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Trace DNA Recovery: Insights from Dubai Police Casework

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ABSTRACT: Trace DNA represents a critical form of forensic evidence, frequently recovered from a wide variety of touched or used items. Despite its evidentiary value, trace DNA analysis poses significant challenges due to the minute quantities of DNA involved, as well as the influence of factors such as surface type, collection methods, and environmental exposure. This study systematically examines the success rates and characteristics of trace DNA profiles recovered from six-item categories—tools, stolen items, wearable items, packaging materials, vehicles, and touched items—processed between 2021 and 2023 by the Biology and DNA Section of the Dubai Police Force. A total of 6277 cases were analyzed, encompassing a range of crimes, including homicide, suicide, missing persons, paternity disputes, and burglary. The results demonstrated an overall trace DNA success rate of 64%, with wearable items yielding the highest success rate at 76% and packaging materials yielding the lowest at 54%. Detailed analysis of positive DNA trace samples revealed significant variability in DNA profile types across item categories. Wearable items and touched items predominantly yielded full single (FS) DNA profiles, reflecting their reliability as sources of singular and high-quality DNA. Conversely, stolen items and packaging materials showed a greater prevalence of full mixed (FM) DNA profiles, highlighting their association with complex mixtures due to handling by multiple contributors. Tools and vehicles, meanwhile, exhibited higher rates of partial profiles, presenting unique challenges related to surface irregularities and environmental factors. This study emphasizes the importance of tailoring forensic strategies to item-specific characteristics, as well as the need for systematic mechanisms to categorize trace samples. Addressing operational challenges such as manual sorting and leveraging automation or AI-based systems can further streamline trace DNA analysis. The findings also underscore the importance of data sharing and standardization across forensic laboratories to enhance trace DNA recovery protocols and improve reliability in forensic investigations. Future research should focus on the effects of material properties, environmental exposure, and collection techniques on DNA retention, advancing the field of trace DNA profiling and its applications in forensic science.

Keywords: Forensic science; Trace DNA; Touch DNA; DNA recovery; Cotton swab; PrepFiler Express™ Forensic DNA Extraction Kit; Investigator Quantiplex Pro Quantification Kit; GlobalFiler™ PCR Amplification Kit; DNA profiling; STR analysis; Forensic casework; DNA success rate

1. Introduction

The concept that offenders both leave and carry trace evidence during criminal acts was initially proposed by Locard over a century ago and later elaborated upon by Inman and Rudin [1,2]. This foundational idea led to the development of various forensic disciplines dedicated to detecting such traces. A significant milestone in forensic science was the groundbreaking discovery by Sir Alec Jeffreys and his colleagues [3,4], who demonstrated the ability to generate distinct genetic profiles from biological materials and applied this technology to identify individuals involved in criminal activities. Over time, technological advancements have enabled the rapid and cost-effective generation of highly discriminating DNA profiles from diverse biological sources [5–7]. Moreover, the establishment of standardized practices across jurisdictions, the implementation of offender DNA databases, and the enactment of

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associated legislation [8–11] have progressively elevated the role of DNA in forensic investigations. These methodologies have also been instrumental in identifying victims of disasters and missing persons [12–23], as well as exonerating individuals wrongfully accused of crimes [12–19].

A major breakthrough emerged with the discovery that DNA could be recovered from non-visible biological material left on surfaces through direct contact with the skin [24,25]. This observation expanded the range of items suitable for DNA profiling and broadened the application of DNA analysis to various scenarios [5,12,16,26–29]. Initially met with skepticism within the forensic community, the ability to generate DNA profiles from touched objects has since been validated and embraced as a valuable tool by law enforcement agencies. Today, trace samples collected from touched or used objects are commonly sampled from crime scenes and often represent the majority of samples processed for DNA profiling [14,30,31].

Touch or trace DNA has become a crucial type of forensic evidence, as it can be recovered from a wide range of touched items or surfaces, establishing connections between suspects and crimes. Common sources of trace DNA include tools, weapons, clothing, and various other touched or used items. Trace DNA is transferred to surfaces not exclusively through the hand but also via other means, as the DNA-bearing cells may originate from multiple parts of the body [32]. This highlights the complex dynamics of DNA transfer and underscores the need to consider these variations when analyzing forensic evidence. However, recovering and analyzing this type of DNA presents unique challenges compared to other biological evidence, as the quantity of DNA collected is influenced by multiple factors [25,32–34]. These factors include the surface nature, collection and extraction methods employed [27], as well as the passage of time and environmental conditions [35,36]. The limited quantities and potential degradation of trace DNA have presented significant hurdles in forensic casework [8].

To address these challenges, forensic laboratories validate collection techniques and develop protocols to enhance trace DNA recovery [37–50]. Despite these efforts, there is limited published data on trace DNA recovery rates from real-world casework, which hampers the development of robust trace DNA profiling practices [31,34,51]. The importance of sharing data collection successes and comparing trace DNA recovery rates has been emphasized in numerous studies [13,52], particularly as laboratories frequently encounter similar items and scenarios in casework [34,53]. The collation of in-house casework data is invaluable for understanding the prevalence of specific profile types from similar objects and situations, especially when consistent methodologies are applied to a significant number of cases. Transparency and the availability of relevant data to other stakeholders, where appropriate, are critical to advancing the field of trace DNA profiling.

The General Department of Forensic Science and Criminology, established in 1981, has become one of the largest forensic laboratories in the Middle East, handling over forty thousand forensic cases annually [54]. Within this department, the Biology and DNA Section comprises specialized divisions responsible for biological examinations, DNA profiling, and the handling of reference samples. Despite the growing reliance on trace DNA in criminal investigations, there has been a lack of access to comprehensive DNA success rates across forensic jurisdictions in the UAE, particularly concerning samples collected from handled objects. Notably, no published review of trace DNA success rates in the UAE exists, leaving a critical gap in the literature.

This study aims to address this gap by examining the success rate of trace samples collected from DNA casework conducted by the Biology and DNA Section of the Dubai Police General Department of Forensic Science and Criminology. The study focuses on items touched or used by hand, including wearable items, and provides insights into trace DNA recovery from these objects. By sharing these findings, the study seeks to advance the understanding of trace DNA profiling practices and inform future forensic protocols.

2. Materials and Methods

2.1. Study Sample Collection and DNA Extraction

Samples were collected by moistening a sterile cotton swab with approximately 100–150 µL of molecular-grade water, applied using a plastic spray bottle [32,37]. The swabs were rubbed over the surface of the items to collect trace DNA and then air-dried before processing. DNA was extracted using the PrepFiler Express™ Forensic DNA Extraction Kit (Thermo Fisher Scientific, Waltham, MA, USA) on a Hamilton Automated Liquid Handler, following the manufacturer's recommendations. Quantification of the extracted DNA was performed using the Qiagen Investigator Quantiplex Pro Quantification Kit on a QuantStudio 5 Real-Time PCR (qPCR) system with HID Real-Time PCR analysis software (Thermo Fisher Scientific). All protocols adhered to the manufacturer's guidelines to ensure reproducibility and consistency across samples.

2.2. DNA Amplification and PCR

The extracted DNA samples were amplified using the GlobalFiler™ PCR Amplification Kit (Thermo Fisher Scientific) on the ABI GeneAmp® 9700 PCR System (Thermo Fisher Scientific). A 29 or 30 cycle protocol was used depending on the DNA input volume and sample quality, as per the manufacturer's recommendations. Each PCR reaction consisted of:

- 15 µL of input volume containing the extracted DNA (diluted if necessary),
- 7.5 µL of Master Mix, and
- 2.5 µL of Primer Set, yielding a total reaction volume of 25 µL.

2.3. Capillary Electrophoresis and STR Data Analysis

Following amplification, the PCR products underwent size separation and detection using an ABI 3500 Genetic Analyzer (Thermo Fisher Scientific). For each reaction, 1 µL of PCR product was combined with 9.6 µL of Hi-Di™ formamide and 0.4 µL of GeneScan™ 600 LIZ® Size Standard v2.0. Samples were denatured at 95 °C for 5 min and rapidly cooled on ice for 5 min before capillary electrophoresis on a 36-cm capillary array with POP-4™ polymer. Standard injection settings of 1.2 kV for 24 s were employed. Each plate included an allelic ladder injection (1 µL per well) to ensure accurate allele designation. STR profiles were analyzed using GeneMapper® ID-X Software Version 1.5 with a minimum detection threshold of 75 RFUs, as determined by in-house validation, ensuring the consistency and reliability of results specific to the laboratory environment.

2.4. Categorization and Figure Generation

To provide an overview of annual case volumes, Figure 1 depicts the annual volume of cases processed by the Biology and DNA section within the General Department of Forensic Science and Criminology at Dubai Police Force between 2021 and 2023. These data were compiled by recording the total number of cases received each year to assess workload trends over time. For Figure 2, data were collected from the DNA quantification and amplification processes across multiple forensic cases. This figure provides an overview of the total number of samples processed and how DNA profiling outcomes were determined. Subsequently, data for Figure 3 were gathered by analyzing trace DNA samples. These samples were categorized into six distinct item types—tools, stolen items, wearable items, packaging, vehicles, and touched items—to examine how different evidence categories may influence DNA recovery and profiling. Finally, Figure 4 was generated by selecting 100 positive DNA trace samples from each of the six categories described above. Recovered DNA profiles were classified into four groups—full single (FS), full mixture (FM), partial single (PS), and partial mixture (PM)—based on the number of alleles and loci recovered. This categorization method allows for a systematic comparison of DNA profile characteristics among various sample types.. Statistical analysis, including factorial analysis of variance (ANOVA), was conducted using RStudio and Microsoft Excel to identify significant differences across sample categories ($p < 0.05$).

2.5. Data Visualization and Statistical Analysis

Figures were generated using Microsoft Excel and Python's Matplotlib library, ensuring clarity and adherence to journal formatting standards. Percentages for DNA profile types (FS, FM, PS, PM) and the average number of alleles recovered for FM profiles were directly annotated for each sample category. Dual *y*-axes were employed in Figure 4 to represent both percentage distributions and allele counts simultaneously. Gridlines, color schemes, and labels were optimized for readability, allowing for easy interpretation of trends in DNA profile quality across categories.

3. Results

3.1. Number of Cases and Samples

Between 2021 and 2023, the Biology and DNA Section received a total of 6277 cases (Figure 1), with each case comprising one or multiple exhibits. During this period, 14,513 samples were collected from these examined items, averaging 4838 samples per year. Of these, 8592 samples underwent processing for DNA profiling (Figure 2), representing 59.2% of the total samples collected. This selective processing aligns with cost considerations and the strategic decision to retain some samples as backups for potential future use. Prioritization of samples for processing is

typically guided by their relevance to specific case scenarios. Samples not initially processed may undergo analysis at a later stage if required by legal or investigative authorities.

The DNA profiling process yielded 7003 positive DNA results, achieving an overall success rate of 81.5% for all types of samples, including trace samples. This high success rate underscores the efficiency and precision of the Biology and DNA Section in extracting usable profiles from prioritized samples, highlighting robust methodologies for DNA extraction and the effective prioritization of high-quality samples.

An analysis of year-over-year trends reveals that while the total number of cases declined slightly from 2021 to 2023, the total number of samples collected and the proportion of samples processed for DNA profiling remained consistent. The proportion of processed samples relative to collected samples (59.2%) indicates a sustained operational focus on prioritizing relevant exhibits while adhering to cost constraints. This proportional stability reflects the section's commitment to balancing resource efficiency with investigative needs.

The DNA profiling success rate of 81.5% highlights the operational efficiency of the Biology and DNA Section. Retaining unprocessed samples as backups provides flexibility, allowing for future analysis if needed by courts or investigators. This dual approach of selective processing and strategic backup retention ensures that the department remains agile in responding to evolving case requirements.

Positive DNA results, defined as profiles with alleles present at a minimum of eight loci, contribute significantly to case resolutions and legal outcomes. These profiles are generated using the GlobalFiler™ PCR Amplification Kit, ensuring compliance with stringent forensic standards by including eight CODIS Core Loci and the Amelogenin locus. This rigorous methodology ensures that the DNA profiles meet the highest standards of forensic reliability, thereby supporting both investigative objectives and the integrity of evidence presented in legal contexts.

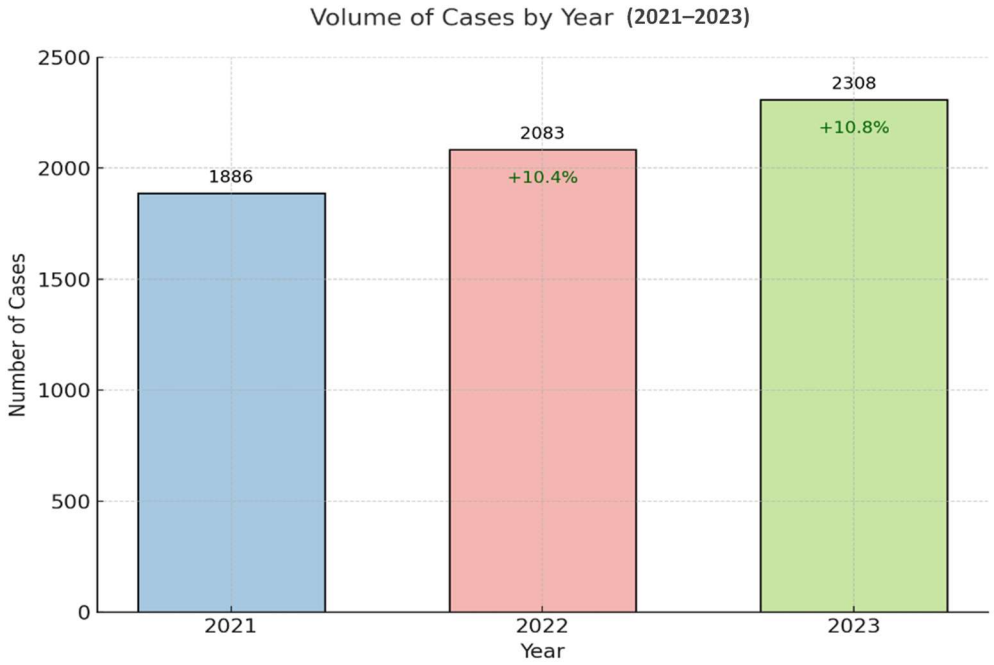

Figure 1. The volume of cases received by the Biology and DNA section within the General Department of Forensic Science and Criminology at Dubai Police Force between 2021 and 2023. A total of 6277 cases were received during this period, with an average of 2092 cases per year. The data shows a steady increase in case volume, with a 10.4% rise in 2022 and a further 10.8% increase in 2023 compared to the previous years.

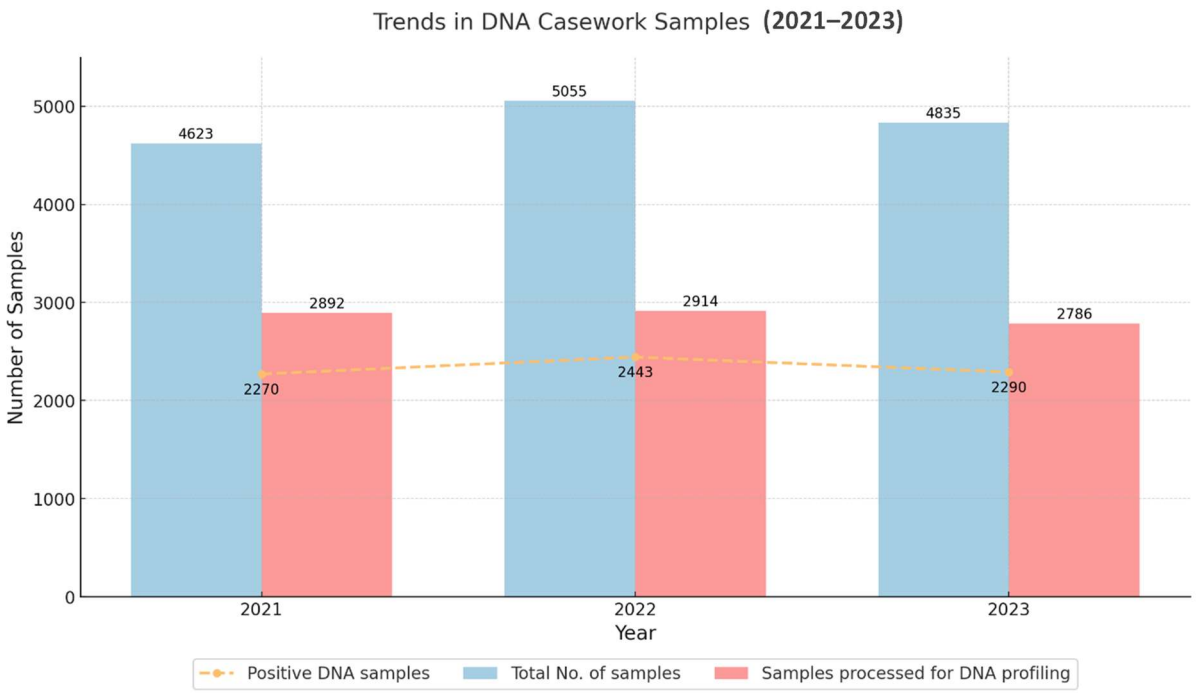

Figure 2. The data for the Biology and DNA section within the General Department of Forensic Science and Criminology at Dubai Police Force from 2021 to 2023. It includes the total number of samples received (n = 14,513, average of 4838), samples processed for DNA profiling (n = 8592, average of 2864, 59.2% of total samples), and the number of positive DNA samples (n = 7003, average of 2334, 81.5% of processed samples).

3.2. Trace DNA Success Rates

Between 2021 and 2023, trace DNA samples comprised a substantial proportion of the samples subjected to DNA profiling, accounting for 64% of the total processed samples. These samples were systematically categorized into six distinct groups, as illustrated in Figure 3. The categorization was established to enable a more detailed examination of sample types and their relevance to various forensic case scenarios. The groups included:

- Tools: DNA samples were collected from handles or grips of items such as screwdrivers and improvised weapons (e.g., knives, axes, machetes, and bats).
- Stolen items: Samples were obtained from the sides, handles, or zippers of frequently stolen objects, including mobile phones, wallets, and handbags.
- Wearable items: DNA was retrieved from internal areas or surfaces of clothing, shoes, jewelry, glasses, and similar articles.
- Packaging: DNA samples were extracted from sealed portions of materials such as plastic bags or containers used for drug storage.
- Vehicles: Sampling locations included steering wheels, door handles, and gear shafts from cars, motorcycles, trucks, and other vehicles.
- Touched items: This group encompassed a variety of everyday objects (e.g., cups, bottles, cans, and lipsticks), with samples collected from sides, handles, or other accessible surfaces.

This systematic categorization, as visualized in Figure 3, provided a comprehensive framework for analyzing the diverse origins of trace DNA samples processed during this time frame and facilitated the assessment of their utility in forensic investigations.

The overall trace DNA success rate was 64%, corresponding to positive DNA profiles for 3489 samples. Success rates varied significantly across the six categories. Wearable items demonstrated the highest success rate, achieving 76%, while packaging materials exhibited the lowest success rate at 54%. The remaining categories, including tools, stolen items, vehicles, and touched items, exhibited an average success rate of 62%, closely aligning with the overall benchmark.

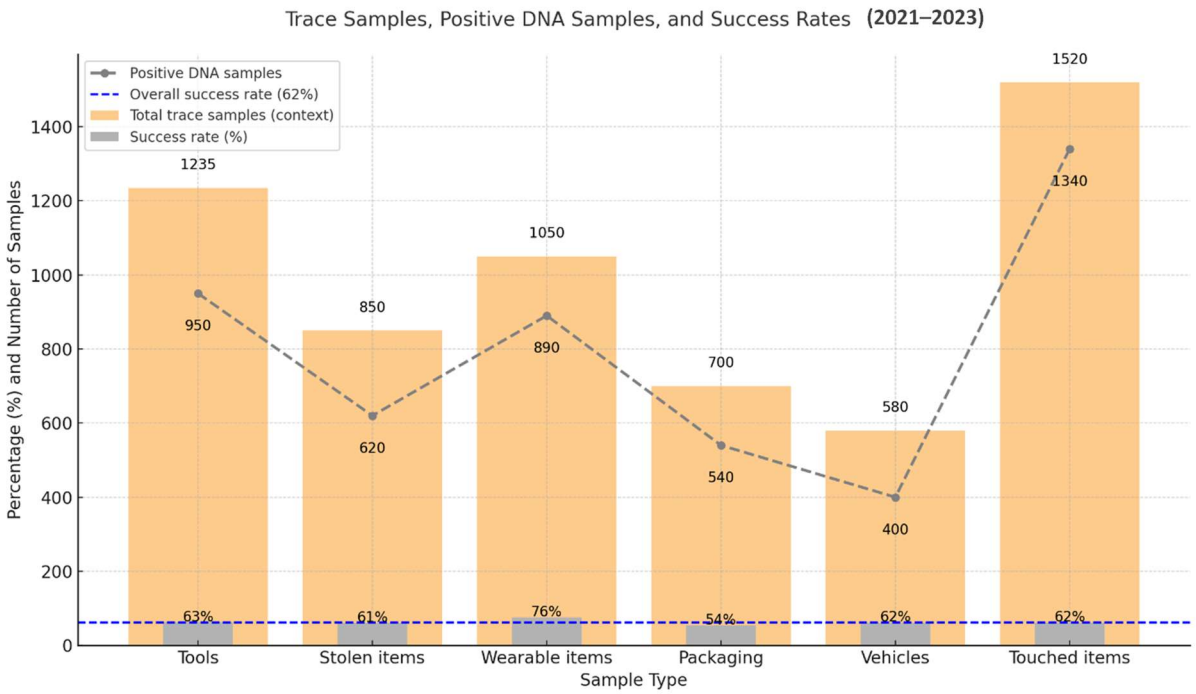

Figure 3. Success rates of positive DNA trace samples and the absolute number of positive DNA samples processed across six categories during the period 2021 to 2023. The chart provides a comprehensive view of total trace samples, positive outcomes, and efficiency. Categories such as wearable items show the highest success rate (76%) and a significant number of positive samples (890), while packaging has the lowest success rate (54%) with 540 positive samples.

3.3. Variability in DNA Profile Types Across Item Categories

To evaluate the quality of recovered DNA profiles, 100 randomly selected positive DNA trace samples from each of six categories (tools, stolen items, wearable items, packaging, vehicles, and touched items) were analyzed. The type of DNA profile recovered was found to be significantly influenced by the sampled item's category ($p < 0.05$), reflecting the dynamics of DNA retention and recovery across different objects. The recovered DNA profiles were classified into four categories: full single (FS), full mixture (FM), partial single (PS), and partial mixture (PM).

Wearable items and touched items yielded the highest proportion of full single (FS) DNA profiles, suggesting that these items, which frequently involve direct and prolonged contact with individuals, are conducive to recovering complete and singular DNA profiles. Conversely, stolen items and packaging produced a significantly greater proportion of full mixed (FM) DNA profiles, likely due to their nature as shared or frequently handled objects, which leads to contributions from multiple individuals. Tools and packaging generated the highest proportion of partial single (PS) DNA profiles, potentially reflecting the limited or inconsistent deposition of DNA on these items or the degradation of DNA due to environmental exposure. Meanwhile, tools and vehicles were associated with the greatest proportion of partial mixed (PM) DNA profiles, possibly resulting from intermittent or indirect contact with these items, which complicates the recovery of distinct contributors. These findings, summarized in Figure 4, underscore the substantial impact of the type of item on the quality and complexity of DNA profiles recovered in forensic investigations.

In-depth analysis of full mixed (FM) DNA profiles further demonstrated that the average number of alleles recovered was significantly influenced by the sampled item's category ($p < 0.05$), providing additional insights into the complexity of DNA mixtures. Stolen items yielded the highest average allele count (157 alleles), followed by packaging (129 alleles) and touched items (119 alleles). Tools and vehicles showed moderate average allele recovery (107 and 102 alleles, respectively), while wearable items exhibited the lowest average allele count (84 alleles). The high allele counts observed for stolen items and packaging likely reflect the frequent handling of these items by multiple individuals, leading to more complex mixtures. In contrast, wearable items may recover fewer alleles in FM profiles due to the dominance of DNA from a single primary contributor.

These findings have important implications for forensic investigations. The high proportion of full single (FS) DNA profiles recovered from wearable and touched items highlights their reliability in providing complete, singular DNA profiles, which are particularly valuable for individual identification. In contrast, the predominance of full mixed (FM) DNA profiles in stolen items and packaging underscores the challenges posed by complex mixtures in forensic

analysis, as these profiles often require advanced computational methods for deconvolution. Additionally, the high prevalence of partial single (PS) and partial mixed (PM) DNA profiles in tools and vehicles suggests that these items are more likely to yield degraded or low-quantity DNA, emphasizing the need to optimize sampling and analytical strategies when processing such items.

Overall, the results presented in Figure 4 illustrate the variability in DNA recovery and profile quality across item types. These insights provide critical guidance for prioritizing sample collection strategies and tailoring forensic methodologies to maximize the evidentiary value of recovered DNA profiles in forensic casework.

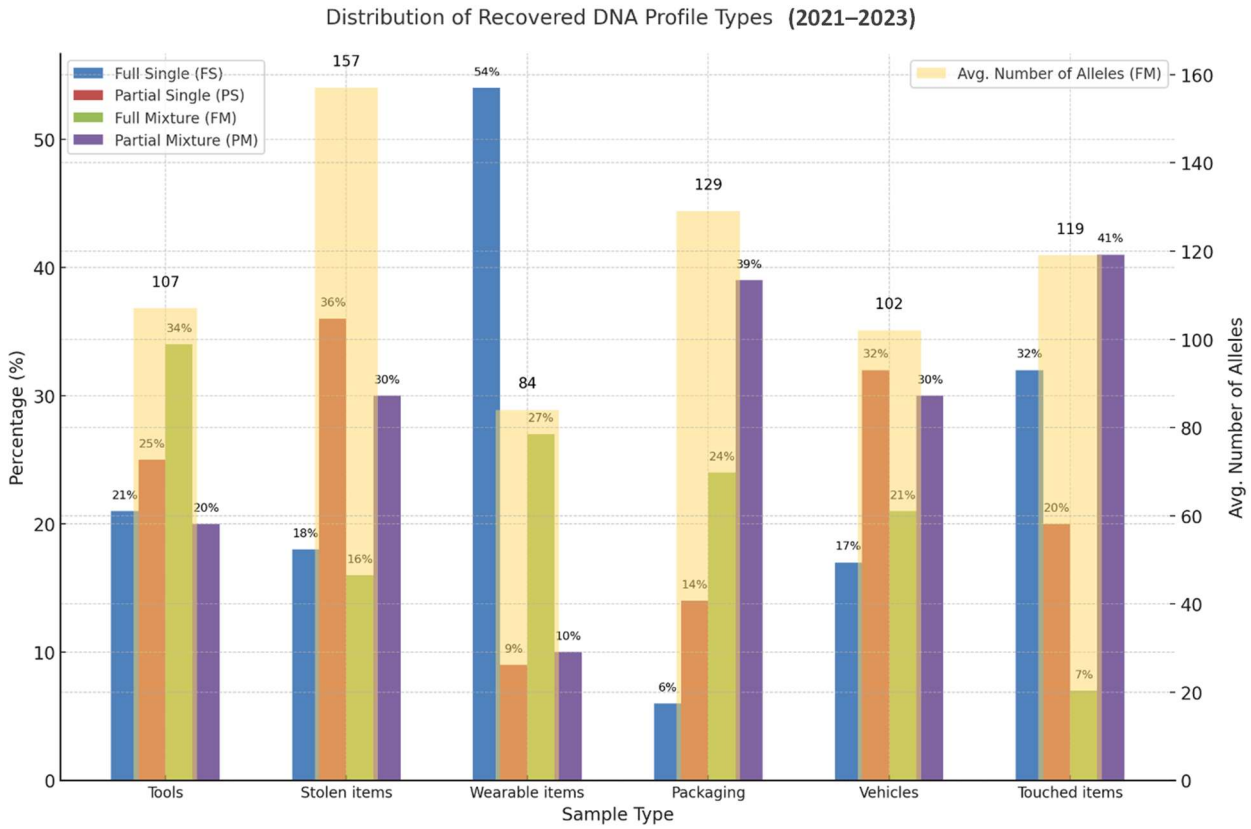

Figure 4. Randomly selected positive DNA trace samples from each of the six groups (tools, stolen items, wearable items, packaging, vehicles, and touched items; n = 600). The recovered DNA profiles are categorized into four types: full single (FS), full mixture (FM), partial single (PS), and partial mixture (PM). All partial DNA profiles contain alleles in nine loci or more. The figure also includes the average number of alleles recovered in full mixture (FM) DNA profiles, represented as yellow bars overlaying the green FM bars and annotated with their respective values. The dual y-axes depict the percentage distribution (left axis) and average number of alleles (right axis), providing insights into the recovery rates and profile types across the six groups.

4. Discussion

4.1. Variability in DNA Profile Types Across Item Categories

The analysis of positive DNA trace samples from six distinct categories provides significant insights into the variability of DNA recovery and the complexity of recovered DNA profiles. The study underscores the critical role that the type of item plays in determining DNA profile quality and its implications for forensic investigations. Wearable items and touched items yielded the highest proportion of full single (FS) DNA profiles, likely due to direct and prolonged contact with the wearer's skin. The porous nature of fabric materials in wearable items enhances DNA retention, making these items particularly reliable sources for generating singular DNA profiles. These findings align with previous studies that emphasize the importance of consistent and sustained contact for high-quality DNA recovery [55].

Conversely, stolen items and packaging materials yielded a greater proportion of full mixed (FM) DNA profiles, reflecting the influence of multiple contributors. Stolen items often pass through numerous handlers, and packaging materials frequently used for illicit substances are handled repeatedly during transport and inspection. These findings underscore the evidentiary value of such items, particularly in cases involving multiple suspects, but also highlight the challenges associated with interpreting complex mixtures [55,56].

4.2. Challenges in Recovering DNA from Tools and Vehicles

Tools and vehicles produced higher proportions of partial single (PS) and partial mixed (PM) DNA profiles, illustrating the difficulties in recovering complete DNA profiles from these substrates. The textured or irregular surfaces of tools can inhibit the deposition or retention of biological material, while environmental exposure and contamination further complicate recovery from vehicles. The study suggests targeted swabbing of high-contact areas and the use of enhanced DNA extraction buffers as strategies to improve recovery from such challenging items. These challenges align with earlier research emphasizing the influence of surface texture and environmental factors on DNA retention and recovery [55,56].

4.3. Implications of DNA Profile Complexity

Further analysis of full mixed (FM) DNA profiles revealed significant variability in the average number of alleles recovered across item categories. Stolen items and packaging materials yielded the highest allele counts (157 and 129 alleles, respectively), reflecting their association with complex mixtures. Wearable items, by contrast, yielded lower allele counts (84 alleles), indicating simpler profiles dominated by a single contributor. These differences emphasize the importance of tailored forensic strategies for analyzing diverse evidence types. Items with complex profiles, such as packaging and stolen goods, may require advanced computational methods for deconvolution, while simpler items, like wearable items, are more straightforward to interpret.

4.4. Ethical Considerations in DNA Profiling

The recovery of complex DNA profiles, particularly full mixed (FM) profiles from items such as stolen goods and packaging materials, presents significant ethical challenges in forensic investigations. One primary concern is the potential for misattribution of DNA contributors, particularly in cases involving multiple individuals. For example, an FM profile recovered from a commonly handled object, such as a stolen wallet, may contain DNA from both a suspect and an innocent bystander. Without robust validation and interpretation guidelines, there is a significant risk of implicating the wrong individual, leading to wrongful accusations or convictions. This issue is further complicated by the sensitivity of trace DNA profiling, where even minute quantities of DNA can be detected and analyzed. The presence of a person's DNA on an object does not necessarily confirm their involvement in a crime, as secondary or tertiary transfer of DNA can occur. In such scenarios, DNA might be indirectly transferred through an intermediary surface or another individual, raising important questions about how such evidence should be evaluated in criminal investigations.

Another ethical consideration involves the interpretation of probabilistic results in mixed profiles [57]. Tools such as STRmix™, a widely adopted probabilistic genotyping software, have become invaluable in deconvoluting complex DNA mixtures [58]. These tools apply advanced statistical models to interpret mixtures, assess the likelihood of various contributors, and generate results expressed as likelihood ratios. While STRmix™ enhances the ability to handle complex DNA profiles, its use also presents challenges. The statistical nature of its results must be clearly explained to non-expert stakeholders, such as legal professionals and juries, to avoid misinterpretation or overconfidence in the reliability of the findings. For example, likelihood ratios provide a measure of the strength of the evidence, but jurors may mistakenly interpret these ratios as absolute proof of guilt or innocence without proper explanation. Additionally, profiles derived from low-template or degraded DNA introduce further uncertainty, amplifying the need for careful consideration of their admissibility in court.

The adoption of STRmix™ by the Biology and DNA Section within the General Department of Forensic Science and Criminology of the Dubai Police reflects a commitment to leveraging advanced technologies to tackle the complexities of DNA profiling. However, its use underscores the necessity of rigorous validation protocols and transparent communication of results to ensure the responsible application of probabilistic genotyping in criminal justice.

To address these challenges, forensic laboratories must prioritize the development of clear and standardized guidelines for interpreting complex DNA profiles. Validation studies assessing the reliability of methods like STRmix™ are essential, particularly in cases involving low-template DNA or secondary transfer. Furthermore, training programs for forensic analysts should focus on equipping them with the skills to communicate the strengths, limitations, and probabilistic nature of DNA evidence effectively in court [59,60]. Engaging legal professionals in understanding complex DNA profiles is equally critical to ensuring that evidence is weighed appropriately during criminal proceedings. By addressing these ethical challenges, forensic science can uphold the integrity and reliability of DNA evidence in the justice system.

4.5. Operational Challenges and Recommendations

Operational challenges in trace DNA analysis remain a significant bottleneck in forensic workflows, as evidenced by the labor-intensive manual sorting and categorization process observed in this study. Assigning trace DNA samples to specific categories, such as tools, vehicles, or wearable items, was crucial for identifying trends and refining protocols. However, this process required considerable time and resources, highlighting the need for automation to improve efficiency and consistency.

Automation presents a viable solution to streamline sample management and processing [57]. For instance, AI-driven image recognition systems could be implemented to analyze photographs of evidence and categorize items based on predefined parameters. These systems, trained on extensive datasets of forensic evidence, could rapidly and accurately classify items, eliminating the need for manual sorting. Similarly, robotic systems can handle physical evidence, such as swabs or tubes, by scanning barcodes and linking them to associated metadata in Laboratory Information Management Systems (LIMS). Such automation would reduce human error and free forensic experts to focus on higher-value analytical tasks.

Additionally, forensic laboratories could adopt enhanced workflow management systems to further optimize trace DNA processing. Digital tools like LIMS can track evidence from collection to analysis, integrating metadata about item type, collection conditions, and processing methods. Pre-categorization protocols established during evidence collection could simplify downstream workflows by standardizing item labeling and prioritization at the crime scene. For challenging items, such as tools and vehicles, clear sampling guidelines should focus on high-contact areas to maximize DNA recovery.

Standardized protocols tailored to different item types are essential to address substrate-specific challenges. For example, textured surfaces, commonly found on tools, often require specialized swabbing techniques or enhanced extraction buffers to improve DNA recovery. Similarly, DNA recovery from chemically treated or impermeable materials, such as packaging, may benefit from targeted modifications to standard protocols. By integrating these strategies into forensic workflows, laboratories can overcome operational challenges, enhance efficiency, and improve the quality of trace DNA analysis.

4.6. Importance of Data Sharing and Future Directions

Data sharing represents a pivotal opportunity for advancing trace DNA profiling by promoting standardization and collaboration across forensic laboratories. Despite the critical insights generated by in-house casework data, forensic laboratories often lack mechanisms for sharing findings on trace DNA recovery. A centralized framework for data sharing could address this gap and foster a more unified approach to forensic investigations.

One approach to facilitate data sharing is the establishment of centralized databases for tracing DNA recovery data. These databases could aggregate anonymized casework data, including success rates, profile characteristics, and methodological details, enabling laboratories to identify trends in DNA recovery across diverse item types and environmental conditions. Managed by government agencies or international forensic organizations, such as INTERPOL or the European Network of Forensic Science Institutes (ENFSI), such repositories would ensure accessibility and standardization.

Recent advancements in human genomics underscore the importance of incorporating large-scale genomic data into forensic databases. Studies such as He et al. (2024) [61] demonstrate the potential of population genomics to uncover genetic admixture and cultural exchanges, which could enhance the inclusivity and accuracy of forensic databases. By integrating genomic insights from diverse populations, forensic laboratories can improve DNA match reliability and ensure equitable representation in forensic investigations.

Collaborative platforms could further enhance data sharing by fostering communication between laboratories. Online forums, workshops, and conferences could serve as venues for sharing best practices and discussing challenges in trace DNA profiling. Peer-reviewed publications and public reports offer another avenue for disseminating findings, particularly for novel methodologies or substrate-specific challenges, such as those encountered with tools and vehicles. Laboratories could also conduct meta-analyses of shared data to identify patterns in DNA recovery and inform the development of universally accepted protocols.

Forensic Investigative Genetic Genealogy (FIGG) represents another transformative advancement in forensic genetics. As noted by Wang et al. (2024) [62], FIGG leverages extensive genealogical databases to expand pedigree tracing and enhance case resolution, particularly in complex cases involving diverse populations. The global application

of FIGG highlights its potential for addressing investigative gaps, emphasizing the need for cross-jurisdictional collaboration and data sharing to maximize its impact in forensic casework.

However, data sharing presents challenges, particularly regarding privacy and confidentiality. Anonymization of genetic data is critical to prevent misuse while ensuring compliance with privacy laws and ethical guidelines. Additionally, laboratories must agree on standardized metrics for reporting DNA recovery rates and profile quality to ensure comparability across jurisdictions. Technological infrastructure, such as secure data-sharing platforms, should be developed to support laboratories with limited resources in participating effectively in collaborative initiatives.

Future directions for data sharing include leveraging machine learning to analyze shared datasets for predictive insights into trace DNA recovery. For example, algorithms could identify factors influencing recovery success rates, such as environmental exposure or item type, enabling laboratories to optimize their protocols. Additionally, insights into DNA shedding dynamics [63], can help refine strategies for evidence collection and recovery under varying conditions. Longitudinal studies investigating DNA degradation under varying storage conditions could also benefit from pooled data, providing valuable insights for evidence preservation. By prioritizing data sharing, forensic science can advance its methodologies, enhance the reliability of trace DNA analysis, and contribute to more consistent outcomes in criminal justice.

5. Conclusions

This study underscores the variability in DNA recovery across six-item categories and its implications for forensic investigations. The findings demonstrate that item-specific characteristics significantly influence DNA profile quality, with wearable and touched items yielding higher proportions of full single (FS) profiles, while stolen items and packaging are associated with more complex full mixed (FM) profiles. Tools and vehicles, on the other hand, often produce partial profiles, reflecting the challenges posed by their surface textures and environmental exposure.

The study highlights the importance of tailored forensic approaches to maximize the evidentiary value of trace DNA. Recommendations include systematic categorization of trace samples based on item type, improved collection and analysis protocols, and the integration of automation to address operational challenges. Data sharing among forensic laboratories is essential to standardize methods and advance trace DNA profiling practices globally.

Future research should continue to explore the dynamics of DNA retention and degradation, particularly for challenging substrates, to refine forensic methodologies further. By addressing these challenges and implementing the recommendations presented here, forensic laboratories can enhance the reliability and efficiency of trace DNA profiling, ultimately improving outcomes in criminal justice.

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Author Contributions

Conceptualization: S.K.A. and W.G.; Methodology: S.K.A.; Formal Analysis: S.K.A.; Investigation: S.K.A.; Data Curation: S.K.A., A.A.A., N.I.A. (Nashmi I. Aidarous), H.M.A., A.M.A. (Amna M. Alrazouqi), A.M.A. (Alanoud M. Alsaadi), S.M.A., A.F.A., N.I.A. (Noura I. Aldabal), M.A.A. and M.M.S.; Writing—Original Draft Preparation: S.K.A.; Writing—Review and Editing: S.K.A. and W.G.; Visualization: S.K.A.; Supervision: H.J.A.

Ethics Statement

Not applicable.

Informed Consent Statement

Not applicable.

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Declaration of Competing Interest

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

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