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Brief Communication

# Double swab technique for collecting touched evidence

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#### Abstract

Touched evidence is often submitted to forensic laboratories for DNA analysis. Classical stain recovery technique, involving one wet cotton swab, is commonly used for recovering the touched evidence. Double swab technique, using a wet cotton swab followed by a dry cotton swab, was compared with the classical technique for recovering the touched evidence. The wet cotton swabs and the dry cotton swabs were individually extracted. DNA extracts were quantified and amplified at 15 polymorphic loci. DNA recovered in some of the second dry swabs contained sufficient amount of DNA to yield a DNA profile. This study shows that the double swab technique improves the quality of the resulting DNA profiles. The double swab technique for recovering touched evidence at crime scenes is recommended.

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Keywords: Forensic science; Touched sample/evidence; Double swab technique; Crime scenes; DNA typing; Short tandem repeat

#### 1. Introduction

Evidentiary touched items are seized and submitted to crime laboratories for DNA analysis since van Oorschot and Jones have reported that DNA profiles could be obtained from handled objects [1]. DNA recovered from these objects was thought to have originated from epithelial cells [2]. A number of studies have examined the primary and secondary transfer of DNA by using single dampened cotton swabs for collecting DNA samples from touched objects [2–4]. The current sensitivity of the detection instruments and PCR–STR techniques has been able to produce full DNA profiles at or below 100 pg of purified DNA [5]. Full DNA profiles from single cells could be obtained using six forensic STR markers [6].

Double swab technique was originally advocated by Sweet et al. for recovery of saliva from skin. A wet cotton swab and a second dry cotton swab are applied onto the same surface of interest in the double swab technique. The use of the double swab technique improved the recovery of saliva compared to the use of the classical stain recovery technique [7]. Furthermore, the double swab technique was also used to retrieve trace level of DNA in the study of the primary and secondary DNA transfer [8–11]. Even though the double swab technique has been applied in these studies, the usefulness and advantages of using the technique to recover touched DNA samples have not been discussed.

In this study, the classical stain recovery technique and the double swab technique for recovering DNA on touched objects were evaluated. Experiments were carried out to examine the efficiency in the use of the double swab technique to obtain sufficient DNA to yield reportable DNA profiles. The use of the double swab technique for touched evidence collection at crime scenes was also discussed.

#### 2. Materials and methods

### 2.1. Samples and swabbing

Skin cells sloughed off during contact were collected by a wet swab first and then by a dry swab following the double swab technique [7] on the surfaces of various articles found in this laboratory (Table 1). The wet swabs were prepared

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by dipping the sterile cotton bud swab (Sterile swabs from Medical Wire & Equipment, Corsham, Wiltshire, England) into sterile water. The target surface was swabbed by a wet swab and then a dry swab with the same swabbing protocol. The surface was swabbed for about 15 s using moderately strong pressure and circular motions. The swabs were rotated along its long axis allowing every side of the swabs to come into contact with the target surface. A total of 20target areas were swabbed in this study. The moisture left by the wet swab was absorbed by second dry swab. The wet and the dry swabs were air-dried after swabbing and then individually extracted.

## 2.2. Extraction, quantitation and amplification

All these swabs were subjected to automated DNA extraction in Genesis Freedom 200 (Tecan) using DNA IQ<sup>™</sup> (Promega) kit according to the manufacturer's

Table 1

Summary of DNA typing results for DNA samples recovered from the first wet swab and the second dry swab over the same area of samples

Area	Description	DNA amount (ng/µl)	Number of alleles detected (>150 rfu)				
			0	1–5	6–10	11-20	>20
Wet swa	b						
1	Computer mouse	0.054		$\sqrt{4}$			
2	Computer keyboard	0.174		• • •			$\sqrt{(25)}$
3	Metal door handle	0.188					$\sqrt{(27)}$
4	Security keypad	0.062		$\sqrt{(1)}$			• • •
5	Light switch	0.072		$\sqrt{(3)}$			
6	Press of water dispenser	<0.023	$\checkmark$	• • • •			
7	Paper ring file	0.121			$\sqrt{6}$		
8	Stapler	0.066			• • • •	$\sqrt{(12)}$	
9	Bench surface	<0.023	$\checkmark$			• • •	
10	Punch	0.088	·		$\sqrt{8}$		
11	Computer mouse	0.06		$\sqrt{(1)}$	• • • •		
12	Computer keyboard	0.77		• • • •			√(26)
13	Metal door handle	0.042	$\checkmark$				• • • •
14	Security keypad	0.183	v			<sub>√</sub> (16)	
15	Light switch	<0.023		$\sqrt{(1)}$		v	
16	Press of water dispenser	0.046		v		√(19)	
17	Paper ring file	0.472				v	√(27)
18	Stapler	0.043	$\checkmark$				V
19	Bench surface	0.074	v	$\sqrt{(5)}$			
20	Punch	0.079		v (-)	√(9)		
Total			4	16			
	L						
Dry swa 1	Computer mouse	0.089				√(18)	
2	Computer house	0.206				$\sqrt{(10)}$	/(22)
3	Metal door handle	0.200				√(16)	√(32)
3 4	Security keypad		/			$\sqrt{(10)}$	
	Light switch	<0.023 0.054	$\checkmark$		/(11)		
5 6	Press of water dispenser		/		√(11)		
	-	<0.023	$\checkmark$				
7	Paper ring file	<0.023					
8	Stapler	0.031					
9	Bench surface	0.026					
10	Punch	<0.023	$\checkmark$		110		
11	Computer mouse	0.053		14.	$\sqrt{6}$		
12	Computer keyboard	0.099		$\sqrt{(1)}$		/(11)	
13	Metal door handle	0.074		((2))		$\sqrt{(11)}$	
14	Security keypad	0.042		$\sqrt{(2)}$			
15	Light switch	<0.023	,	$\sqrt{(1)}$			
16	Press of water dispenser	0.025	$\checkmark$			((17)	
17	Paper ring file	0.065			1100	$\sqrt{(17)}$	
18	Stapler	0.081			√(9)		
19	Bench surface	<0.023	$\checkmark$		11.0		
20	Punch	0.091			√(10)		
Total			8	12			

All samples were subjected to automated extraction using DNA IQ<sup>TM</sup> according to the manufacturer's recommendations. For all samples, the final elution volume was 40  $\mu$ l. The table shows the number of alleles detected in bracket for each sample.

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