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Evaluating the impact of sandy surface contamination on trace DNA recovery from wearable fabrics: A comparative study of collection methods and extraction kits

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Abstract

Touch DNA evidence plays a pivotal role in forensic investigations, particularly in the absence of visible biological fluids. However, trace DNA recovery is influenced by multiple factors, including substrate type, collection technique, extraction method, and environmental exposure. Despite widespread adoption of both cotton swabbing and tapelifting methods, little is known about their comparative performance under real-world environmental stressors such as sand contamination, which is common in arid and desert regions.

This study evaluated the efficiency of two collection methods Copan cotton swabs (CS) and SceneSafe Fast™ minitapes (MT) and two DNA extraction kits PrepFiler Express BTA™ and QIAamp® DNA Investigator Kit in recovering Touch DNA from 100 fabric-based items (face masks, T-shirts, and caps) exposed to sandy outdoor environments. DNA concentration, STR profile completeness, and total allele count were analyzed using standardized protocols. Statistical methods included factorial ANOVA, chi-square analysis, and Pearson correlation to assess method performance and inter-variable relationships.

Cotton swabs consistently outperformed minitapes in DNA yield and profile integrity across all fabric types. The combination of cotton swabs with Prep Filer extraction produced the highest DNA concentrations (mean >2.0 ng/µL) and yielded full STR profiles in a majority of cases. In contrast, minitape sampling, particularly when combined with QIAamp extraction, resulted in lower recovery and an increased rate of partial or mixed profiles. A strong positive correlation ($r > 0.8$) was observed between DNA concentration and STR profile completeness. These findings indicate that adhesive-based sampling methods are substantially hindered by sand interference, reducing their forensic value in contaminated conditions.

The results emphasize the need for adaptive forensic DNA protocols that account for environmental contaminants such as sand. Cotton swabbing in combination with Prep Filer Express BTA™ extraction represents a robust and reliable strategy for maximizing trace DNA recovery from wearable items in sandy or dusty outdoor settings. This research provides critical guidance for improving DNA evidence collection in real-world casework and supports the development of optimized trace DNA workflows for challenging environments.

Keywords: Forensic Genetics; Trace DNA; DNA Extraction; DNA Recovery; Copan Cotton Swab; Scenesafe Fast™ Minitape

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1. Introduction

Trace DNA is a vital forensic resource often recovered from crime scenes, playing a central role in linking individuals to criminal events [1–6]. Unlike biological fluids, it is commonly deposited through casual contact with surfaces such as tools, doorknobs, or clothing, offering valuable probative evidence when other biological traces are absent [2,7–9]. However, the effectiveness of Touch DNA analysis is frequently limited by fluctuations in both the quantity and integrity of DNA recovered. These variations are influenced by factors such as the surface's chemical and physical attributes [10–11], environmental degradation [12–14], and disparities in collection procedures [10–11,15–18]. Additional complexity arises from inconsistencies in moistening agents and the number of adhesive lifts applied, both of which can significantly impact DNA recovery efficiency [19–25].

Beyond collection-related challenges, differences in extraction and quantification protocols [2,4,12,26–30], potential contamination, and individual variability in DNA shedding further complicate the recovery process [31–38]. Therefore, the selection of appropriate sampling tools such as cotton swabs, nylon swabs, or adhesive tapes—must be carefully matched to surface characteristics for optimal outcomes [10–11]. For instance, smooth, non-porous surfaces like plastic and glass are better suited to swabbing [10,20], while porous materials like fabrics often require adhesive tape-lifting to achieve reliable results [39–44].

In response to the shortcomings of traditional sampling methods, novel collection strategies have emerged. These include hybrid approaches like combining cotton and microFLOQ® swabs for direct amplification, as well as the use of microbial wet-vacuum devices and advanced decontaminants to improve recovery rates [23,44–46]. Such innovations highlight the ongoing evolution in trace DNA collection methods. Notably, the wide variation in DNA yield observed across different surfaces and environmental contexts supports the call for adaptive, case-specific sampling protocols [47–50].

Keeping pace with shifting forensic needs demands not only methodological innovation but also flexibility in investigative approaches. This necessitates the integration of evolving technologies with responsive sampling strategies to address modern crime scene challenges effectively [51–52]. Moreover, traditional DNA workflows—particularly those relying on silica-based extraction can suffer from sample loss, an issue especially problematic in low-template or environmentally degraded samples [1,53]. In light of these challenges, direct amplification techniques that circumvent extraction and quantification have gained traction for preserving limited material while accelerating analytical turnaround [17,22,54].

Building on these foundations, the present study seeks to evaluate how sandy environments a common condition in outdoor crime scenes, particularly in arid regions affect the recovery of trace DNA from wearable fabric items such as shirts, face masks, and caps. Specifically, this research compares the efficacy of cotton swabbing versus adhesive tapelifting, in conjunction with two widely used DNA extraction kits: PrepFiler Express BTA™ and QIAamp® DNA Investigator. The goal is to determine the optimal combinations of tools and methods for reliable Touch DNA recovery under sandy conditions, enhancing forensic readiness for real-world scenarios.

2. Materials and Methods

2.1. DNA Recovery

This study employed two trace DNA collection tools to assess recovery efficiency from wearable items exposed to sandy outdoor environments: the Copan cotton swab (150C; referred to as CS) and the SceneSafe Fast™ minitape (K545; referred to as MT). These tools were selected based on their widespread use in forensic DNA casework and their previously reported performance across porous and non-porous surfaces. All collection procedures were conducted under standardized and controlled conditions to enable a fair comparative analysis.

Prior to use, each cotton swab was moistened with 100 µL of sterile distilled water using a calibrated plastic spray bottle to ensure consistent wetting, as previously described in other studies [2,19,24]. The CS was then applied to the fabric surface using moderate pressure and a rotational technique to maximize the contact area and promote efficient DNA uptake. In contrast, the MT required no moistening or preparation. Each piece of tape was pressed onto the sampled surface and lifted 16 consecutive times, in line with recommendations shown to optimize DNA recovery without oversaturation or diminishing returns [55].

2.1.1. Sample Set and Environmental Conditions

A total of 100 fabric items were included in this study, comprising

- 30 disposable surgical face masks
- 50 T-shirts (cotton-polyester blends)
- 20 baseball caps (mixed polyester and cotton)

All items were sourced from actual forensic case submissions involving outdoor crime scenes. A unifying factor among these items was their exposure to sandy environments, with visible dust and sand particles embedded in the fabric at the time of recovery. This condition was deemed critical for simulating real-world challenges in arid and desert climates, such as those frequently encountered in the Gulf region.

2.1.2. Sampling Strategy

For consistency and internal comparison, both CS and MT were used on each item. Each item was divided into two symmetrical sampling zones, clearly demarcated using sterile single-use templates to avoid cross-contamination. The sampling design was item-specific

- Face masks: The inner surface was split vertically right half sampled with CS, left half with MT.
- T-shirts: A 10 × 10 cm area on the chest or upper back was selected and equally divided CS on the right, MT on the left.
- Baseball caps: The interior sweatband was split across the center half for CS, half for MT.

Between each sampling session, all tools and workspaces were decontaminated using 10% bleach followed by 70% ethanol, and single-use gloves were worn throughout to prevent contamination.

2.2. DNA Extraction and Amplification

Samples collected using both the Copan cotton swabs (CS) and the SceneSafe Fast™ minitapes (MT) underwent DNA extraction using two commonly adopted forensic kits to compare efficiency under sandy conditions. The first method utilized the PrepFiler Express BTA™ kit (Thermo Fisher Scientific), referred to as EX1, which was performed on the AutoMate Express™ Forensic DNA Extraction System, following the manufacturer's recommended protocol. The second method employed the QIAamp® DNA Investigator Kit (Qiagen), referred to as EX2, which was performed manually in accordance with Qiagen's published guidelines. To optimize recovery from nylon swabs in EX2, NAOBasket™ adapters were used as recommended by Copan Diagnostics.

For CS samples, the entire swab head was subjected to extraction. In the case of MT samples, only the lower adhesive portion of each tape was processed. The final elution volume for both methods was standardized to 50 µL to ensure comparability.

DNA quantification was conducted using the Qiagen Investigator Quantiplex Pro Quantification Kit on the QuantStudio 5 Real-Time PCR (qPCR) System. Analysis was performed using HID Real-Time PCR Analysis Software v1.3, strictly adhering to the manufacturer's recommendations to ensure reproducibility and quality control.

DNA amplification was carried out using the GlobalFiler™ PCR Amplification Kit (Thermo Fisher Scientific) on an ABI GeneAmp® 9700 Thermal Cycler, following the recommended protocol for 29 amplification cycles. Post-amplification, samples were size-separated and analyzed using the ABI 3500 Genetic Analyzer.

Each injection mixture was composed of

- 1 µL of PCR product
- 9.6 µL of Hi-Di™ formamide
- 0.4 µL of GeneScan™ 600 LIZ® Size Standard v2.0

To ensure accurate STR allele sizing, 1 µL of the appropriate allelic ladder was added per run in each 96-well plate. All procedures were performed under sterile conditions to prevent cross-contamination.

2.3. Data Analysis and Quality Control

Prior to capillary electrophoresis, all amplified DNA samples were denatured at 95 °C for 5 minutes and rapidly cooled on ice for 5 minutes to ensure effective single-stranded DNA separation. Capillary electrophoresis was performed using a 36-cm capillary array and POP-4™ polymer on the ABI 3500 Genetic Analyzer (Life Technologies), with injection parameters set at 1.2 kV for 24 seconds. STR profile data were processed using GeneMapper® ID-X Software Version 1.5 with default analytical thresholds and filters, and a detection threshold of 75 relative fluorescence units (RFUs) was applied to distinguish genuine allelic peaks from background noise.

Quantitative analysis of RFU values was conducted by recording the total peak height for homozygous loci and summing the peak heights of both alleles for heterozygous loci. Total allelic signals were calculated per sample to estimate STR profile richness. Partial profiles, stutter artifacts, and allelic drop-out events were manually reviewed and logged for transparency in interpreting low-template samples.

Negative controls including extraction blanks, reagent blanks, and amplification blanks—were processed alongside each sample batch to monitor for potential contamination. No DNA was detected in any control, confirming the reliability and integrity of the laboratory workflow.

All statistical analyses were performed using RStudio (R version 4.2.3), with initial data curation handled in Microsoft Excel. A factorial analysis of variance (ANOVA) was used to evaluate the effects of collection method, extraction kit, and surface type on DNA concentration and allele counts. Post hoc comparisons were assessed using Tukey's HSD test where appropriate. For categorical data (profile completeness types), a chi-square (χ^2) test of independence was used to examine associations between sampling method and profile outcome. To assess the relationship between DNA yield and STR profile quality, a Pearson correlation analysis was performed using numerically assigned profile completeness scores (FS = 4, FM = 3, PS = 2, PM = 1), and the correlation was visualized using linear regression. Statistical significance was set at $p < 0.05$ for all tests unless otherwise specified.

3. Results

3.1. Quantitative DNA Yield as a Function of Collection and Extraction Methods

Quantification results revealed substantial variability in DNA recovery as a function of both the sampling method and the DNA extraction kit used. As illustrated in Figure 1, cotton swabs consistently yielded higher DNA concentrations than minitapes across all tested surface types namely disposable face masks, T-shirts, and baseball caps. The combination of cotton swabs with the PrepFiler Express BTA™ extraction kit produced the highest mean DNA concentrations, reaching 2.22 ng/µL on T-shirts, 2.46 ng/µL on face masks, and 2.01 ng/µL on caps. In contrast, the lowest mean yields were observed for minitapes used in conjunction with the QIAamp® DNA Investigator Kit, with mean recoveries of 0.90 ng/µL, 1.02 ng/µL, and 0.81 ng/µL for the same surfaces, respectively.

The effect of method combination was statistically significant across all surfaces, as confirmed by a one-way ANOVA ($F = 269.05$, $p < 0.0001$). These results underscore the compounded influence of both collection and extraction strategies on overall DNA recovery, particularly in contexts involving particulate interference such as sand. Furthermore, cotton swabs demonstrated superior mechanical interaction with dusty and fibrous materials, likely contributing to their enhanced recovery efficiency over adhesive-based sampling methods such as minitapes.

3.2. Impact of Sampling Technique on STR Profile Completeness

STR typing outcomes were assessed by categorizing profiles into four qualitative classes based on allelic completeness and mixture status: Full Single-source (FS), Full Mixed (FM), Partial Single-source (PS), and Partial Mixed (PM). The distribution of these profile categories is presented in Figure 2. The cotton swab method yielded a significantly higher proportion of complete profiles comprising 40% FS and 35% FM compared to minitapes, which showed a predominance of partial profiles (25% PS and 20% PM). These differences were consistent across all item types and reflect a decline in STR data integrity associated with the minitape method under sandy or dusty conditions.

Chi-square analysis revealed a statistically significant difference in the distribution of profile types between cotton swabs and minitapes ($\chi^2 = 9.68$, $df = 3$, $p = 0.0215$). These findings suggest that sampling efficiency not only affects DNA yield but also directly influences the likelihood of generating interpretable STR profiles, particularly in trace DNA contexts where template quantity and integrity are already compromised.

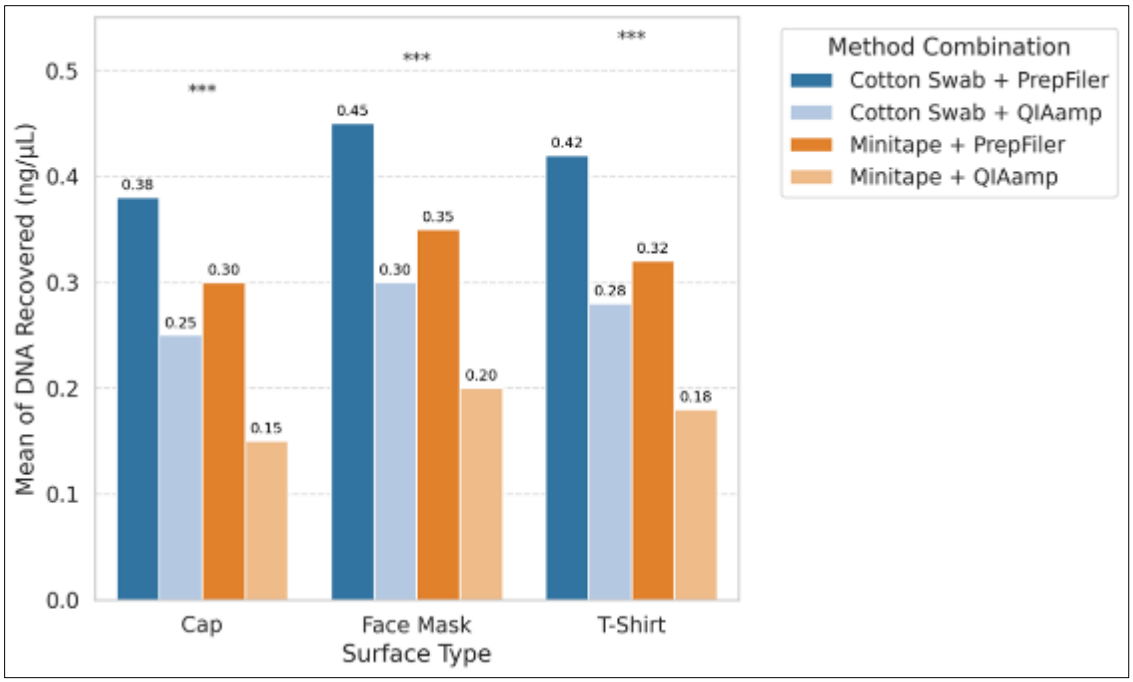

Figure 1 Mean DNA concentrations (ng/µL ± standard deviation) recovered from three types of wearable fabric items disposable face masks, T-shirts, and caps contaminated with sand are presented for four collection and extraction method combinations: Cotton Swab + PrepFiler, Cotton Swab + QIAamp, Minitape + PrepFiler, and Minitape + QIAamp. Each bar represents the mean of replicate measurements obtained from a combined total of 100 items sampled under standardized conditions. The results indicate that cotton swabs consistently yielded higher DNA recovery than minitapes across all surface types, with the highest concentrations observed for the Cotton Swab + PrepFiler combination. In contrast, the Minitape + QIAamp combination produced the lowest yields, likely due to compromised adhesion efficiency caused by sand and reduced extraction performance. Statistically significant differences (***$p < 0.001$) were observed between the highest- and lowest-performing method pairs on all surface types. These findings underscore the critical impact of method selection on trace DNA recovery in challenging environmental conditions such as sandy outdoor scenes

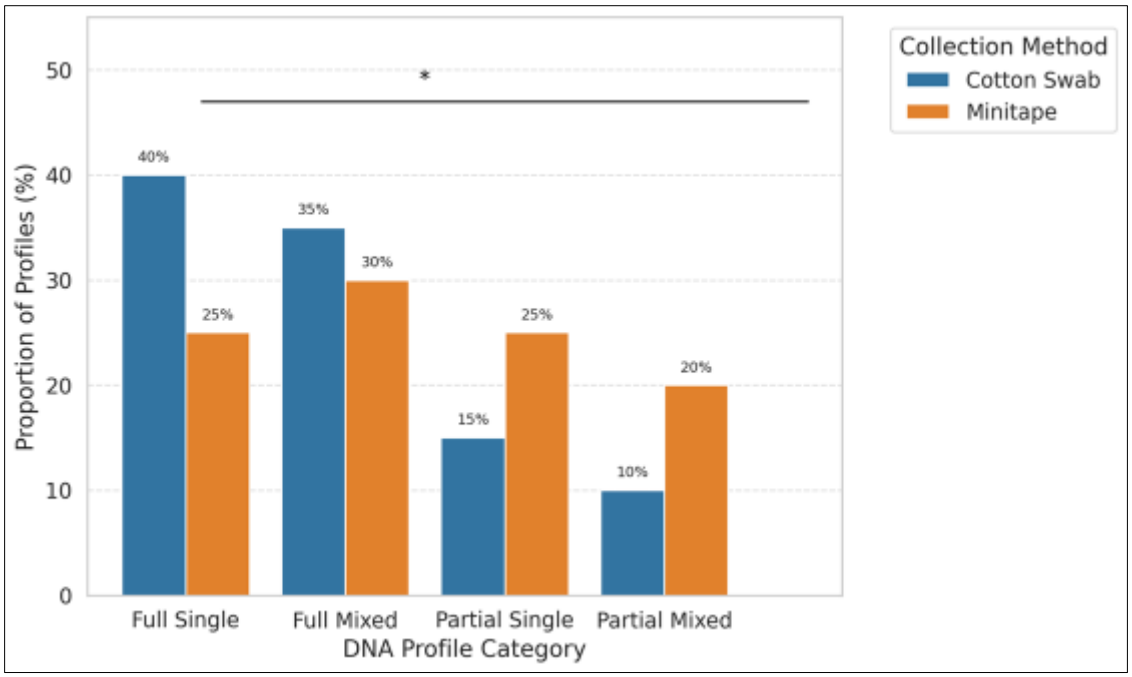

Figure 2 Distribution of DNA profile completeness categories—Full Single (FS), Full Mixed (FM), Partial Single (PS), and Partial Mixed (PM) obtained from sandy wearable fabric surfaces using two collection methods: cotton swabs and minitapes. Proportions are based on a total of 100 samples pooled across face masks, T-shirts, and caps. Cotton swabs yielded a greater proportion of complete profiles (40% FS and 35% FM), while minitapes resulted in higher frequencies of partial profiles (25% PS and 20% PM), indicating reduced recovery efficiency under particulate contamination. Profile classifications were determined by allele count and signal integrity, with full profiles comprising all expected STR loci and partial profiles including at least nine loci. A chi-square test revealed a statistically significant difference in the overall distribution of profile types between the two collection methods (χ^2 = 9.68, df = 3, p = 0.0215). The asterisk (*) and connecting bracket line above the bars visually indicate this significant difference in overall profile distribution. These findings further support the superior performance of cotton swabs in maintaining profile completeness in the presence of environmental contaminants such as sand

3.3. Correlation Between DNA Concentration and STR Profile Quality

To investigate whether DNA yield correlates with the completeness of STR profiles, we assigned numerical scores to each profile type (FS = 4, FM = 3, PS = 2, PM = 1) and plotted them against DNA concentrations. The resulting scatterplot and regression analysis are shown in Figure 3. A clear positive relationship emerged, with higher DNA concentrations associated with more complete STR profiles (n = 40). Samples yielding greater than 2.0 ng/µL frequently resulted in FS or FM profiles, while those below 1.5 ng/µL were predominantly associated with partial or mixed outcomes.

This relationship supports the inference that DNA quantity is a key determinant of STR typing success, and by extension, that suboptimal collection or environmental degradation may directly compromise downstream interpretability. These data emphasize the value of using both sensitive sampling tools and robust extraction methods to optimize not just DNA recovery, but also the forensic utility of the resulting profiles.

3.4. STR Allele Recovery Across Surfaces and Methods

In addition to profile type, we evaluated the number of STR alleles recovered per sample as a quantitative measure of profile richness. Results are summarized in Figure 4, which compares allele counts for cotton swabs and minitapes across the three substrate types. Across all surfaces, cotton swabs consistently yielded a significantly higher number of alleles. For instance, average allele counts for face masks reached 43.1 alleles with cotton swabs versus 31.8 with minitapes. Comparable trends were observed for T-shirts (42.7 vs. 29.5) and caps (41.3 vs. 28.2).

Statistical analysis confirmed significant differences for all surfaces using one-way ANOVA: face masks ($F = 1661.49$, $p < 0.0001$), T-shirts ($F = 2193.51$, $p < 0.0001$), and caps ($F = 1605.56$, $p < 0.0001$). These results reinforce the superior capacity of cotton swabs to maximize allele recovery from fabric items contaminated with sand and dust, conditions that likely interfere with adhesive-based sampling.

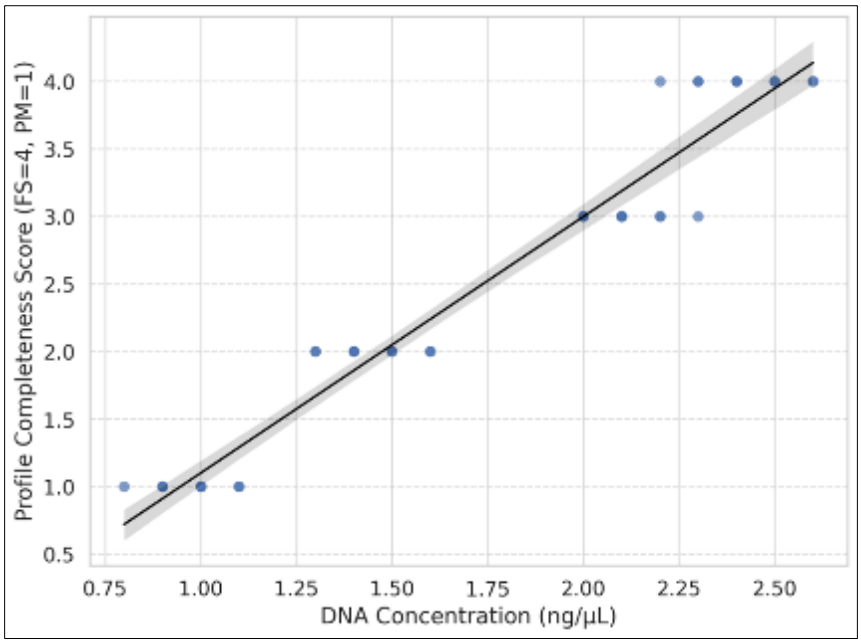

Figure 3 Correlation between DNA concentration (ng/µL) and STR profile completeness score (n = 40). Each point represents a sample recovered from sandy fabric surfaces, with completeness scores assigned as follows: Full Single (FS = 4), Full Mixed (FM = 3), Partial Single (PS = 2), and Partial Mixed (PM = 1). A positive linear trend is evident, showing that higher DNA concentrations are associated with more complete STR profiles. The regression line (black) illustrates this association, with lower-yielding samples (<1.5 ng/µL) often producing partial or mixed profiles. These findings support the inference that DNA yield critically influences the quality of forensic profiles under sandy environmental conditions

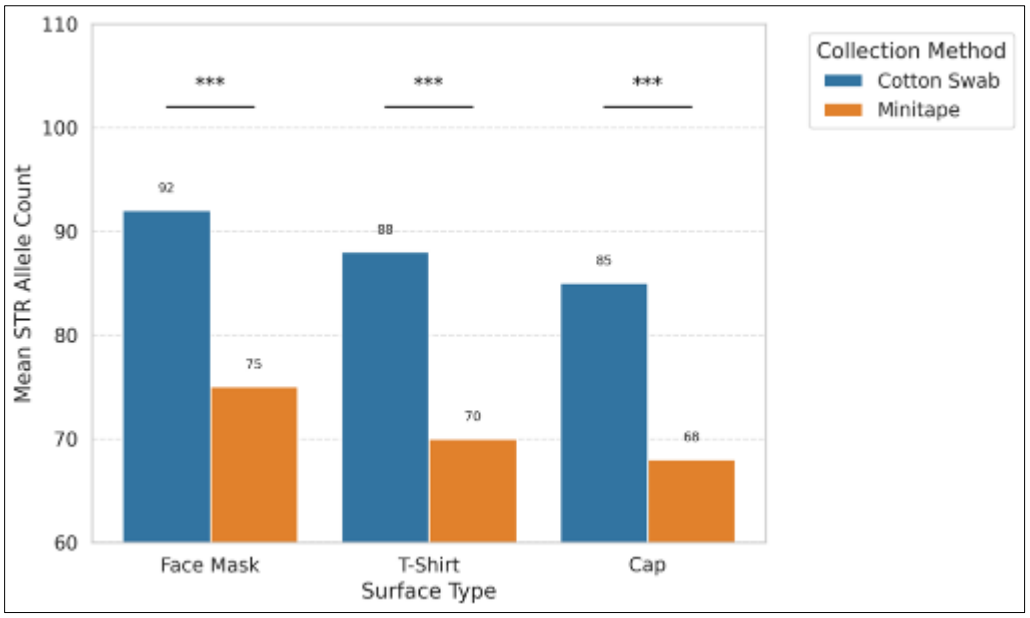

Figure 4 Mean STR allele counts recovered from three types of sandy wearable fabric surfaces face masks, T-shirts, and caps using cotton swabs and minitapes. Bars represent average allele counts per method per surface, with error bars indicating standard deviation. Cotton swabs consistently yielded significantly more alleles across all surface types. One-way ANOVA revealed strong statistical differences between collection methods for each surface: face mask ($F = 1661.49$, $p < 0.0001$), T-shirt ($F = 2193.51$, $p < 0.0001$), and cap ($F = 1605.56$, $p < 0.0001$), denoted by asterisks (***) and horizontal brackets. These results confirm the superior efficiency of cotton swabs in recovering STR alleles from trace DNA under sandy and dust-contaminated conditions

4. Discussion

4.1. Overview and Significance of Findings

This study examined the impact of sandy contamination on the effectiveness of two widely used DNA collection methods cotton swabbing and minitape tapelifting alongside two extraction systems, across common wearable items. The findings reveal that environmental interference, particularly from sand, substantially reduces the efficacy of adhesive-based tapelifting methods, while cotton swabs paired with magnetic bead-based extraction (PrepFiler Express BTA™) consistently yielded superior DNA quantities, more complete STR profiles, and higher allele recovery. These results not only reinforce the critical role of method selection in trace DNA analysis but also challenge prevailing assumptions about the universal applicability of minitape systems, especially under harsh environmental conditions.

These observations are especially relevant in forensic contexts within arid or desert regions where particulate contamination is frequent. By focusing on wearable items such as face masks, T-shirts, and caps—evidence types increasingly encountered in modern investigations this study directly informs operational casework and contributes novel insight into forensic DNA sampling under environmental stressors.

4.2. Comparative Analysis with Prior Research

Previous work by Alketbi and Goodwin (2019) [12] confirmed that sandy surfaces substantially reduce the efficiency of trace DNA recovery, particularly on non-porous items such as glass and textured plastic. Their recommendation to use nylon swabs in combination with PrepFiler in desert conditions aligns with our finding that cotton swabs—although slightly different in material—significantly outperform minitapes in sandy environments. Our data expand on this by showing that even porous and fabric-based items, such as face masks and caps, exhibit reduced recovery when tapelifting is employed under sandy exposure.

In contrast, other research (e.g., Alketbi and Goodwin, 2025 [16]) reported that minitapes outperformed swabs on clean face masks in robbery cases, citing higher DNA concentration and profile completeness. However, that study was conducted on items uncontaminated by environmental agents like dust or sand. Our findings suggest that while minitapes may perform well under controlled indoor conditions, their efficiency deteriorates substantially in outdoor, particulate-heavy scenarios, where sand clogs adhesive surfaces and prevents effective DNA collection.

Likewise, Alketbi (2022) [39] and Verdon et al. (2014) [41] highlighted the potential of minitapes on clean fabric substrates and recommended multiple tape applications to increase yield. However, our standardized protocol using 16 presses per area showed diminishing returns under sandy conditions, likely due to adhesive saturation and particulate interference. This is supported by Stoop et al. (2017) [55], who also noted optimal tape usage is highly dependent on surface type and environmental cleanliness—highlighting the need for adaptive protocols.

4.3. Methodological Implications and Optimization

This study clearly demonstrates that PrepFiler Express BTA™ extraction kit delivers superior performance when paired with either sampling method. This finding is in line with previous results by Stoop et al. (2017) [55], who reported that magnetic bead-based kits outperform conventional organic extractions when used with SceneSafe Fast™ minitapes. However, our data indicate that the extraction kit cannot fully compensate for inefficiencies caused by collection method or substrate contamination.

Further, the strong correlation observed between DNA concentration and STR profile completeness (Figure 3) underscores the interdependence of upstream and downstream processes. Low-yield samples—often caused by ineffective sampling directly resulted in partial or mixed profiles, emphasizing the need to prioritize high-yield collection approaches in real-world conditions.

4.4. Contribution to Forensic Practice

This research provides novel insights with immediate operational relevance. Notably, while previous studies have focused on ideal laboratory conditions, our study simulates field realities where sandy contamination compromises standard procedures. By using authentic casework items exposed to outdoor conditions, we offer a real-world validation of collection-extraction combinations.

The results contradict a growing trend in some jurisdictions to favor tapelifting as a universal method across fabrics. While Verdon et al. (2014) [41] and Alketbi and Goodwin (2022) [42] supported minitape use on small areas or

polyester fabrics, our findings caution against overgeneralizing its effectiveness under sandy or dusty field conditions. Instead, cotton swabs demonstrate more reliable performance, especially when used with bead-based extraction workflows.

4.5. Study Strengths, Limitations, and Future Directions

A key strength of this study is its realistic sampling context including 100 case-derived items subjected to natural environmental contamination. Additionally, the use of both quantitative (DNA concentration, allele count) and qualitative (profile type) measures allowed a comprehensive assessment of forensic value.

Nonetheless, limitations exist. The study did not evaluate DNA degradation indices, which could further clarify environmental impacts on DNA integrity. Moreover, while cotton swabs performed better overall, additional comparisons involving flocked nylon swabs or hybrid swabbing methods (e.g., microFLOQ® swabs) may yield different outcomes under similar conditions.

Future studies should explore additional variables such as humidity, UV exposure, and surface microtopography, and assess novel decontamination techniques or enhanced adhesive formulations to improve tapelifting reliability under adverse environmental conditions.

5. Conclusion

The present study provides robust empirical evidence supporting the superiority of cotton swabs combined with PrepFiler Express BTA™ extraction for recovering trace DNA from fabric-based evidence exposed to sandy outdoor environments. In all measured parameters DNA yield, STR profile completeness, and total allele count—this combination outperformed minitape collection and QIAamp®-based extraction workflows. The findings are particularly relevant for forensic practitioners operating in desert climates or other particulate-rich environments, where sand can impede standard collection techniques such as tapelifting.

Collectively, the data demonstrate that the combination of cotton swab sampling and PrepFiler extraction consistently yielded superior results across all tested parameters: DNA concentration, STR profile completeness, and total allele counts. Moreover, a strong correlation was observed between DNA yield and the quality of STR profiles, emphasizing the interdependence between upstream collection efficiency and downstream genotyping success. These findings have important implications for trace DNA recovery in arid and dusty environments, where methodological optimization is critical for generating reliable forensic evidence.

This study underscores the necessity of adapting trace DNA protocols to match environmental realities. The selection of collection tools and extraction strategies must be guided not only by laboratory efficacy but also by practical field conditions. By providing data-driven recommendations grounded in real-world case samples, this research contributes meaningful advances to the optimization of forensic DNA workflows and reinforces the need for environment-specific sampling strategies.

Compliance with ethical standards

Acknowledgments

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Disclosure of conflict of interest

The authors declare that there are no conflicts of interest financial or personal that could have influenced the conduct or outcomes of this research.

Statement of ethical approval

This study was conducted in accordance with the ethical policies and procedures of the General Department of Forensic Science and Criminology, Dubai Police General Headquarters, Dubai, United Arab Emirates. All methodologies including

sample acquisition, data handling, and analytical protocols were reviewed and approved by the department to ensure adherence to institutional and internationally recognized ethical standards. The research was carried out with full commitment to ethical integrity and forensic best practices.

Author Contributions

S.K.A. was responsible for evidence sampling, experimental execution, data processing, and drafting of the manuscript. W.G. provided supervisory input, critically revised the content, and contributed to the refinement of the final version. Both authors have reviewed and approved the completed manuscript.

Data Availability Statement

No datasets were generated or analyzed for this study that are applicable for public sharing.

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