Literature Review: Evaluation of the Effect of Swab Type and DNA Isolation Protocol on the Success of Touch DNA Genetic Profiling

Nurul Hidayah*

Department of Magister Biomedicine, Faculty of Medicine, Universitas Sriwijaya, South Sumatera, Indonesia
**Corresponding Author: nurulhidayah200201@email.com*

Abstract

Touch DNA, trace DNA transferred upon contact with a surface is often very low in quantity and susceptible to degradation, making the success of Short Tandem Repeats (STR) profiling highly dependent on the collection method (swab type and technique) and DNA isolation protocol. A variety of collection devices (cotton, rayon, flocked/nylon, foam, microFLOQ) and isolation approaches (spin-column/silica, magnetic-bead, organic/phenol-chloroform; direct/LCN workflows) have been reported to produce different results on different substrates and sample conditions. Assess comparative evidence regarding the influence of swab type and DNA isolation protocol on the quality and efficacy of genetic profiling in touch DNA samples; identify best practices and research gaps for forensic/biomedical applications. The journal search identified 10 journals that met the specified inclusion criteria. The studies used case-control and cohort study designs. While some differences in the results were found for each study, they nevertheless shared similarities in the DNA isolation methods used for tracking and touch DNA. Based on the review results, it can be concluded that swab selection (type, material) and sampling techniques (swabbing, tape lifting, micromanipulation) are very important, especially for difficult surfaces such as metal or rough surfaces. Sample pre-processing (handling, storage, surface cleaning, contamination prevention) must be optimized to minimize DNA loss.

Keywords: *Touch DNA, swab type, profiling STR*

Abstrak

Literature Review: Evaluasi Pengaruh Jenis Swab dan Protokol Isolasi DNA terhadap Keberhasilan Profil Genetik Touch DNA. DNA sentuh, DNA jejak yang ditransfer saat kontak dengan permukaan seringkali jumlahnya sangat sedikit dan rentan terhadap degradasi, sehingga keberhasilan pembuatan profil Short Tandem Repeats (STR) sangat bergantung pada metode pengumpulan (jenis dan teknik usap) dan protokol isolasi DNA. Berbagai perangkat pengumpulan (katun, rayon, flocked/nilon, busa, microFLOQ) dan pendekatan isolasi (spin-column/silika, magnetic-bead, organik/fenol-kloroform; alur kerja langsung/LCN) telah dilaporkan menghasilkan hasil yang berbeda pada substrat dan kondisi sampel yang berbeda. Menilai bukti komparatif mengenai pengaruh jenis usap dan protokol isolasi DNA terhadap kualitas dan efikasi pembuatan profil genetik dalam sampel DNA sentuh; mengidentifikasi praktik terbaik dan kesenjangan penelitian untuk aplikasi forensik/biomedis. Pencarian jurnal mengidentifikasi 10 jurnal yang memenuhi kriteria inklusi yang ditentukan. Studi-studi tersebut menggunakan desain studi kasus-kontrol dan kohort. Meskipun terdapat beberapa perbedaan hasil pada masing-masing studi, namun keduanya memiliki kesamaan dalam metode isolasi DNA yang digunakan untuk pelacakan dan sentuhan DNA. Berdasarkan hasil tinjauan, dapat disimpulkan bahwa pemilihan sampel (jenis, bahan) dan teknik pengambilan sampel (swabbing, pengangkatan pita, mikromanipulasi) sangat penting, terutama untuk permukaan yang sulit seperti logam atau permukaan kasar. Pra-pemrosesan sampel (penanganan, penyimpanan, pembersihan permukaan, pencegahan kontaminasi) harus dioptimalkan untuk meminimalkan kehilangan DNA.

Kata Kunci: Sentuh DNA, jenis usap, profil STR (Pengulangan Tandem Pendek)

Introduction

"Touch DNA" can be defined as DNA transferred from a person to an object through contact with the object itself. In the literature, this form of evidence is also called "contact DNA," "trace DNA," or "transfer DNA." Many studies support the DNA deposited through touch originating as mentioned separate keratinocytes.[1] In particular, cell-free DNA has proven to be a reliable source of genetic material, often yielding higher yields than its cellular counterpart, although considerable doubt remains about its origin. It remains unclear whether cell-free DNA originates directly from bodily fluids or is released after cell degradation due to touch. Reports of fragmented DNA traces deposited from freshly washed hands suggest that DNA changes begin within the organism.[2]

However, contact DNA samples are generally known to contain low levels of DNA, and the presence of degraded genetic material, regardless of its origin, makes genotype detection challenging. Degraded DNA is not the only component of contact deposits that can compromise forensic profiling. The presence of small amounts of available genetic material, sometimes even below the minimum threshold of modern, highly sensitive commercial STR (Short Tandem Repeats) kits, is another common phenomenon found in contact samples. In this contingency, PCR amplification can miss the detection of short DNA fragments even when the procedure is implemented with additional cycles to maximize yield.[1]

The laboratory methods used also influence the success of touch DNA analysis. Once recovered, the standard workflow for processing touch DNA evidence involves first DNA extraction, which has many approaches, and then DNA quantification, which is essential for determining the quantity and quality of the extracted DNA.[3] This process is crucial for deciding which downstream genotyping method to use and the proportion of the initial amount of evidence to submit for potential destructive analysis, thus achieving a more informed interpretation of the results of further analysis.[4] However, the DNA extraction and quantification processes both result in the loss of some of the original sample and increase the likelihood of introducing exogenous DNA. The amplification phase often involves the use of one of the most commonly used commercially available kits for criminal cases.[2]

Methods

This review was performed in accordance with the preferred reporting items for literature review guidelines based on journal searches in PubMed, Researchgate, Scopus, and Google Scholar, the keywords are touch DNA, DNA isolation, DNA extraction, STR profiling, DNA forensics, and biometric fingerprints. This research uses a literature review method with reference sources from journals.[3]

Based on the results of a search of Web of Science, ScienceDirect, and Pub Med journals with the keywords Touch DNA, swab type, profiling STR (Short Tandem Repeats), researchers selected 10 journals according to these keywords with a time span of 2020-2025. In searching for articles and journals to expand or narrow the search, thus facilitating the selection of articles or journals to be used. Data search using the Web of Science, ScienceDirect, and Pub Med databases based on the keywords "Touch DNA, swab type, profiling STR (Short Tandem Repeats)" found 100 articles. Then, eliminated in the screening and assessment process because they did not match the criteria for swab type and DNA isolation to the genetic profile of touch DNA. So that left 12 journals that met the criteria. Of the 12 journals that could be used, only 10 others did not have full text available. The journal search process to obtain the final selected journal is shown in figure 1.

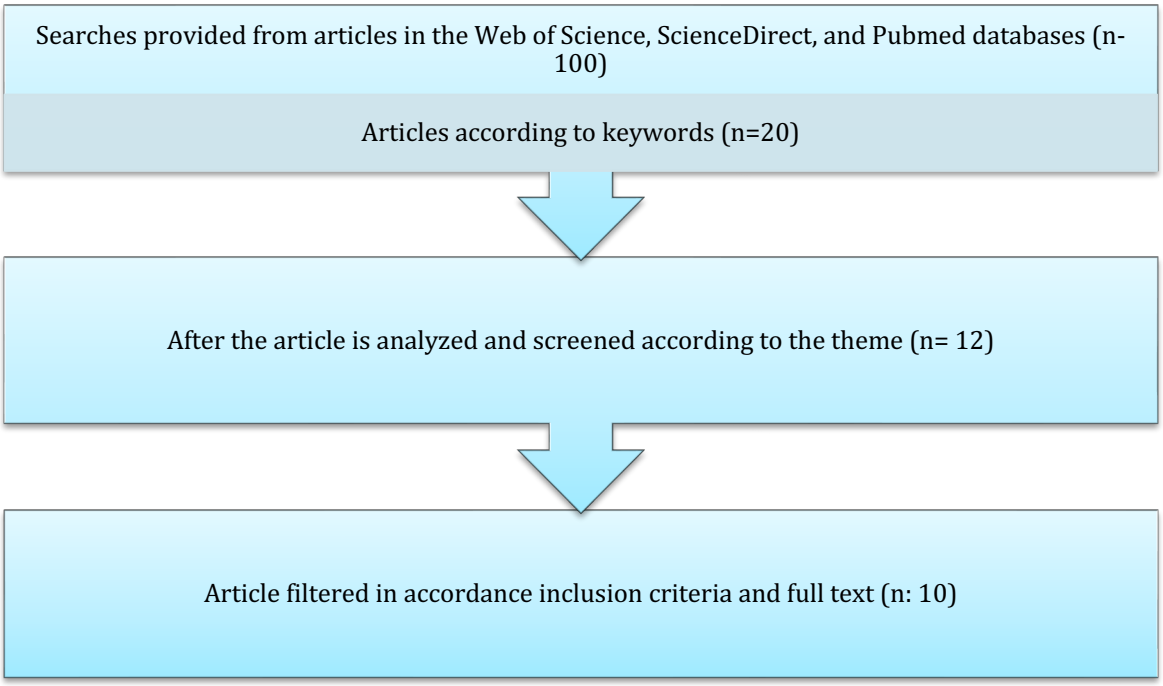

Figure 1. Flowchart related to the steps of a systematic literature review

Results and Discussion

Collecting and analyzing touch DNA, especially when the expected amount of genetic material is low, can be both challenging and invaluable for investigations.[4] Touch DNA testing is limited by the difficulty of obtaining not only sufficient quality DNA to generate a complete profile, but also sufficient material to allow for repeat testing.[5,6] Therefore, optimizing the procedure is crucial, even to increase the success rate of STR typing. The most common variable is that Flocked nylon swabs yield the highest amount of DNA and the most complete STR profiles.[7]

And then, studies investigating touch DNA often exhibit wide variability across experimental settings, with few papers examining this topic cross-sectionally. This analysis was designed to conduct a literature review on touch DNA, focusing on comparing the efficacy of different sampling methods. Because there is significant variability in the presentation of results and the type of data used to compare touch DNA scenarios, we evaluated the performance of three categories of collection techniques (single swab vs. double swab vs. other methods) by analyzing the average number of STR alleles, the percentage of informative profiles, and the quantity of touch DNA obtained.[6] This variability in results can be partly explained by the fact that there is currently no consensus on which aspect of the analysis is most suitable for comparing DNA traces. DNA quantity appears to be ineffective, from an investigative perspective, as it does not correlate with profile quality and does not provide any information about the presence of more than one contributor. However, it can provide insight into the efficacy of the procedure, the purpose of the study, and aid in the interpretation of research findings. On the other hand, several experimental studies evaluate results by analyzing profile composition. This subgroup is also considered to provide a broader perspective on the topic.[7]

Table 1. Journal summary

No	Researcher name and citation	Research title	Population	Method	Results and types of statistical tests	Conslusion
1.	Saamia, V., Yudianto, A., Nurjayadi, M., & Novitasari, N. (2023)[7]	Touch DNA viability on various substrates from different shedder levels. Medical Journal of Indonesia	9 Participants (High, medium, low Shedders)	Analytical research method with case control	$p = 0.97$ for substrate type; $p = 0.053$ for sampling method; $p < 0.001$ for shedder rate	The individual's shedding level significantly impacts DNA yield and profiling quality.
2.	Saamia, V., Yudianto, A., et al. (2023)[9]	Evaluation of 20 CODIS Core STR Loci for Touch DNA Analysis.	9 Donors (High, medium, low Shedders)	Analytical research method with case control	Concentrations below 0.0625 ng/µl cause amplification failure.	The amount of DNA is very important for the success of STR amplification.
3.	Alketbi, S.K., & Carta, L. (2025)[2]	Uncovering the Persistence of Touch DNA on Human Skin and its Implications for Violent Crime Investigations.	168 samples) + 72 additional samples for post-activity conditions (showering/sweating).	Observation method with a cross-sectional	The number of perpetrator alleles decreased significantly after 48 hours and was undetectable after 72 hours ($p < 0.05$). After washing or sweating, perpetrator DNA was completely removed within 6 hours ($p < 0.05$).	ANOVA analysis showed statistical significance ($p < 0.05$) for all main factors, confirming that DNA collection should be performed as quickly as possible to avoid loss of alleles.
4.	Watherston, J., Watson, J., Bruce, D., Ward, J., & McNevin, D. (2021)[10]	Efficient DNA Profiling Protocols for Disaster Victim Identification	7 human remains donors	Observation method with a cross-sectional	Wilcoxon Signed Rank Test to test the differences between methods on the number of alleles and DNA degradation with a p value < 0.05 is considered significant.	Nail and distal phalangeal sampling is effective for DVI with high DNA yields and is faster than bone.
5.	Rupf, S., Helmus, P., Hecker, P., Büttner, M., & Rothschild, M. (2021)[1]	Suitability of Specific Soft Tissue Swabs for the Forensic Genetic Identification of Human Remains	120 soft tissue samples from 20 human remains	Observation method with a cross-sectional	One-way ANOVA and post-hoc Tukey test were used to compare results between swab types and organs. Flocked nylon swabs yielded the highest DNA count and the most complete STR	Flocked nylon swabs are recommended as the best soft tissue collection tool for forensic DNA identification.

					profiles (≥95%) compared to other types ($p < 0.01$).	
6.	Alketbi, S. K. (2022)[4]	Analysis of Touch DNA	Total >5000 case samples	Observation method with a cross-sectional	ANOVA and t-test with a significance level of $p<0.05$ or $p<0.001$ to assess differences between conditions (swab type, extraction, time, temperature)	The combination of cotton swabs and microFLOQ (CS+MF) is recommended to maximize DNA recovery. Immediate refrigeration after collection and the use of surface-specific methods increase success rates by up to 17%.
7.	Thornton, J. E. (2023)[5]	Analysis of Touch DNA Recovered from Metal Substrates	Touch DNA samples from metals (copper, brass, stainless steel) using 45–135 replicates, as well as cell-free DNA (cfDNA) and cellular	Observation method with a cross-sectional	Two-way ANOVA and Student's t-test ($p<0.05$) to compare efficiency between methods and metal types.	Touch DNA recovery from metals is influenced by the interaction of metal ions with cfDNA. M-Vac techniques and nuclease-free water humidification are recommended for non-porous metals. cfDNA plays an important role in the genetic profiling of metal surfaces.
8.	Mateen et al. (2020)[3]	Generating DNA Profile from Low Copy Number DNA: Strategies and Associated Risks	DNA copy number is low, <100 pg	Observation method with a cross-sectional	Increasing the PCR cycle rate up to 34 times can improve the detection of low-quantity DNA. Mini-STR and nested PCR are effective for degraded DNA. The high-fluorescence method (ET-16) increases detection to 62.5 pg of DNA.	Advanced PCR techniques and biochemical modifications allow DNA profiling from very small samples, but increase the risk of forensic misinterpretation. Laboratory validation standards and the use of Likelihood Ratios are required for more accurate statistical interpretation.

9.	Wiegand et al., 2020[8]	Recovery Techniques for Contact DNA Traces	60 touch DNA samples from different surfaces (metal, glass, plastic, fabric)	Analytical research method with case control	Flocked nylon swabs demonstrated the highest efficiency in contact DNA capture compared to cotton. The magnetic bead extraction method produced purer DNA with a higher amplification rate ($p < 0.05$).	Flocked nylon swabs and magnetic bead-based extraction techniques are the best methods for obtaining DNA from contact traces, offering high amplification yields and low degradation risk. The choice of isolation tool and protocol is crucial for the success of genetic profiling.
10.	Wang et al. (2022)[6]	Development of a Microneedle Swab for Acquisition of Genomic DNA from Buccal Mucosa.	30 healthy human volunteers (aged 20–45 years). DNA samples were obtained from the buccal mucosa using two methods: conventional swab (cotton swab) and microneedle swab (MNS).	Analytical research method with case control	A paired t-test was used to compare differences in DNA yield (ng/μL) between MNS and cotton swabs. Significance was set at $p < 0.05$.	Microneedle Swab (MNS) effectively obtains high-quality genomic DNA in twice the amount compared to traditional cotton swab methods.

Many factors can influence the quantity and success of genetic material recovery, schematically grouped into three categories: variables affecting sample preparation, deposition, and analysis. The concept of good or bad shedder status is discussed. Although the biological and genetic factors influencing this status are largely unknown, age, gender, and certain activities (e.g., touching DNA-free objects, wearing gloves, rubbing fingers on body parts) appear to influence the amount deposited.[8] Generally, men shed more DNA than women, especially younger men compared to older men, and handwashing can reduce the amount available. Conversely, physical activity involving sweating leads to increased DNA transfer. Closely related to this issue is the impact of body location; for example, hands, fingertips, or palms can potentially facilitate DNA deposition.

DNA profiling analysis aims to identify biological material used by crime scene investigators or police forensic investigators. Biological evidence can be left virtually everywhere during criminal activity, from wooden murder weapons to doors with metal handles.[7,8] Considering this, in everyday forensic practice, different material compositions must be investigated, with varying results. Some authors have reported increased epithelial cell sloughing on rough, porous substrates, while non-porous substrates adhere to genetic material less readily.[7] Thus, fabric and cotton appear to be better DNA collectors than plastic or glass surfaces, and it has been shown to be more difficult to consistently recover tactile DNA from metal surfaces.[8] The mode and duration of contact also influence the amount of genetic material transferred. It has been shown that DNA deposition increases when pressure or friction is involved, directly proportional to the applied intensity. Conversely, the influence of time on the amount of DNA produced during handling/wearing remains controversial. Although recent studies have proposed a linear correlation between the variables, previous papers have ruled out any such relationship, suggesting the origin of traces in a single transfer step upon initial contact. In addition, the possibility of interaction between other investigative methods, such as the enhanced dactyloscopic method, the enhanced blood smear method, and the DNA typing technique, cannot be excluded.[9]

Because every step of the operation involves a wide variety of equipment and techniques, as well as methods for sample recovery, processing, and analysis, DNA analysis results can be influenced by a combination of a single forensic approach to the scene and the following laboratory procedures.[10-11] From a methodological perspective, the collection of tactile DNA traces can involve the use of various sampling devices, such as swabs, adhesive tape, or directly examining the evidence, in whole or in part. Considering its cost-effectiveness and minimal training requirements, the use of swabs is one of the most versatile and widely used methods.[6] They can be applied dry or moistened with various agents and in a variety of materials.[10] For example, standard cotton swabs have traditionally been preferred for the collection of biological fluids and, although further research is needed, have shown a tendency for organic residues to become trapped in the cotton fibers, reducing sample availability.[11] When DNA traces are expected to be recovered, a double swab technique can be implemented. This consists of a wet swab and a second dry swab applied sequentially to the desired surface, aimed at maximizing recovery.[9] Although the effectiveness of this method has not been fully discussed, it is commonly used to enhance the collection of cellular material. When other procedures are used, effective alternatives include "cutting" the soft tissue sampling area or adhesive tape that lifts off the solid surface. The latter sampling method is quick and easy, and tapes with better adhesion have been reported to produce higher trace DNA yields than swabs, although the stickiness, stiffness, and size of the tape make interpretation of the results more difficult.[11]

Conclusions

A journal review of several studies related to swab types and DNA isolation for touch DNA genetic profiling found that the collection of useful touch DNA evidence should not hinder the selection of an appropriate sampling method. Less common sampling procedures, such as FTA paper scraping, are also recommended. A more comprehensive understanding of profiling based on object type and history, identifying the most appropriate areas to target for DNA sampling, and the impact of additional factors, such

as duration, frequency, and mode of contact, is needed. Furthermore, further research into the mechanisms of DNA shedding, including gender differences, the effects of activities performed prior to deposition, and other factors that may influence the amount of DNA deposited, is urgently needed in forensic science. The ability to recognize, harmonize, and improve these aspects will undoubtedly enhance the value of DNA evidence.

Conflict of Interest

While current scientific opinion on this topic remains questionable, this review contributes to the debate by offering an updated perspective on recent developments. While single sampling appears to be more efficient than alternative methods, double sampling does not improve early touch DNA collection.

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