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TECHNICAL NOTE

CRIMINALISTICS

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The Utility of Polyester and Cotton as Swabbing Substrates for the Removal of Cellular Material from Surfaces*

ABSTRACT: Various types of cotton and polyester fabrics were tested to ascertain the optimal physical and chemical characteristics of fabrics needed for the removal of cellular material from surfaces. DNA quantitation values obtained on dried saliva stains showed no difference between cotton and polyester across all constructions and solvent conditions. Fabrics used dry and with water yielded higher quantitation values than those used with isopropanol. Quantitation values were also higher for wovens and nonwovens than knits across all solvent conditions. Low thread count fabrics used with water yielded higher quantitation values, but no correlation between thread count and quantitation values was observed with dry fabrics. A low thread count woven fabric, however, outperformed other tested fabrics when swabbing object surfaces in a highly used room. Full DNA profiles from fingerprints on glass surfaces were obtained with low thread count woven and nonwoven fabrics but not with the knit fabric tested.

KEYWORDS: forensic science, forensic DNA typing, DNA swabbing media, cellular removal from surfaces, cotton, polyester

With the advent of low copy number (LCN) DNA testing, maximizing the amount of cellular material removed from a surface prior to testing is critical. Although researchers have studied several aspects of LCN DNA recovery including extraction technique, the relationship between the amounts of time a surface comes into contact with skin, the propensity of individuals to shed cells, the substrate surface being contacted, and environmental factors acting on the sample (1,2), the importance of swabbing medium has not been extensively reported. As LCN DNA is defined as samples containing a maximum concentration of 100 picograms of DNA (*c.* 20 epithelial cells; [3]), inefficient removal of cellular material could further exacerbate problems associated with stochastic fluctuation, allelic dropout, and insufficient genotyping results.

This study deals with determining the chemical and the physical properties of fabrics best suited for forensic DNA typing. In addition, this study examines the role that polarity of solvent plays in combinations with different fabrics in optimizing DNA recovery. One hypothesis of the role of the solvent is to facilitate the binding of the fabric and the cell by effectively bonding to both the cell and fabric surfaces. Polar solvents are expected to form hydrogen bonds with carbohydrates, which are rich in hydroxyl groups, present on the membranes of epithelial cells.

The characteristics of an efficient fabric include both recovering epithelial cells from the substrate and releasing them into the sample during extraction. Both of these conditions must be met to yield DNA concentrations sufficient for useable genotyping results.

Given the diverse nature of different types of fibers, the variation in chemical properties may influence how effectively they recover epithelial cells from a substrate. Fibers can be natural, semi-synthetic (derived from natural fibers, such as cotton or cellulose), or completely synthetic. Fibers are intertwined to form yarn, which is used to produce fabrics. Fabrics are textile structures produced by interlacing two sets of yarn (woven fabrics), interlocking series of loops of one or more yarns (knit fabrics), or textile fibers bonded or entangled together by either thermal, mechanical, solvent, or chemical means (nonwoven fabrics; [4]).

The different fabric constructions may preferentially affect the ability of epithelial cells to adhere to fabrics. Nonwoven fabrics may be held together tightly or loosely (generally tightly but could be held loosely as in a swab), knit fabrics more tightly, and woven fabrics have yarns that are more loosely held together. Similarly, the different methods of assembly can cause fabrics to have different absorbent qualities affecting the amount of solvent applied to the fabric.

The thread count of a woven fabric may also influence the ability of the fabric to recover epithelial cells. Thread count is used as a measure of the coarseness or fineness of a fabric and is the sum of the number of threads in both the length and width directions contained in one square inch of fabric (5). High thread count fabrics have more groups of fibers (threads) per unit length than low thread count fabrics.

Sample types used in the study include both touch DNA and saliva samples on glass. As DNA is isolated from epithelial cells present in saliva, it was deemed a good sample model for ascertaining the potential of each of the fabrics to recover cellular material in LCN DNA cases.

Materials and Methods

All materials used including pipettes, tubes, glass substrates, fabrics, and reagents were thoroughly sterilized using a Stratalinker 2400 (Stratagene, La Jolla, CA). Pipettes and glass substrates were

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washed with 0.25% bleach, water, and ethanol. All sample preparation was performed in a sterilized environment to prevent contamination between samples, as well as contamination from the analyst. The appropriate substrate and negative controls were tested where applicable.

Test Fabrics

This study utilized 10 different types of cotton and 10 different types of polyester to determine which were most conducive to the greatest DNA recovery. Nine of the cotton fabrics and nine of the polyester fabrics originated from a large sheet of fabric and were cut into 1 × 1 cm squares. One cotton and one polyester fabric were in swab form, similar to those used in typical forensic science casework.

Table 1 shows the characteristics of each of the fabrics used in this study including weave type, thread count and classification, and thread orientation. Woven fabrics showing a thread count between 97 and 124 were considered low thread count fabrics, those showing a thread count between 137 and 150 were considered middle thread count fabrics, and those with a thread count greater than 168 were considered high thread count fabrics.

Saliva Samples

Each polyester and cotton fabric sample was tested on 4-μL stains of neat saliva heat-fixed to glass microscope slides by placing the slide on a hot plate. Each fabric was tested in five replicate runs to determine the efficiency of each at recovering epithelial cells from a glass substrate using water (polarity index = 10.2) and isopropyl alcohol (polarity index = 3.9), respectively, to moisten the swab. The fabrics were also tested dry on 4 μL of neat saliva to determine their efficiency at recovering epithelial cells from a glass substrate, when no solvent is used. In addition, 4-μL stains of 1:100 saline-diluted saliva stains heat-fixed to glass microscope slides in the same manner were tested with each fabric using water as a solvent.

Cuttings of fabric utilizing solvents were held with sterile tweezers, while 100 μL of solvent was applied with a pipette to ensure each fabric sample was moistened with the same volume. The cotton swabs (Puritan—Catalog # 25-803 2WC; Puritan Medical, Guilford, ME) and polyester swabs (Puritan—Catalog # 25-806 1PD) were held by the wooden or plastic applicators, respectively, while moistening and swabbing, instead of using tweezers. After the fabric was swabbed over the dried saliva stains, they were placed in 1.5-μL microcentrifuge tubes.

DNA Extraction and Quantitation

Saliva samples were extracted within 24 h of preparation using a modified protocol specifically designed for LCN DNA samples originally proposed by Schiffner et al. (2). Changes made to this procedure include the use of 18 mg/mL proteinase K instead of the originally proposed 0.78 mg/mL, and 1 ng of poly A RNA was used to coat the Microcon® 100 (catalog 42413; Millipore, Billerica, MA) in a total volume of 25 μL instead of the proposed 200 μL. The extracts were subsequently stored at 4°C prior to quantitation. Previous work showed that this method was far superior to Chelex® extraction (Biorad Laboratories, Hercules, CA) in differentiating the ability of different fabrics to remove cellular material (6).

DNA of sample extracts were quantified in duplicate using a Corbett Rotorgene 6000 Real-Time PCR instrument (Qiagen, Valencia, CA) employing the SYBR Green qPCR method using *Alu* sequence-specific primers proposed by Nicklas and Buel (7).

Statistical Analysis

No assumption of normality was made on any of the data sets. As a consequence, only nonparametric tests were used to compare populations at data. All statistical tests were performed at the 95% confidence interval, and comparisons were made using either the Mann–Whitney test (8) or the Kruskal–Wallis test (8). The Mann–Whitney test is designed for pairwise comparisons of nonparametric data, and the Kruskal–Wallis test is useful to compare nonparametric data from more than two groups (the Kruskal–Wallis test is the nonparametric equivalent of a one-way analysis of variance test). Tests for significance between polyester and cotton were conducted

TABLE 1—*Description of fabrics used in study.*

Fabric Type	Weave Type	Thread Count per in^2	Thread Count Classification	Thread Orientation*
Cotton 1 (C1)	Woven	97	Low	Over 1, Under 1
Cotton 2 (C2)	Knit	n/a	n/a	n/a
Cotton 3 (C3)	Woven	137	Middle	Over 1, Under 1
Cotton 4 (C4)	Woven	150	Middle	Over 1, Under 1
Cotton 5 (C5)	Woven	117	Low	Varying orientations
Cotton 6 (C6)	Woven	140	Middle	Over 1, Under 1
Cotton 7 (C7)	Woven	124	Low	Over 1, Under 3
Cotton 8 (C8)	Woven	193	High	Over 1, Under 1
Cotton 9 (C9)	Woven	177	High	Over 1, Under 3
Cotton 10 (C10)	Nonwoven (swab)	n/a	n/a	n/a
Polyester 1 (P1)	Nonwoven	n/a	n/a	n/a
Polyester 2 (P2)	Woven	198	High	Over 1, Under 1
Polyester 3 (P3)	Knit	n/a	n/a	n/a
Polyester 4 (P4)	Knit	n/a	n/a	n/a
Polyester 5 (P5)	Woven	119	Low	Over 2, Under 2
Polyester 6 (P6)	Knit	n/a	n/a	n/a
Polyester 7 (P7)	Nonwoven	n/a	n/a	n/a
Polyester 8 (P8)	Woven	168	High	Over 1, Under 1
Polyester 9 (P9)	Woven	122	Low	Over 1, Under 1
Polyester 10 (P10)	Nonwoven (swab)	n/a	n/a	n/a

n/a, not applicable.

*Thread orientation refers to the position of the weft threads in relation to the warp threads. As an example, an ''over 2, under 2'' orientation demonstrates that one warp thread is woven over two weft threads then under two weft threads along the entire length of the fabric. Concurrently, one weft thread is woven over two warp threads, then under two warp threads along the entire width of the fabric.

across all three solvent conditions. Pairwise comparisons included all wovens versus all nonwovens, all knits versus all wovens, and all knits versus all nonwovens. Statistical analysis was also performed to ascertain the effect of solvent conditions and thread count on DNA quantitation.

Touch Samples

Fabrics that routinely showed high quantitation values in the saliva studies (fabrics which produced one of the top two median values in at least one of the four test groups: neat saliva using fabrics with water, neat saliva using dry fabrics, neat saliva using fabrics with isopropanol, and 1:100 diluted saliva using fabrics with water) were also moistened with 100 μL of water and used to swab a computer keyboard, the top of a desk, a door handle, and top of a table in a highly used area. A different area of each location was sampled with each swab. The samples were then subsequently extracted and DNA quantitated.

Triplicate samples of the same high-performing fabrics in the saliva studies were also used to swab fingerprints on a glass surface. The samples were prepared by pressing bare fingers down on sterilized glass microscope slides for 2 min after rubbing both hands together for 1 min to help facilitate even distribution of the sloughed off epithelial cells to each finger. Each of the chosen fabrics was moistened with 100 μL of water, swabbed over the entire area where one fingerprint was made, and placed in 1.5-μL microcentrifuge tubes. After DNA extraction and quantitation, samples were genotyped using Powerplex® 16 (Catalog # DC6531; Promega Corporation, Madison WI). One-half (0.5) nanograms of template DNA was added to the amplification reaction, which was prepared according to the amplification protocol in the Promega Powerplex 16 Technical Manual (9). Positive and negative amplification controls were analyzed with each run.

Results

Table 2 lists all the range and median DNA quantitation results for neat saliva swabbed with each fabric using all three solvent conditions. Using the Kruskal–Wallis test ($\alpha = 0.05$), a comparison between all polyester and cotton fabrics across all three solvent conditions was made resulting in a p-value of 0.644. This indicates that there was no significant difference between polyester and cotton irrespective of fabric structure in DNA recovery. A pairwise comparison of the results obtained for the 1:100 diluted saliva using water as the solvent (range and median values listed in Table 3) utilizing the Mann–Whitney test ($\alpha = 0.05$) also showed no significant difference between polyester and cotton (p-value = 0.236).

Statistical analysis of solvent conditions using data from all fabrics, and construction was also performed on the neat saliva samples utilizing the Kruskal–Wallis test ($\alpha = 0.05$). The resulting mean of ranks for the three solvent conditions separates the solvent conditions into two significantly different groups. Quantitation values using isopropanol as the solvent were significantly lower than quantitation values obtained using water as a solvent or employing the fabrics dry. No statistical difference was observed in DNA quantitation values between fabrics using water and fabrics used dry.

Using the Mann–Whitney test ($\alpha = 0.05$), no significant difference was observed between wovens and nonwovens (p-value = 0.413), but quantitation values for wovens and nonwovens were significantly higher than those for knits (p-value = 0.029 for wovens versus knits and $p = 0.008$ for wovens versus nonwovens). These results were obtained despite comparatively high values obtained with sample P6 using water as a solvent. No other knit fabric gave similar values.

Woven fabrics were also compared by examining the effect of low, medium, and high thread count on DNA quantitation values irrespective of fiber type using both water as a solvent and no solvent on the neat saliva samples using the Kruskal–Wallis test ($\alpha = 0.05$). Using the fabrics dry, no statistical difference was observed based on thread count. However, low thread count woven fabrics gave statistically significant higher values DNA quantitation values when using water as a solvent.

High performing fabrics selected to be tested on a computer keyboard, the top of a desk, a door handle, and the top of a table in a highly used area included two low thread count cotton woven fabrics (C1 and C7), a cotton nonwoven swab (C10), and one polyester knit fabric (P6). Each of the selected fabrics yielded one of the top two median DNA quantitation values in at least one of the four test groups: neat saliva using fabrics with water, neat saliva using

TABLE 2—*Range and median DNA quantitation results for neat saliva swabbed with all fabrics using various solvent conditions.*

Solvent		Water		Dry		Isopropanol	
Fabric Number	*N*	Range (ng/μL)	Median (ng/μL)	Range (ng/μL)	Median (ng/μL)	Range (ng/μL)	Median (ng/μL)
C1	5	17.67–56.47	37.41	42.28–59.09	42.55	7.26–11.41	10.35
C2	5	5.39–17.12	11.10	13.47–43.75	37.76	3.23–4.19	3.31
C3	5	11.63–28.02	21.06	14.39–39.39	29.23	2.79–5.73	3.78
C4	5	5.33–21.61	16.01	22.98–28.53	26.31	3.19–4.29	3.84
C5	5	14.97–51.94	23.59	19.82–45.37	37.72	2.90–5.49	5.10
C6	5	10.88–20.44	16.33	20.95–26.64	23.74	4.19–5.85	4.82
C7	5	44.33–54.57	52.32	55.10–62.17	55.70	4.83–7.46	5.54
C8	5	14.77–47.77	22.11	33.10–38.69	34.05	3.15–3.59	3.45
C9	5	8.65–18.77	11.20	11.04–46.00	29.04	3.06–6.04	5.04
C10	5	17.39–28.47	22.90	22.21–48.08	36.12	4.54–6.19	5.97
P1	5	15.19–28.73	18.49	16.02–36.00	28.34	1.04–1.84	1.30
P2	5	12.46–20.07	16.70	19.05–22.70	19.28	0.67–1.78	1.07
P3	5	12.97–35.77	18.81	11.66–12.00	11.75	1.71–3.40	1.74
P4	5	11.00–24.94	23.23	13.39–21.40	21.10	0.72–1.11	1.00
P5	5	13.53–52.45	20.65	16.76–38.79	18.85	1.18–1.98	1.20
P6	5	33.81–99.24	55.96	11.88–23.77	22.58	0.75–1.40	0.92
P7	5	8.67–43.50	16.08	12.68–25.24	14.08	0.69–2.26	1.41
P8	5	7.60–64.82	38.51	23.84–40.12	33.68	0.19–0.93	0.78
P9	5	22.48–49.09	45.61	12.53–45.87	29.70	0.88–1.51	1.36
P10	5	20.51–85.65	40.70	34.90–43.45	38.20	1.80–3.82	1.82

TABLE 3—*Range and median DNA quantitation results for 1:100 diluted saliva swabbed with all fabrics using water as a solvent.*

Fabric Number	Range (ng/μL)	Median (ng/μL)
C1	1.94–5.54	3.23
C2	0.36–1.51	1.12
C3	0.36–3.88	1.11
C4	0.64–1.73	1.06
C5	0.90–2.38	1.39
C6	0.69–1.16	1.14
C7	1.08–3.23	2.16
C8	0.40–1.14	0.80
C9	0.10–0.17	0.11
C10	0.14–3.12	0.50
P1	0.92–3.12	1.18
P2	0.13–0.78	0.20
P3	0.88–3.09	1.08
P4	0.96–2.75	1.48
P5	0.21–0.37	0.32
P6	1.19–3.44	2.01
P7	0.11–0.48	0.21
P8	0.17–0.56	0.21
P9	0.12–1.64	0.39
P10	0.65–1.69	1.13

TABLE 4—*Range and median DNA quantitation results for swabbing of computer keyboards, desk surfaces, door handles, and table surfaces in high traveled areas.*

Fabric Number	Area Swabbed	DNA Quantitation Results (ng/μL)
C1	Computer keyboard	1.05
C1	Top of desk	0.48
C1	Door handle	0.45
C1	Top of table	0.47
C7	Computer keyboard	0.002*
C7	Top of desk	0.002*
C7	Door handle	0.004*
C7	Top of table	0.005*
C10	Computer keyboard	0.003*
C10	Top of desk	0.002*
C10	Door handle	0.002*
C10	Top of table	0.004*
P6	Computer keyboard	0.0005*
P6	Top of desk	0.005*
P6	Door handle	0.001*
P6	Top of table	0.006*

*Cycle threshold values exceed negative control.

dry fabrics, neat saliva using fabrics with isopropanol, and 1:100 diluted saliva using fabrics with water. Table 4 shows the DNA quantitation results of the swabbing. The quantitation for each area using C1 shows substantially higher values than the other three fabrics. Values using C1 on these surfaces ranged from 0.45 to 1.05 ng/μL, while all other fabrics demonstrated values in the per 10^3 ng/μL range.

These same four fabrics were tested on samples of fingerprints on a glass surface. Higher median DNA quantitation values were obtained with the two low thread count cotton woven fabrics (3.0 ng/μL for C1, 2.7 ng/μL for C7) compared to the values obtained with the cotton nonwoven swab (0.46 ng/μL for C10) and the polyester knit fabric (0.65 ng/μL for P6). Subsequent genotyping of each of the three test samples for each fabric using Powerplex 16® was then compared. Of 24 possible alleles, complete profiles were obtained with C1 and C7, a maximum number of 23 alleles were obtained with C10, and a maximum number of 15 was obtained from P6 using a relative fluorescence units threshold of 100 (Table 5).

TABLE 5—*Range and median DNA quantitation and genotyping results for swabbing of fingerprint samples on a glass surface using water as a solvent.*

Fabric Number	*N*	Range (ng/μL)	Median (ng/μL)	Maximum Number and Percentage of Alleles Obtained
C1	3	2.66–4.33	3.00	22 (92%)
C7	3	0.76–4.68	2.70	24 (100%)
C10	3	0.41–0.74	0.46	23 (96%)
P6	3	0.43–0.94	0.65	15 (63%)

Discussion of Results

The data presented in this study indicate that cotton and polyester fabrics show no statistical difference in their ability to remove cellular material from surfaces and in yielding quantities of DNA during the extraction process. A review of the literature finds both concordant and contradictory findings to the results of this study. Although a review of the literature yielded no studies showing the affect of swabbing materials on subsequent DNA quantitation, three studies have reported on the role that swabbing materials might play in genotyping. One study reported that fibers with reduced ability for hydrogen bonding, such as polyester and acrylic, were not as effective as fibers, such as cotton and rayon, in producing DNA profiles after blood was placed on the fabric and allowed to dry (10). Conversely, another study indicated that although allelic intensities were poorer with polyester compared to cotton and nylon on touch hand samples directly applied to fabrics, full DNA profiles were still able to be obtained with polyester when used as a sample substrate in producing DNA profiles (11).

These studies have contributed the difference in the ability of various types of fabrics to generate DNA profile to the types of functional groups present. For instance, the O-H groups present on cotton and rayon, and the N-H groups of nylons and wools are capable of strong molecular bonding with nucleic acid chains and cell membranes. Conversely, polyesters and acrylics contain polar carbonyl and cyano groups, respectively, that will permit relatively weaker dipole–dipole interactions with nucleic acid chains and cell surfaces (12).

This study differs from the previous studies in that biological material was not directly applied to the fabrics but rather used to swab surfaces using various solvent conditions and that a DNA extraction technique was used. Previous studies also did not consider the role of fabric construction of substrates in the generation of DNA profiles. Because no statistical difference was observed in DNA quantitation values between polyester and cotton over all solvent conditions tested, factors in addition to hydrogen-bonding capability and dipole–dipole interactions are likely to play a significant role in ascertaining the ability of a substrate to remove cellular material from surfaces.

If based simply on chemistry alone, cotton would be expected to have significantly higher DNA quantitation values than polyester. As mentioned, cotton would be expected to be an effective DNA recovery substrate because cotton is comprised of repeating units of cellulose that consists of an abundance of hydroxyl (OH) groups, offering enormous hydrogen-bonding potential whether used dry or moistened with water.

When a dry cotton fabric is used to swab cellular material, the hydroxyl groups on the fabric may directly form hydrogen bonds with the hydroxyl groups of the carbohydrates on the outside of the cell membrane. Similarly, the hydroxyl groups of cotton can attract water and contribute to the high absorptivity of cotton. These hydroxyl groups can readily bind via a hydrogen bond to the

available hydrogen atoms in the water molecule. As the water molecule has two available hydrogen atoms, the second hydrogen atom may participate in hydrogen bonding with the hydroxyl groups on the carbohydrates surrounding the outside of the cellular membrane.

Conversely, polyester is a manufactured, long-chain synthetic polymer composed of units of an ester of a substituted aromatic carboxylic acid. Even though polyester is less polar than cotton resulting in weaker molecular bonding interactions with cellular membranes and nucleic acids, it did not yield significantly lower DNA quantitation values than cotton when tested on the saliva stains.

Although the polarity of the fabrics themselves yielded no significant difference in DNA quantitation values, the polarity of the solvent used did produce a statistical difference. Fabrics using isopropanol as a solvent yielded comparably low DNA quantitation values. This may be attributable to the presence of only one polar hydroxyl group on the isopropanol molecule. Thus, only one hydrogen bond can form between either the solvent and fabric or the solvent and an epithelial cell but not to both simultaneously. It is likely that because the solvent is added to the swab prior to swabbing, very few hydroxyl groups on the fabric will be available for cellular recovery greatly reducing the amount of DNA extracted from the swab.

The statistical analysis that compared DNA recovery efficiency for the different woven fabrics based on thread count demonstrated that woven fabrics with a low thread count have a preferential ability to retrieve epithelial cells from a glass surface using water as a solvent. Based on quantitation results, the two most efficient cotton fabrics were low thread count woven fabrics (C1 and C7). The larger spaces between individual threads in lower thread count fabrics may allow epithelial cells to penetrate to the interior of the fabric. Conversely, epithelial cells may only be able to interact with the exterior of the fabric because of the smaller spaces between threads in larger thread count fabrics.

A reasonable explanation can be formulated as to why there was no significant difference between thread counts when a dry fabric was used and a significant difference when water was used as a solvent. When no solvent is used, the epithelial cells most likely only bind to the surface of the fabric, regardless of the presence of large or small spaces between the threads. When water is used as a solvent, the water penetrates into the fabric and draws the epithelial cells into the interior. Efficient interactions between the interior of the fabric, the solvent, and epithelial cells may be greater in low thread count fabrics. In higher thread count fabrics, the absorbance of the solvent to the interior of the fabric did not have as great an effect on the penetration of the epithelial cells, because the spaces between the threads is small. This could clearly be a benefit, when swabbing samples with a lower concentration of epithelial cells as seen when comparing the data from C1 and C7 both low thread count woven fabrics. Although C7 outperformed C1 using whole saliva samples, the reverse was true with the 1:100 diluted saliva samples. Perhaps the lower thread count of C1 (97 as opposed to 124) can account for this.

The advantage of using a low thread count fabric was clearly evident when examining the results from Table 4. Of the four fabrics used to swab a computer keyboard, the top of a desk, a door handle, and the top of a table, the only fabric yielding a significant quantity of DNA was C1. It appears that the difference in the ability to remove cellular material from surfaces becomes apparent only at lower concentrations of DNA.

The benefit of using water was clearly demonstrated with P6, a polyester knit fabric. Although comparatively high quantitation results were observed with the fabric moistened with water on both the whole and 1:100 diluted saliva samples, much lower results were observed on the fabric used dry on the whole saliva samples. Values obtained with the dry fabric were less than half of those obtained for the same fabric using water on the whole saliva samples (22.58 ng/μL and 55.96 ng/μL, respectively). The comparatively high values obtained with P6 with water are not reflective of the low values obtained for the knit fabrics as a group in this study (C2, P3, and P4 gave comparatively low DNA quantitation results under all solvent conditions) considering that woven fabrics gave statistically higher DNA quantitation results. Conversely, nonwoven fabrics were not statistically different from woven fabrics, when compared across all solvent conditions with the dried saliva samples but were also significantly higher than knit fabrics. This may be simply because of the ease with which swabs can be used on surfaces compared with fabrics that required the use of a tweezer. The physical environment between the nonwoven swabs and the low thread count woven fabrics did not produce differences in quantitation results with the relatively high levels of DNA found in the dried saliva samples.

Genotyping results of the fingerprint samples (Table 5) also reflected the DNA quantitative differences between woven, nonwoven, and knit fabrics. Of the four fabrics tested, the knit fabric (P6) yielded the smallest percentage of possible alleles (63%) even though a quantity of DNA normally sufficient for genotyping was obtained after extraction (median value of 0.65 ng/μL). The poorer DNA profile obtained with the polyester fabric is consistent with other studies, perhaps suggesting a different mechanism for poor genotyping other than weak nucleic acid or cellular binding to the fabric (10,11).

In conclusion, not only should chemical characteristics be considered when employing a swabbing medium for DNA typing purposes, but physical characteristics of fabrics should be considered as well. Although it seems likely that no single material is best suited for samples with higher quantities of DNA, practitioners may be advised to use a material that will interact well with polar solvents, such as water, and that display a structural environment that will allow cellular material to enter the interior of the fabric, such as those found in low thread count woven fabrics, when sampling surfaces that likely have small quantities of DNA.

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