–14) as compared to 5.3 (range 0–14) for the individual swabbings group. The somewhat higher number of loci in the combined swabbings group could be attributed to the higher yields of input DNA this group exhibited, as noted above.

The ability to successfully obtain at least a partial DNA profile is markedly greater in the group using combined swabbings as compared to that group using individual area swabbings. Table 3 shows only 5% of the samples in the combined swabbing group failed to yield a DNA profile, as compared to 32% in the individual swabbing group. This could be attributed once again to the higher yield of DNA resulting from combining swabbings as compared to that obtained from swabbings of a limited area of the firearm.

Size of Profiles Between Individual Areas of a Firearm

Table 4 is a summary of the mean number of loci along with sample size for the different individual swabbing areas analyzed within the individual swabbing group. Only those regions of the firearm represented at least three times in this study are recorded in this table. Regions of the firearm represented less than three times are not included in this table but are discussed.

This study, along with that of Polley et al. (1), demonstrates that the grip of the gun is the best area for obtaining the most complete profiles. This can be attributed to the grip of the gun being the area that an individual would touch most in terms of time and surface area. Sight, front strap, and magazine did not produce any detectable DNA profiles. Back strap produced a DNA profile at one locus and was observed once in this case review. The safety was swabbed once in this case review and produced a profile containing 10 loci.

Additional Comments

As would be expected, a 10-sec injection yielded additional alleles above the 150 RFU interpretation threshold from the DNA profile when compared to the default 5 sec in 92% of the samples reviewed in this study. Data below 150 RFU were not used in this case review and is only used according to our standard operating procedures for exclusionary purposes in casework mixtures involving three or more people.

Not surprisingly, combining swabbings from different areas of the firearm does result in a small increase in the number of mixed profiles obtained (Table 3). Where DNA results were obtained, approximately 78% of combined swabbings resulted in mixtures of two or more people as compared to 64% obtained from swabbings of individual areas. However, this small increase in the number of mixtures observed in the combined swabbing group does not overshadow the fact that it also allows for the detection of more loci.

In this case review, the combined swabbings resulted in two unique CODIS eligible profiles versus six for the individual swabbing group. A unique CODIS eligible profile is defined as a DNA profile originating from a single donor. Multiple profiles obtained from a firearm which are consistent with having originated from the same donor are considered as one unique profile. However, the limited number of samples, as well as CODIS regulations on what can be uploaded, prohibits a meaningful assessment of which group truly offers an advantage over the other in terms of CODIS entries. Guidelines concerning the size and complexity of profiles, both large and small, as well as regulations defining the probative component of a profile, all enter into the admissibility of a profile into CODIS.

Conclusion

There are considerable benefits to processing handler's DNA using combined swabbings rather than analyzing the individual swabbings separately. Table 1 shows a noticeable increase in DNA

TABLE 1—*Total DNA yields (real-time PCR): combined swabbings versus individual swabbings.*

Combined swabbings (ng) from 16 separate firearms															
20.6	8.0	7.5	6.3	6.2	5.8	3.8	3.0	2.4	1.6	1.5	1.2	0.9	0.7	0.6	0.3
Individual swabbings (ng) from a total of 5 firearms															
14.4	3.4	2.4	1.6	1.5	1.4	1.2	0.9	0.8	0.7	0.2	0.2	0.1	0.1	0.02	<0.02

Note: Values listed within the combined group represent total DNA yields from the combined swabbings from each of 16 separate firearms. Values listed in the individual group represent total DNA yields from each of 16 individual areas from a total of five separate firearms.

TABLE 2—*Size of DNA profiles (no. of loci): combined swabbings versus individual swabbings.*

Combined swabbings (no. of loci) from 19 separate firearms																		
14	14	14	13	13	12	10	9	9	8	8	7	6	5	5	3	1	1	0
Individual swabbings (mean no. of loci) from a total of 18 firearms																		
14.0	13.2	9.5	9.0	7.7	5.5	5.5	5.0	5.0	5.0	3.3	3.0	2.8	2.7	2.0	1.3	1.0	0.0	

Note: Values listed within the combined group represent total number of loci obtained from combined swabbings from each of 19 separate firearms. Values listed in the individual group represent mean number of loci obtained from individual areas taken from each of 18 separate firearms.

TABLE 3—*Comparison of profiles obtained from combined swabbings versus individual swabbings.*

	Combined Swabbings	Individual Swabbings
Total samples	19*	53†
No DNA profile	1	17
Incomplete profile	2	9
Partial single profile	2	3
Full single profile	0	1
2 person mixture	5	18
>2 person mixture	9	5

*The total number of firearms represented in this group.
†The total number of individual area swabbings from among 18 different firearms represented in this group.

TABLE 4—*Size of profiles from individual swabbings of specific areas on firearm.*

Swabbing area	Total Swabbings in Study	Average No. Loci
Grip	16	7.9
Slide	12	5.7
Hammer	3	4.0
Trigger	5	3.4
Cylinder	4	0.5

Note: This table reports on only those areas represented three of more times in this study.

yield for the combined swabbing group versus the individual swabbing group. A comparison of the results in Table 2 also shows that the higher DNA yields observed in the combined swabbings group over that of the individual swabbing group resulted in a corresponding increase in the mean number of loci detected for that group (8.0 loci vs. 5.3 loci).

There does not appear to be an increase in the number of profiles that can be uploaded into CODIS by combining individual area swabbings prior to extraction. Neither category appears to provide a high percentage of CODIS suitable profiles, suggesting that handler's DNA from firearms is not often a viable source for such investigative purposes. This conclusion is supported with a study conducted by Tambasco and Simons (23).

The data provided in this case review suggest that combining individual region swabbings prior to extraction for handler's DNA from firearms markedly increased the amount of samples worked in the laboratory that yielded interpretable DNA results. Eliminating individual area swabs used for sample collection minimizes the amount of time and work needed for sample processing. It also reduces the amount of extraction chemistry and laboratory consumables utilized. Most importantly, it provides the best approach for obtaining profiles which can be used for associations to known standards of potential handlers of a firearm.

The police department uses as many as six swabs to collect handler's DNA from a firearm. In order to minimize the loss of DNA which inevitably occurs when combining multiple extractions and concentrating down to a single tube, it is suggested that the handler's DNA from a firearm be collected on a minimal amount of swab material to maximize DNA yield and minimize sample loss due to unnecessary manipulation.

This review was presented to the police department, along with the suggestion that all areas of a firearm (trigger, grips, hammer, cylinder release, magazine, slide, strap, front sight) be collectively swabbed with only two swabs.

Acknowledgments

I would like to thank Daniel Gandor, Ph.D.; William Frank, M.S.; Jeanne Richeal, M.S.; Megan Neff; and Rodney Anderson from the Forensic Science Center at Chicago and Kara Stefanson from the Cook County State's Attorney's Office for their critical review of this manuscript. I would also like to thank Brian Schoon, M.S.F.S, from the Forensic Science Center at Chicago for his involvement in presenting this case review to the individuals responsible for changing the collection procedure of handler's DNA from firearms.

References

1. Polley D, Mickiewicz P, Vaughn M, Miller T, Warburton R, Komonski D, et al. An investigation of DNA recovery from firearms and cartridge cases. Can Soc Forensic Sci J 2006;39(4):217–28.
2. Farley MA, Harrington JJ. Forensic DNA technology. Chelsea, MI: Lewis Publishers, 1991.
3. Giusti A, Baird M, Pasquale S, Balazs I, Glassberg J. Application of deoxyribonucleic acid (DNA) polymorphism to the analysis of DNA recovered from sperm. J Forensic Sci 1986;31(2):409–17.
4. Hochmeister MN, Budowle B, Borer UV, Eggman U, Comey CT, Dirnhofer R. Typing of deoxyribonucleic acid (DNA) extracted from compact bone from human remains. J Forensic Sci 1991;36(6):1649–61.
5. Laber TL, O'Connor JM, Iverson JT, Liberty JA, Bergman DL. Evaluation of four deoxyribonucleic acid (DNA) extraction protocols for DNA yield and variation in restriction fragment length polymorphism (RFLP) sizes under varying gel conditions. J Forensic Sci 1992;37(2):404–24.
6. Lee HC, Gaensslen RE, Pagliaro EM, Guman MB, Berka KM, Keith TP, et al. The effect of presumptive test, latent fingerprint and some other reagents and materials on subsequent serological identification, genetic marker and DNA testing in bloodstains. JFI 1989;36:339–58.
7. Walsh PS, Varlaro J, Reynolds R. A rapid chemiluminescent method for quantitation of human DNA. Nucleic Acids Res 1992;20(19):5061–5.
8. Waye JS, Presley LA, Budowle B, Shutler GG, Fourney RM. A simple and sensitive method for quantifying human genomic DNA in forensic specimen extracts. BioTechniques 1989;7(8):852–65.
9. Waye JS, Michaud D, Bowen JH, Fourney RM. Sensitive and specific quantification of human genomic deoxyribonucleic acid (DNA) in forensic science specimens: casework examples. J Forensic Sci 1991;36(4): 1198–203.
10. Budowle B, Hulow W, Lee S, Klevan L. Using a CCD camera imaging system as a recording device to quantify human DNA by slot blot hybridization. BioTechniques 2001;30:680–5.
11. Applied Biosystems. Quantiblot Kit instructions. Foster City, CA: Applied Biosystems.
12. Applied Biosystems. Quantifiler™ Human and Quantifiler™ Y Kit user's manual. Foster City, CA: Applied Biosystems.
13. Green RL, Roinestad IC, Boland C, Hennessy LK. Developmental validation of quantifiler real time PCR kits for the quantification of human nuclear DNA samples. J Forensic Sci 2005;50(4):809–25.

14. Richard ML, Frappier RH, Newman JC. Developmental validation of a real time quantitative PCR assay for automated quantification of human DNA. J Forensic Sci 2003;48(5):1041–46.
15. Andreasson H, Allen M. Rapid quantification and sex determination of forensic evidence materials. J Forensic Sci 2003;48(6):1280–86.
16. Nicklas JA, Buel E. Development of an alu-based real time PCR method for quantitation of human DNA in forensic samples. J Forensic Sci 2003;48(5):936–44.
17. van der Horst EH, Leupold JH, Schubbert R, Ullrich A, Allgayer H. Taq-Man®-based quantification of invasive cells in the chick embryo metastasis assay. BioTechniques 2004;37(6):940–5.
18. Applied Biosystems. AmpFℓSTR® Profiler Plus PCR Amplification Kit user's manual. Foster City, CA: Applied Biosystems, 1997.
19. Applied Biosystems. AmpFℓSTR® COfiler PCR Amplification Kit user bulletin. Foster City, CA: Applied Biosystems, 1997.
20. Applied Biosystems. 310 Genetic Analyzer Instrument user's manual. Foster City, CA: Applied Biosystems, 1995.
21. Applied Biosystems. GeneMapper ID Software v3.2 user's manual. Foster City, CA: Applied Biosystems, 2005.
22. Applied Biosystems. GeneScan chemistry guide. Foster City, CA: Applied Biosystems, 1995.
23. Tambasco A, Simons RJ. Evaluation of firearm submissions—recovery and analysis of DNA from guns utilizing the PowerPlex® 16 system. MAFS Newsletter 2008; 22–26.

Additional information and reprint requests:
Nicholas J. Richert, B.S.
Illinois State Police
Forensic Science Center at Chicago
1941 W. Roosevelt Rd.
Chicago, IL 60608
E-mail: richern@isp.state.il.us