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TECHNICAL NOTE

Federica Alessandrini,[1] *B.Sc.; Monia Cecati,*[1] *B.Sc.; Mauro Pesaresi,*[1] *M.D.; Chiara Turchi,*[1] *B.Sc.; Flavia Carle,*[2] *Ph.D.; and Adriano Tagliabracci,*[1] *M.D.*

Fingerprints as Evidence for a Genetic Profile: Morphological Study on Fingerprints and Analysis of Exogenous and Individual Factors Affecting DNA Typing

ABSTRACT: Material recovered from 374 fingerprints left by eleven laboratory workers on three different substrates (glass, wood, metal) at a standard pressure time of 30 s, with and without preliminary handwashing, was submitted to morphological, quantitative, and type analysis. Morphological and agarose-gel electrophoresis analysis showed that a non-negligible amount of epidermal corneal cells presented apoptotic alterations. The quantity of DNA recovered from fingerprints ranged between 0.04 to 0.2 ng, and in a significant number of experiments no DNA was detected. Handwashing reduced the amount of DNA recovered from fingerprints. The "shedder status" of the donor was a very important factor, causing inter-individual variations in the amount of DNA left by fingerprints. Spurious alleles from laboratory-based and secondary transfer contamination, stutters, and other artifacts described when analyzing low-copy-number DNA and capable of affecting correct profiles were observed.

KEYWORDS: forensic science, fingerprints, DNA typing, low-copy-number DNA, DNA transfer, forensic identification

Most crimes committed are against property (theft, robbery) and against the person (bodily harm, sexual violence, murder), but very often the perpetrators are not punished, since traces with analyzable biological material that could identify them cannot be found. In Italy in the year 2000, 86.95% of crimes remained unpunished, a percentage that increases to 96.12% in the case of theft (1). Apart from the few cases in which crimes are planned and precautions are taken to prevent leaving any biological traces at the scene, in most crimes of this type, i.e., theft, robbery, bodily harm, etc., criminals do not wear gloves or other devices, and fingerprints are the only evidence available. The literature contains preliminary studies or case histories on the possibility of recovering DNA from fingerprints left on the skin or on rope, cord, wire, etc., used for strangling, on gloves, knives, solid parts of cars and other objects, and on the interference by substances used to highlight fingerprints during later genetic analysis (2,3). These works report isolated experiments dictated by the need to resolve definite cases. Systematic studies of various factors influencing the success of analysis, such as recovery techniques, interference by contaminants, i.e., latent fingerprint enhancers, and amplification protocols of low-copy-number (LCN) DNA usually recovered from fingerprints, are in progress (4–9). Systematic studies of the influence of various modes of contact and type of substrate in the success of PCR analysis have not been exhaustively carried out. Lastly, the relevance of contamination by different subjects due to secondary and tertiary transfers affecting the robustness of results and the usability of analytical results in court must all be considered more deeply. The same origin of the DNA found in these skin contact traces and the influences of individual and exogenous factors in the number of cells left with the fingerprint still remain unclear. Therefore, the use of this substrate for genetic identification is a subject of passionate debate in the forensic community, and further contributions are still necessary to highlight the advantages, difficulties and limitations of DNA analysis from fingerprints.

This study was carried out with the aims of investigating the amount of DNA recovered from various substrates and the influence on it of individual and exogenous factors, as well as the suitability of DNA recovered from fingerprints for personal identification by DNA microsatellites. The importance of contamination by exogenous DNA transfer and the stochastic effects on analysis from sampling minimal amounts of DNA recovered from fingerprints were also considered.

Materials and Methods

Collection of Samples

The fingerprints from eleven persons working in the laboratory were applied to the following clean substrates: glass, metal (alloy metallic surfaces), and wood (cortex of hard wood). Experiments were carried out without washing the hands and immediately after

[1] Istituto di Medicina Legale, Università di Ancona, Policlinico Torrette, I-60020 Ancona, Italy.
[2] Centro di Epidemiologia Biostatistica e Informatica Medica, Università di Ancona, Polo Didattico Torrette, 60020 Ancona.

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vigorous handwashing with antiseptic soap. Fingerprint formations were carried out by pressing for a standard time of 30 s. Three sets of specimens were collected, prepared according to the above conditions, and each was used for morphological, quantitative, and qualitative analyses for a total of 374 samples.

Morphological Analysis

Forty-four thumb fingerprints, four from each of the eleven subjects, prepared from washed hands, were directly applied to slides, air-dried overnight, stained with hematoxylin-eosin or Feulgen, and examined under the light microscope. "Blank" slides used as negative controls were submitted to the same procedures to detect laboratory contamination.

Quantitation Analysis

One hundred and ninty-eight fingerprints, 18 from each subject, from the five fingers of a hand, were prepared from washed (99) and unwashed (99) hands on three different substrates (66 for each substrate).

Typing Analysis

One hundred and thirty-two fingerprints, prepared and subdivided as for quantitation analysis, were analysed.

Recovery of Fingerprint and Extraction of DNA

The surfaces of substrates were first swabbed with digestion buffer (10 m*M* Tris-HCl ph 8, 10 m*M* EDTA pH 8, 100 m*M* NaCl, 0.5% SDS), and residual moisture was then recovered by swabbing the surfaces with a dry swab. Both swabs were immediately immersed in 400 μL of the same digestion buffer. Ten microlitres of 2-mercaptoethanol and 25 μL of Proteinase K (10 mg/mL) were added, and samples were incubated at 56°C overnight (10). DNA was extracted with phenol-chloroform (11). The Microcon-30® device (Amicon, Inc., Beverley, MA) was used to concentrate samples up to 20 μL.

Quantitation of DNA

Quantitation was carried out using the dot-blot procedure with a primate-specific alpha satellite probe, D17Z1 (Gibco-BRL, Gaithersburg, MD) (12). Qualitative tests were performed in 1% agarose-gel stained with ethidium bromide.

Amplification and Electrophoresis of DNA

All material recovered from fingerprints was amplified with the AmpFℓSTR Profiler Plus™ kit (PE/AB) on a GenAmp System 9700 thermal cycler (PE/AB), following the manufacturer's recommendations. PCR amplification was performed in a final volume of 50 μL, composed of 20 μL PCR reaction mix, 10 μL primer set, 1 μL AmpliTaq Gold DNA polymerase, and 20 μL concentrated sample in the following conditions: 1 cycle at 95°C for 11 min; 28 cycles at 95°C for 1 min, at 59°C for 1 min, at 72°C for 1 min; a last cycle of extension at 60°C for 45 min.

For LCN amplification, experiments were performed by increasing the number of amplification cycles from 28 to 34, as suggested by Gill et al. (6), using as PCR template both the DNA from cell line 9947A (diluted to 100, 75, 50, and 25 pg) and fingerprint extracts.

Capillary electrophoresis was carried out on an ABI Prism 310 Genetic Analyzer (Applied Biosystems, Foster City, CA). One microlitre of amplified product and 0.5 μL of internal size standard (GeneScan-500 Rox, PE/AB) were added to 12 μL of deionized formamide. After denaturation, PCR products were run as described previously by Tagliabracci et al. in 1999 (13). Ladders were run at the start and end of the work session. The length of amplified fragments was established from the internal run standard by the Southern Local method using Genescan Analysis 3.1.2 software (PE/AB).

Sample Genotyping

Only peaks above 100 RFU were considered for allele typing, which was carried out by Genotyper 2.5 software (PE/AB). Stutters were recorded when extra bands one full repeat shorter than the main band were present in the pherogram (14). Spurious alleles were identified by comparison with the known genotypes of subjects involved in the experiments. All peaks resulting from capillary electrophoresis analysis were in any case recorded for analysis of amplification dynamics from fingerprints.

Quality Assurance/Quality Control

All pre-PCR operations were made in a vertical laminar flow hood using DNA-free plasticware. Recovery of DNA from surfaces was carried out immediately after fingerprint formation. Negative controls were included in extraction and PCR stages, and positive controls were introduced at the PCR step (15,16). Controls were also made on clean swabs and on swabs passed over clean surfaces without fingerprints.

Statistical Analysis

The inter-individual variability of epidermal corneal cells left from the print of a single finger was analyzed by estimating the coefficient of variation separately for numbers of nucleated cells and of stripped nuclei.

Correlations between epidermal cells left on a slide and DNA recovered from glass substrates (samples in the washed hands condition) were estimated by Spearman's rank correlation coefficient (r_S).

The Fisher exact test was performed to verify differences in profile distribution among substrates. Comparisons among substrates for washed and unwashed experimental conditions were performed using non-parametric analysis of variance for repeated measures (Friedman Test) (17).

A level of probability lower than 5% was considered as statistically significant. The Statistical Analysis System (SAS 8.2; SAS Institute Inc. Cary, NC) was used for all statistical analyses.

Results and Discussion

Quantity of DNA Recovered from Fingerprints

In general, the amount of DNA that can be recovered varied in different experiments for the same donor, ranging from no DNA at all to a few tens or hundreds of picograms. The maximum quantity of DNA recovered from substrates printed for 30 s was 3 ng when the object was touched without preliminary hand washing. In most experiments, however, the amount of DNA recovered was on average between less than 100 and a few hundred picograms. Especially with washed hands, in a high percentage of experiments (48 to 84%, depending on substrate), the amount of DNA recovered was under the detection threshold of 40 pg, which constitutes the cut-off value of the quantitation method adopted (Table 1). Only

TABLE 1—*Range of quantities of DNA (in nanograms) obtained from each subject in 198 tests and total of experiments, expressed in percentages, with detectable quantities of DNA (>0.04 ng).*

	Glass		Wood		Metal	
Subject	Washed	Unwashed	Washed	Unwashed	Washed	Unwashed
1	n.d.–0.04	n.d.–0.4	n.d.–0.2	n.d.–0.2	n.d.–0.04	n.d.–0.2
2	n.d.–0.04	n.d.–0.4	n.d.–0.1	n.d.–0.2	n.d.	n.d.–0.2
3	n.d.	n.d.	n.d.–0.2	0.2–1	n.d.	2–3
4	n.d.	0.04–0.2	0.04	n.d.–0.04	n.d.	n.d.–0.2
5	n.d.	0.04–0.1	n.d.	0–0.1	n.d.	0.04–0.1
6	n.d.	n.d.–0.1	n.d.	0.1–0.4	n.d.	0.04–0.1
7	0.2–0.4	0.04–0.1	n.d.	n.d.–0.04	n.d.	0.04–1
8	0.2–1	n.d.–0.2	n.d.	n.d.–0.04	n.d.–0.04	0.04–0.1
9	0.2–0.4	0.04–0.2	n.d.–0.04	0.2–2	n.d.–0.04	0.2–0.4
10	0.04–2	n.d.–0.2	n.d.–0.04	n.d.–0.1	n.d.	0.04–0.1
11	0.04–0.1	0.2–1	n.d.–0.04	0.4–1	n.d.–0.04	0.2–2
			Total >0.04			
n (%)	17 (52)	19 (57)	12 (37)	26 (79)	5 (16)	30 (91)

TABLE 2—*Comparison of DNA recovered from three different substrates from washed and unwashed hands: results of non-parametric analysis of variance.*

		Substrates Median (25^{th}–75^{th} percentile)			
Mode	No.	Glass, ng	Wood, ng	Metal, ng	F_r (p)*
Washed	11	0.04 (0–0.4)	0.04 (0–0.1)	0 (0–0.04)	5.27 ($p > 0.05$)
Unwashed	11	0.2 (0.1–0.4)	0.2 (0.1–1)	0.2 (0.04–1)	0.46 ($p > 0.05$)

* Friedman test.

for some subjects whom we could classify as good shedders did the amount of DNA recovered reach a few nanograms at most. Among our samples, there were three donors (Table 1: Donors 9,10,11) who deposited on average much more DNA than others, with positive amplification and typing results in all experiments when the hands were unwashed.

Differences in the maximum quantity of DNA recovered from the three substrates were not statistically significant with either washed or unwashed hands (Table 2).

The quantity of DNA recovered in controlled experiments was less than that reported by van Oorschot and Jones (4) and Ladd et al. (18), but in those experiments the objects were handled for a long time, or several times, or with the palms rubbed together or against the objects. Our experimental results agree with those performed using similar methods of collecting samples (10). The arbitrary time of 30 s for printing that we adopted was not an important factor for DNA recovery, because DNA is normally lost at the first contact (4), and this printing time only represents a standardized procedure to verify other factors that may influence DNA analysis from fingerprints.

The quantity of DNA that can be recovered from fingerprints generally depends on two main factors: (1) the amount of DNA left by touching objects; (2) the suitability of recovery and extraction techniques. Other factors, such as substrate characteristics, action of atmospheric agents, contact times, etc., are secondary factors, which occasionally intervene but which are in any case capable of influencing results.

In experiments in which substrate, time, and mode of touching are all standardized, the reasons for the different quantity of DNA left in fingerprints depend on individual factors. The experiments of Lowe et al. (9) showed that the amount of DNA left on an object by touching it presents an inter-individual variability that allows subjects to be grouped as good or poor shedders. Apart from diseases affecting keratinization and desquamation of the stratum corneum, such as psoriasis and carcinoma, this increased loss of corneal cells may be due to accelerated turnover of epidermal maturation and differentiation under overexpression of epidermal growth and transforming growth factors, as well as the influence of other agents regulating keratinocyte cycle times (19).

The second factor affecting DNA recovery depends on the suitability of techniques for its recovery from different materials. It must be borne in mind that the quantity of DNA left on the substrate and lost during the extraction procedure may be up to 90%, depending on substrate and extraction methods used (20).

To differentiate between these two main aspects of the matter, morphological analysis of fingerprints left by subjects was carried out in order to verify the amount of nucleated cells left on a slide after thumb pressure for 30 s (Table 3). Nucleated cells and stripped nuclei left from the print of a single finger were generally limited to a few units (median = 3; range = 0 to 14) and, as expected, depended on the surface of contact, i.e., finger size. In some individuals, however, the number of nucleated cells and stripped nuclei left on the substrate was always greater than in others (up to 14 units) and independent of the surface of contact, according to the different amounts of DNA harvested from the fingerprints.

The recovery of DNA resulting from quantitation analysis is a small percentage of that expected from the number of cells observed in morphological analysis, indicating that most DNA is lost during harvesting and extraction operations. Another factor to be considered is the quality of the DNA recovered, because the loss of

epidermal corneal cells is related to apoptosis, also known as programmed cell death, in which nuclei are affected by alterations causing DNA fragmentation into multiples of 180 to 200 bp or larger (21). This may be important in the successive step of amplification, because the presence of many competitive DNA template targets deriving from fragmentation processes may affect the success of amplification, even with large amounts of template. The quality of DNA recoverable from fingerprints was evaluated by both agarose-gel electrophoresis and morphological analysis of epidermal corneal cells left by fingerprints. Since the detection threshold was close to 1 ng, only in the cases of good shedders, where the recovered DNA exceeded this limit, did agarose gel electrophoresis show positive results, with relevant amounts of degraded DNA. According to molecular evidence, "stripped nuclei" and "tingible bodies" (Fig. 1), expressions of apoptosis, were commonly found together with nucleated cells in morphological analysis of fingerprints directly stained on glass (Table 3).

TABLE 3—*Interindividual variability of epidermal cells left on a slide after thumb pressure for 30 s (max number of cells from four experiments). Considerable inter-individual variability was observed for both nucleated cells and stripped nuclei.*

Subject	Nucleated Cells	Stripped Nuclei	Total
1	1	1	2
2	1	3	4
3	2	0	2
4	3	0	3
5	1	2	3
6	0	0	0
7	1	2	3
8	5	3	8
9	9	4	13
10	6	8	14
11	0	1	1
Mean	3	2	5
Standard Deviation	3	2	5
Coefficent of variation (%)	100	100	100

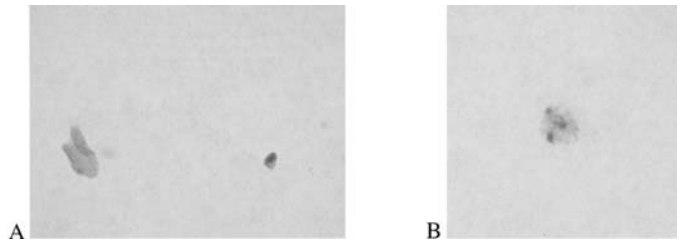

FIG. 1—*Direct microscopic examination of fingerprints imprinted on slide:* A: *keratinocyte (left) and stripped nucleus;* B: *tingible body (Feulgen).*

The statistical correlation existing between the maximum quantity of DNA recovered and the number and features of epidermal cells left on fingerprints was evaluated by Spearman's test. The rank correlation coefficient showed a good correlation of 0.80 for stripped nuclei (95% C.I. 0.58 to 1.02) and a low one of 0.43 for nucleated cells (95% C.I. 0.06 to 0.92).

Data indicated different effectiveness of recovery and extraction methods of DNA from nucleated cells and stripped nuclei, perhaps because extraction of DNA from stripped nuclei is easier than that from nucleated cells. A further consideration is that the status of "good shedder" depends on the number of stripped nuclei in the keratinized corneal layer of epidermidis and left on fingerprints. This status thus depends on individual accelerated turnover in the differentiation of keratinocytes.

DNA Typing

Amplification was carried out on a set of DNA samples without preliminary quantitation, since early experiments showed that the DNA that could be recovered from fingerprints was in most cases insufficient for either approach. Complete profiles were obtained in only 31.8% of experiments, and negative results, with no profiles at all, were observed in 13.6%, whereas the largest quota (54.5%) was composed of partial profiles (Table 4). No statistical significant differences were observed among the different printing substrates, but preliminary handwashing drastically reduced the success of amplification due to the minimal amount of DNA that it was possible to recover in such circumstances. Locus dropouts mainly involved high-molecular-weight loci (only 9.09% for Amelogenin, as opposed to 60.6% for D18S51), whereas allele dropouts were evenly spread among different loci, as observed in similar experiments with LCN of DNA (7).

Peak heights were generally below the level of 150 RFU suggested by the manufacturer for allele assignment, but clear differentiation from background noise could still be made.

Spurious alleles, that is, alleles present in the pherogram but not belonging to the subject who has fingerprints (6) and stutter bands (14) were recognizable in some cases. According to the better results in the amplification of low-molecular-weight loci, spurious alleles were more often associated with Amelogenin, D3S1358, and D8S1179 and, as expected, mainly in experiments with unwashed hands (Table 5). Spurious alleles for Amelogenin (8/66 amplifications) and D7S820 (2/66 amplifications) were also observed in fingerprints left on clean surfaces touched with washed hands, probably due to laboratory-based contamination. Stutters also occurred, often associated with D3S1358, vWA, D8S1179, D21S11, and D5S818 loci.

TABLE 4—*Results from AmpFlSTR Profiler Plus amplification of 132 fingerprints. Fisher exact test does not show statistical differences among substrates for each (washed/unwashed) experimental condition.*

	Washed				Unwashed			
	Complete Profile, *n*, (%)	Negative Profile, *n*, (%)	Partial Profile, *n*, (%)	*p**	Complete Profile, *n*, (%)	Negative Profile, *n*, (%)	Partial Profile, *n*, (%)	*p**
Glass	6 (27.3)	4 (18.2)	12 (54.5)	0.067	10 (45.5)	2 (9.1)	10 (45.5)	0.600
Wood	0 (0)	4 (18.2)	18 (81.8)		10 (45.5)	0 (0)	12 (54.5)	
Metal	4 (18.2)	6 (27.3)	12 (54.5)		12 (54.5)	2 (9.1)	8 (36.4)	

* Fisher exact test.

TABLE 5—*Spurious alleles observed in AmpFlSTR Profiler Plus amplification of 132 fingerprints.*

	AMEL	D3S1358	D8S1179	D5S818	vWA	D21S11	D13S317	FGA	D7S820	D18S51
GW	…	…	…	…	…	…	…	…	…	…
GU	…	2	…	…	2	2	…	2	…	2
WW	6	…	…	…	…	…	…	…	2	…
WU	12	2	4	2	2	2	…	2	…	…
MW	2	…	…	…	…	…	…	…	…	…
MU	8	2	2	2	…	…	…	…	…	…

GW = washed hands on glass. WW = washed hands on wood. MW = washed hands on metal.
GU = unwashed hands on glass. WU = unwashed hands on wood. MU = unwashed hands on metal.

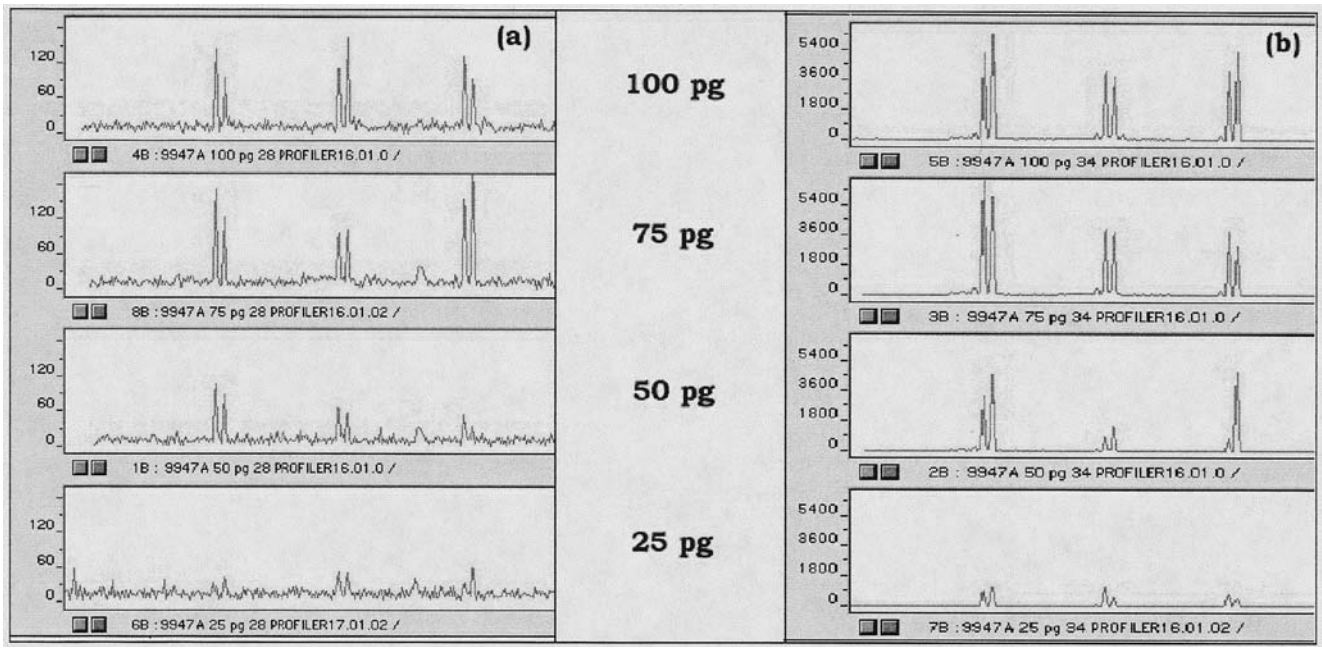

FIG. 2—*Amplification of LCN DNA. Pherograms obtained by amplification at 28* (a) *and 34* (b) *cycles of decreasing amounts (100-75-50-25 pg) of DNA standard from cell line 9947A. After 34 cycles of amplification, positive results with peak heights exceeding 150 RFU were obtained up to 25 pg of DNA template.*

The combined presence of stutters, heterozygote imbalance, and allele dropouts when amplifying <100 pg of total genomic DNA (LCN) has been described elsewhere (6,7). These studies also demonstrated that laboratory-based contamination when amplifying LCN of DNA is impossible to avoid and that this drawback is proportional to the stressing conditions of amplification, mainly the increased number of cycles adopted to enhance the reaction. Spurious bands, or peaks, depending on the typing platform used, are therefore expected events that may hinder correct allele identification and genotype assignment. To minimize these problems and to make the analytical results of LCN analysis of DNA applicable, various strategies have been proposed regarding conditions of amplification and the adoption of guidelines to interpret electrophoretic results (6,22). The small amount of DNA normally recoverable from fingerprints, which means that the entire extract must be used for amplification in order to attempt positive results, makes one of these proposals, i.e., replication of PCR amplification to obtain consensus and to avoid the risk of designating spurious alleles (23), difficult to apply in casework.

Attempts to improve results were carried out by increasing the cycle number of amplifications from 28 to 34. Experiments performed with a series of stock DNA dilutions with distilled water from a human cell line gave a full DNA profile from up to 25 pg of starter template (Fig. 2). The same experiments with DNA extracted from fingerprints did not improve the results meaningfully, because the increase in the peak heights of true alleles was associated with a corresponding magnification of artifacts and the appearance of further peaks, previously absent or masked by background noise, in the allele range. In some instances, spurious alleles with peak heights exceeding those of correct alleles, giving rise to perfect false genotypes, were also observed, as well as multiple ladder-like amplification products (Fig. 3). Amplification controls containing PCR reagents and distilled water did not yield any detectable peaks. The different results obtained from the two templates suggest that the LCN method enhances the amplification of spurious alleles present in fingerprints, but laboratory-based contamination cannot be excluded, since standard negative controls of amplification cannot reveal lower levels of contamination (6).

Contamination by secondary transfer or laboratory-based contamination is therefore a serious problem when working with minimal amounts of template. The high number of spurious peaks may be explained not only by the contamination of fingerprints derived from objects handled by various persons. The low quantity of starting template, which normally enhances the appearance of spurious alleles and stutter bands (6,22), must also be taken into account. Lastly, we must consider that some artifacts are determined by

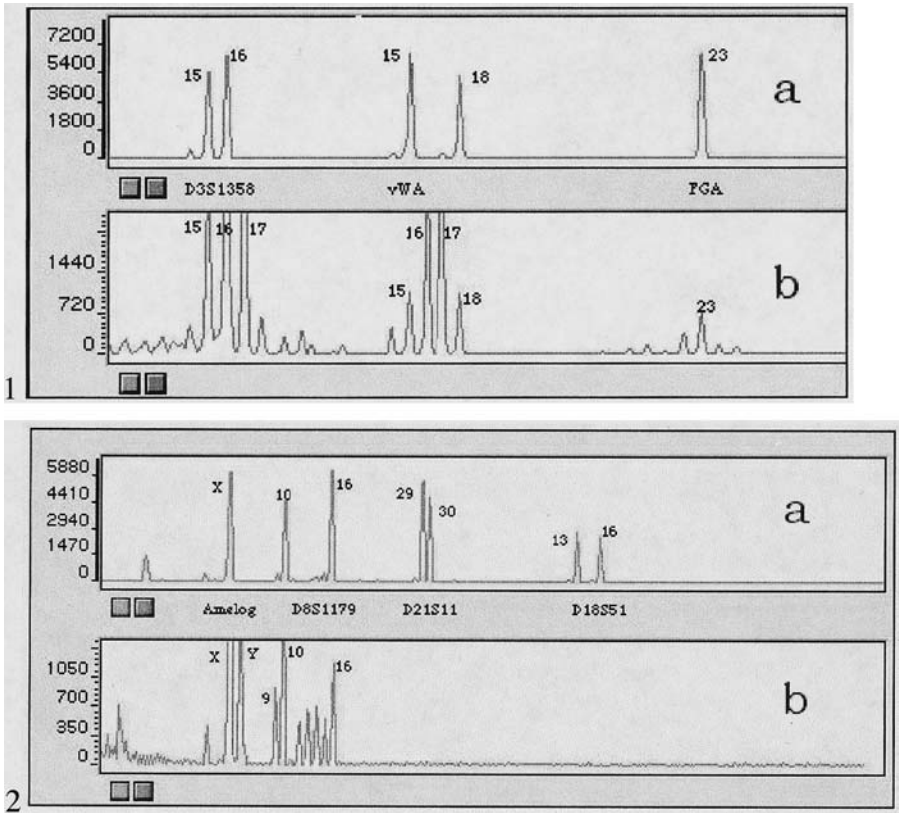

FIG. 3—*Artifacts that may result when typing LCN of DNA from fingerprints (34 cycles of amplification). Pictures 1a and 2a: correct profiles obtained from 1 ng of DNA extracted from saliva at 28 cycles of amplification from two different subjects. Pictures 1b and 2b: artifacts in amplification at 34 cycles performed on DNA recovered from fingerprints of same subjects. A decrease in peak heights of larger fragments (1b at FGA and vWA) for true alleles is also visible. 1a: allele assignment: D3 15–16, vWA 15–18, FGA 23. 1b: accessory alleles for D3 and vWA loci with peak heights greater than those of true alleles. 2a: allele assignment: Amelogenin X, D8 10–15, D21 29–30, D18 13–16. 2b: Y-accessory allele for Amelogenin and ladder-like accessory peaks for D8.*

degradation of DNA by apoptosis and physical or chemical exogenous agents capable of damaging nucleated epidermal cells and producing DNA fragments of a few hundred basepairs (19,25,26).

DNA Transfer and Assessment of a Profile

All studies carried out on DNA fingerprints from fingerprints have dealt with secondary transfer of DNA, a condition in which one individual transfers DNA left by another person, on hands or objects (skin to skin to object, or skin to object to skin). Tertiary transfer has also been described when the DNA lost on one object is transferred by a poor shedder to a different object (skin to object to skin to object). The impact of these phenomena in the field of forensics is a serious problem, because their variable contributions in fingerprint formation can give, each time, mixed or poorly interpretable profiles or profiles left by individuals not involved in the crime scene. In a series of experiments using a model of manual strangulation, Rutty (27) recently observed the persistence of contamination from offender fingers for at least ten days after the contact. In their experimental conditions, Ladd et al. (18) reached the conclusion that secondary transfer is unable to affect the interpretation of DNA profiles from case samples, because of the minimal contribution from the second individual, but the possible different combinations of "shedder status" hypothesized for donors may compromise the identification of the correct or last handler of the object, as observed by Van Oorschot and Jones (4).

The impact of DNA transfer in our experiments was established by evaluating the percentage of accessory alleles added to correct profiles combined with the decrease in accessory alleles between experiments with unwashed and washed hands. When fingerprints were made after subjects had touched objects of routine use, including computer keyboards used by many people, mixed alleles from multiple donors were observed. In many cases, the peaks of accessory alleles reached those of true alleles, hindering definite allele typing. When allele dropouts were associated in these cases and only two alleles were present, incorrect assignments were sometimes made. Since small alleles are preferentially amplified even in minimal amounts, as in the case of contamination, the number of spurious alleles was inversely proportional to the size of the loci considered, according to locus dropout data.

Conclusions

Our study confirmed that it is possible to recover DNA from fingerprints with quali-quantitative features suitable for positive identifications. The quantity of DNA recovered from an object after a single contact is limited to a few nanograms at most. The amount of DNA left in fingerprints probably depends on donor shredder status and on random factors rather than on scientific rules. Most DNA is lost during harvesting and extraction procedures, and a further amount is degraded by apoptosis affecting epidermal corneal cells.

Amplification is able to generate full or incomplete profiles in a high percentage of experiments. Additional alleles derived from DNA transfer by unprotected hands or laboratory-based contaminations are observed with non-negligible frequency. Profiles are also affected by locus dropout, spurious alleles, and stutters, arti-

facts described in LCN analysis of DNA. Nevertheless, almost one third of the number of fingerprints left on various objects by pressure could be typed correctly for all ten loci investigated in this study, and a further relevant percentage gave partial but correct profiles. This study therefore showed that genetic fingerprints from fingerprints is a promising tool in the forensic scenario and may become courtroom-spendable when a series of precautions are taken to ensure very careful and proper analyses, avoiding or minimizing factors that could affect the results in any analytical step and leading to incorrect identifications in casework.

First of all, the recovery of DNA from evidence surfaces should be performed on the largest possible number of sites, as well as on those where the suspect is believed to have left fingerprints. The combined evaluation of profiles obtained from different points of the object may give useful information on possible mixtures of DNA by multiple handlers and DNA transfer. Restrictions on the number of people touching the evidence and measures avoiding primary transfer from investigators and laboratory staff must be adopted, as well as strict anti-contamination practice in later analytical steps involving not only work area and equipment but also analytical strategies. A database containing the genetic profiles of laboratory personnel is a necessary measure to detect accessory alleles from this source. Negative controls for extraction and negative/positive controls for amplification should also be considered. The LCN of DNA available for analysis also means that laboratory conditions such as those suggested for mtDNA analysis by the ISFG (28) should be arranged and set up to minimize the possibility of contamination.

Typing results must be evaluated like those deriving from other biological evidence, when the above-mentioned precautions and the rules of allele assessment suggested by Gill et al. (6,14) to differentiate them from artifacts are observed. A full or partial profile with peaks clearly emerging from the background noise, above the rfu threshold adopted in one's own laboratory—which may vary from one to another—showing one or two alleles for all loci investigated, should be considered as a positive result for later comparison with the genetic profile of a suspect. The possible contemporary presence of artifacts deriving from amplification of LCN and DNA recovered from fingerprints left on objects by multiple handlers means that the use of multiple allele profiles is problematic, even when proposed rules for interpretation of mixed profiles are observed (29). However, the influence of DNA transfer in interpreting a match should always be kept in mind when dealing with this particular matrix.

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Additional information and reprint requests:
Adriano Tagliabracci
Istituto di Medicina Legale
Policlinico Torrette
I-60020 Ancona (Italy)
Fax no.: + 39 071 596 4723
E-mail: tagliabr@unian.it