Experiments on the DNA contamination risk via latent fingerprint brushes

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Abstract. One of the crucial tasks of a crime scene investigation is the search for latent fingerprints. The most common technique for the detection and development of latent fingerprints is the use of brushes with carbon black powder. As DNA analysis of latent fingerprints is already a common technique to obtain additional information, 51 used latent fingerprint brushes were analyzed to check if the brushes may be a source of DNA contamination. On 86% of the tested brushes, DNA could be observed in partial or full profiles, mostly as DNA mixtures. Following these pre-testing results, a secondary transfer study was carried out with used and artificially contaminated brushes. The typing results of these tests could prove a limited DNA contamination risk via latent fingerprint brushes via secondary transfer. © 2005 Elsevier B.V. All rights reserved.

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1. Introduction

As the analysis of small amounts of DNA has been improved especially in the last years using “low copy number” typing strategies, the police more frequently requests DNA testing of latent fingerprints that are not analyzable for dactyloscopy because of smearing or incompleteness. Often enough, this is the last possibility to obtain crucial information leading to a suspect by database search or to match evidence to a suspect. 

In contrast to other contact stains taken directly from the evidence, latent fingerprints have normally been treated with powder using dactyloscopy brushes made from glass fibers or bird feathers. According to SOCOs from the Cologne Police Department, these brushes are typically used for several weeks up to months on numerous different crime scenes. This led us to the assumption that DNA from powder-treated fingerprints may be
contaminated by DNA from other crime scenes or other evidence from the same crime scene. The area for visualization of fingerprints is selected arbitrarily which means even huge surfaces (e.g. doors) are treated with powder, and even when no fingerprint was found, human cells (e.g. skin debris, saliva) may adhere to the brush. In this study, we present the results of our investigations regarding the DNA contamination risk via latent fingerprint brushes. The main parts of the investigations were separated into three phases.

2. Materials and methods

Phase 1: Analyzing the brushes: 51 different fingerprint brushes (used at crime scenes from several weeks to many years, originating from Germany, the Netherlands, Switzerland, Austria, obtained from the Federal Criminal Office [BKA] and the Cologne Police Department) were analyzed by DNA extraction (Phenol/Chloroform and Centricon/Microcon treatment) of some of the fibers or feathers that were cut from every brush. The resulting DNA samples were quantified using Quantifiler™ and 7000 SDS (Applied Biosystems). All samples were typed with AmpfSTR SEfiler™ on a 3100 Avant genetic Analyzer (AB).

Phase 2: Finding ‘good shedders’ [1]: Fingerprints of 12 volunteers taken on clean glass slides as well as blank control samples from the slides were recovered with cotton swabs and analyzed as described above to find persons that transfer a high amount of cell debris on surfaces by touching them (‘good shedders’). These people were used for phase 3.

Phase 3: Secondary transfer study [2]: Based on the results from the Phase 1, we chose 11 fingerprint brushes that provided good typing results, 2 brushes where no DNA was found and 1 unused brush as negative control for the secondary transfer study. Furthermore, based on the results of Phase 2, two of the twelve donors brushed their hands and foreheads once a day for a week with an unused fingerprint brush. These two artificially contaminated brushes were added to the secondary transfer study. The resulting 16 fingerprint brushes were taken to brush a defined area (12 × 12 cm²) on an acetate sheet with dactyloscopic carbon black powder. For every brush, new powder was used, and the surface was prepared with a thin film of paraffin oil to imitate real fingerprints consisting mostly of fat and protein. The target area was divided into two regions, one about 6 cm² that is comparable to a fingerprint’s size and one consisting of the remaining area. Both regions were swabbed separately and the swabs were put into the DNA extraction and further DNA typing was performed as described above.

3. Results and discussion

Phase 1: Table 1 shows the DNA typing results of the 51 different fingerprint brushes that were investigated in the first part of our study. The extracted DNA yield varied in a range from 0 to 80 pg/μL. From 28 brushes we obtained full DNA profiles with the AmpfSTR SEfiler™, another 16 showed partial profiles (86% of all). In most cases DNA mixtures from two or more persons were detected. In five cases, however, a full DNA profile from a single person was detected with partially high signal intensities suggesting that it may have arisen from a blood or saliva stain.

Phase 2: For the artificially contaminated brushes we looked for so called ‘good shedders’ as described previously [2]. Two of twelve glass slides with fingerprints showed ‘good shedder’
characteristics, i.e. a full profile without additional alleles. Besides that, five glass slides showed full profiles with additional alleles. Partial profiles/no alleles were obtained from another five. Blank controls gave no typing result. The two ‘good shedders’ were used for the artificial contamination of unused fingerprint brushes.

**Phase 3:** The typing results of the secondary transfer tests could prove a limited DNA contamination risk via latent fingerprint brushes. On the large \((12 \times 12 \text{ cm}^2)\) area, we were able to detect DNA on the surfaces in four cases that were treated with the fingerprint brushes including both from artificially contaminated brushes and from two of the used ones. From the artificially contaminated brushes and one of the originally used brushes, we could find full DNA profiles from single persons. Complete DNA profiles of the two ‘good shedders’ were obtained. For the originally used brush, the DNA profile was not detected when analyzing the brush directly. Moreover the signal intensities were very high which led us to the assumption that blood or saliva probably adhered to the fibers. In the fourth case, we detected a partial profile with several allelic dropouts.

Regarding the swabbed areas in fingerprint size, a secondary transfer with a full profile could only be obtained from one of the artificially contaminated brushes. Concerning all other tests including negative controls, from the fingerprint size area and the remaining area, mostly no alleles could be detected. In rare cases a maximum of three alleles were found. The alleles found were part of the DNA mixture seen directly on the brush. All other samples showed no result or only one or more single allelic peaks.

In summary, following conclusions can be made: (1) Secondary transfer of DNA via used and artificially contaminated latent fingerprint brushes has been clearly demonstrated. (2) ‘Good shedders’ are a strong source for such contaminations. (3) The larger the brushed area, the greater is the risk for contamination; single fingerprints are less affected. (4) Contact of the brush with body fluids such as blood or saliva make secondary transfer highly likely. (5) To avoid secondary transfer, we suggest to change brushes after investigating important crime scenes, or to develop decontamination procedures for brushes.

**Acknowledgment**

We would like to thank our colleagues in numerous German and Swiss police crime labs who have donated their fingerprint brushes for this study.

**References**


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**Table 1**

DNA typing results (AmpF/STR SEfiler™) obtained from the analysis of 51 fingerprint brushes

<table>
<thead>
<tr>
<th>No. of brushes</th>
<th>Typing results</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>23</td>
<td>+++</td>
<td>Results in all typed STRs</td>
</tr>
<tr>
<td>5</td>
<td>+++</td>
<td>Single profile in all typed STRs</td>
</tr>
<tr>
<td>6</td>
<td>++–</td>
<td>Partial profile with rare allelic dropouts</td>
</tr>
<tr>
<td>10</td>
<td>+ –</td>
<td>Partial profile with allelic and full STR-dropouts</td>
</tr>
<tr>
<td>3</td>
<td>– (+)</td>
<td>No result with artificial peaks</td>
</tr>
<tr>
<td>4</td>
<td>–</td>
<td>No peaks observed</td>
</tr>
</tbody>
</table>