Effect of common fingerprint detection techniques on subsequent STR profiling

Bryan Bhoelai a, Bas J. de Jong a, Marcel de Puit b, Titia Sijen a,*

a Department Human Biological Traces (R&D), Netherlands Forensic Institute, The Netherlands
b Department Digital Technology (Fingerprints), Netherlands Forensic Institute, The Netherlands

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DNA profiling of latent fingerprints can be compromised by fingerprint detection techniques. We found that cyanocrylate (CA) fuming and/or vacuum metal deposition (VMD) did not affect subsequent STR typing. Treatments that involved washing steps like basic yellow or safranin staining reduced DNA quantities. Methods that rely on immersion of items like 1,8-diaza-9-fluorenone (DFO) and ninhydrin staining were found to present the risk of introducing DNA contamination from the staining solution even though the fingerprint DNA was not negatively affected. The use of physical developer was deleterious for the DNA results. When items are handled before a fingerprint is placed, contaminating alleles occur at the fingerprint area. The fingerprint DNA can outstand this background, but due to the large variation for DNA quantities in fingerprints this is not certain and cautious interpretation is appropriate.

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1. Introduction

Both fingerprints and DNA are used as individualizing evidence. Fingerprints cannot be analyzed when prints are badly smudged or distorted but the DNA present in these prints can provide individualizing information. Latent fingerprints have been reported to contain enough DNA for a genetic analysis [1,2]. In the forensic process, the dactyloscopic methods generally precede DNA typing, and it is relevant to study the effects of fingerprint enhancement methods on subsequent DNA profiling [2]. Since the amount of DNA in a latent fingerprint varies tremendously [1,2] an experimental design that allows comparison of treated and untreated fingerprints is imperative. Furthermore, a distinction between alleles of the fingerprint donor and alleles of other donors is appropriate as DNA contamination may arise from various physical developer (maleic acid pre-wash, silver nitrate solution, reductant solution).

For QiAamp-based DNA isolation (Qiagen; standard protocol), fingerprint areas are cut into fragments. Standard profiling uses 5 μl of the 100 μl extract. Alternatively, full extracts were concentrated (to 10 μl) by standard ethanol (EtOH) precipitation using 1 μl GlycoBlue™ (Ambion) as coprecipitant. For STR profiling the AmpFISTR SGM Plus kit (Applied Biosystems) was used. Rfu values complying with donor alleles at all 11 loci were summed, and analyzed with a Grubbs test (P < 0.05) to remove significant outliers. A fingerprint detection technique was regarded harmful for subsequent DNA analysis when the average rfu values at D3S1358, D8S1179 and FGA were 50% or less for the treated halves than that for the untreated halves.

2. Materials and methods

Probands placed fingerprints by pressing fingers of unwashed hands during 60 s on chlorine-free paper or plastic sheets which had been irradiated for 30 min in an UV-crosslinker to remove contaminating DNA. Fingerprint enhancement techniques involved CA fuming (fumed for 10 min at 80% humidity and 120 °C) enhanced by basic yellow or safranin staining, VMD (vacuum <1 x 10^-4 mbar), DFO (with evaporation for 30 min at 100 °C) and ninhydrin (with evaporation for 30 min at 70 °C) and

* Corresponding author at: Laan van Veenburg 6, The Hague 2497 GB, The Netherlands. Tel.: +31 708886666; fax: +31 708886555.
E-mail address: t.sijen@nfi.minjus.nl (T. Sijen).

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was left untreated and the other half was treated with seven different reagents (Table 2). CA fuming and VMD (and the combination of both) did not affect subsequent DNA profiling (Table 2). However, when CA fuming was combined with safranin or basic yellow staining less donor DNA was retrieved. This reduction appears related to the wash step that is used to remove the surplus of stain, as a similar reduction is seen when CA fuming is combined with water washes (Table 2). Ninhydrin or DFO treatment did not affect subsequent DNA profiling. However, blanks (paper sheet immersed in ninhydrin or DFO solution either before or after immersing the series of fingerprints) showed contaminating alleles (10–15 peaks with rfu values up to 150). These alleles did not correspond to the fingerprint donor, which suggests that the staining solutions are susceptible to contamination. Precautions to minimize DNA contamination (e.g., freshly prepared solutions) are recommended when using ninhydrin or DFO to-stain fingerprints that are subjected to DNA analysis. Physical developer was found to be deleterious for DNA profiling (Table 2), which is most likely due to the pre-wash with maleic acid. In many DNA profiles (also from untreated fingerprints halves), non-donor alleles were observed that probably originate from non-donor cell material residing on the hands of the proband as DNA had been cleared from the surfaces by UV-irradiation.

In real casework, surfaces may also contain cell material especially when items have been touched. Therefore, plastic items were touched by several persons after which the proband placed fingerprints at indicated areas. After CA fuming, the full fingerprint areas were collected and subjected to STR typing using the EtOH-precipitated full DNA extract as PCR input. For 12 of the 20 recovered fingerprints full donor profiles were obtained for which the average peak height varied from 6629 to 157 rfu (Table 3). For all 20 fingerprints non-donor alleles were observed, the number varied from 4 to 28. In one profile (Table 3, fingerprint 1) the number of non-donor alleles outnumbered the donor’s (even without considering allele sharing). For some profiles non-donor alleles were substantially lower than donor peaks (Table 3, fingerprints 1–3), but for several profiles the non-donor peaks had similar peak heights (Table 3, fingerprints 16, 18 and 19). Our proband was selected because of consistent positive profiling results from his latent fingerprints, but the majority of the donors we tested appeared to leave much less DNA in their fingerprints. Consequently, we infer that caution is needed when STR profiles of fingerprints are interpreted, as contaminating alleles may be difficult to distinguish from donor alleles.

### 4. Concluding remarks

Full STR profiles can be obtained from a single latent fingerprint also after application of various fingerprint enhancement techniques (e.g., CA fuming, VMD). We did not sensitise STR typing by applying low template techniques, but we did use the full DNA extract in a single amplification. Large variation in fingerprint DNA quantity was observed between donors and more variation can occur depending on length and intensity of the contact, the surface or the presence of body fluids. Non-donor alleles were observed that appear to have several origins like the hands of the donor, the use of a touched surface and fingerprint detection solutions like DFO or ninhydrin. Therefore, STR typing of fingerprints detected by various enhancement techniques is not a guaranteed success and the risks of DNA contamination should be taken into account when interpreting the typing results.

### Conflict of interest

None.

### References