International Journal of Science and Research Archive
eISSN: 2582-8185
Cross Ref DOI: 10.30574/ijsra
Journal homepage: https://ijsra.net/

(REVIEW ARTICLE)

DNA AT THE SCENE DOES NOT MEAN DNA FROM THE CRIME: A PRACTICAL REVIEW OF TRANSFER, BACKGROUND DNA, CONTAMINATION, AND FORENSIC INTERPRETATION

Salem K. Alketbi [1, 2, 3, *]

[1] The Biology and DNA Section, General Department of Forensic Science and Criminology, Dubai Police General Head Quarters, Dubai, UAE.
[2] International Center for Forensic Sciences, Dubai Police General Head Quarters, Dubai, UAE.
[3] School of Law and Policing, University of Lancashire, Preston, UK.
* Corresponding Author; E-mail: alkitbe.11@hotmail.com

ORCID Details
Salem K. Alketbi: https://orcid.org/0000-0002-7773-3953

International Journal of Science and Research Archive, 2026, 20(03), 211–279

Publication history: Received on 26 July 2026; revised on 02 September 2026; accepted on 05 September 2026

Article DOI: https://doi.org/10.30574/ijsra.2026.20.3.1726

ABSTRACT

Modern forensic DNA profiling can provide very strong statistical support for attributing biological material to an individual, while the questions disputed in investigations and courts often concern how, when, and during which activity that material was deposited. This focused critical narrative review evaluates the inferential gap between contributor attribution and crime-level interpretation by integrating evidence on direct and indirect transfer, subsequent transfer, biological reservoirs, persistence, background and prevalent DNA, glove- and packaging-mediated redistribution, contamination, recovery, and activity-level evaluation. Across experimental, operational, and evaluative studies, materially different histories can produce the same source-level DNA observation. DNA quantity, profile completeness, contributor rank, spatial location, and non-detection can inform a comparative evaluation, but none is a stand-alone marker of direct contact, recency, or crime-related deposition. Likewise, a strong source- or sub-source-level likelihood ratio does not automatically provide strong support for an activity proposition. Interpretation should compare explicit competing histories using sufficiently relevant transfer, persistence, prevalence/background, and recovery data while accounting for handling history, contamination opportunities, unknown contributors, and dependence between samples or sites. The review develops a decision framework that starts with the disputed question and preserves the distinction between analytical observation, source attribution, activity evaluation, and ultimate fact-finding. The principal research priorities are realistic proposition-driven datasets, calibrated recovery information, explicit treatment of uncertainty, and reporting practices that keep conclusions at the inferential level supported by the evidence.

Keywords: Trace DNA; Touch DNA; DNA Transfer; Secondary Transfer; Background DNA; Persistence; Contamination; Activity-Level Propositions; Forensic Interpretation

1 INTRODUCTION

DNA evidence is highly persuasive to non-specialists because a profile can provide very strong statistical support for biological attribution. The proposition resolved by that statistic, however, is often narrower than the question before an investigator or court. The disputed issue may be whether the person handled an item, was present during a relevant event, deposited the DNA recently, performed a particular activity, or participated in the alleged offence. These questions occupy different levels within the hierarchy of propositions and require different information for their evaluation [1–3]. A strong answer to "whose DNA is this?" does not, by itself, answer "how did it get there?" or "what does its presence establish about the alleged crime?"

The inferential gap has widened as forensic DNA methods have become more capable of recovering and profiling small, invisible quantities of biological material. Modern trace DNA workflows can generate useful profiles from handled, worn, shared, packaged, and environmentally exposed items that would previously have yielded little or no genetic information [4–6]. Greater analytical sensitivity expands evidential opportunity, but it also reveals more of an exhibit's biological history. DNA detected at a scene or on an item may derive from direct contact during the event of interest, indirect person- or object-mediated transfer, subsequent or tertiary transfer, background or prevalent DNA, persistence from earlier legitimate use, redistribution within an exhibit or its packaging, or contamination introduced after the event [4]. Several of these processes can operate sequentially or simultaneously, allowing materially different histories to converge on the same source-level observation.

Analytical yield and evidential discrimination are different endpoints. A Dubai Police casework series reported 7,003 positive results among 8,592 profiled samples, with substantial variation between evidence categories [6]. Yet a positive profile is not necessarily the result that best distinguishes competing accounts of a case. An analysis of 47,097 forensic samples likewise showed that DNA recovery and investigative added value are not interchangeable endpoints [7]. The same principle applies at trial: even an extremely strong source-level association may provide little discrimination between activities when both the prosecution and defence propositions readily predict the person's DNA. Conversely, a lower-quantity or partial result may be informative if its location, composition, or absence is substantially less expected under one proposition than the other. Evidential value is therefore proposition-dependent rather than a direct function of profile strength [2,3,8].

Over-interpretation occurs when distinct inferential steps are compressed into one narrative. In everyday language, a DNA 'match' may be taken to mean that the person touched the object; a major contributor may be assumed to be the most recent or most important handler; DNA recovered from a particular location may be treated as if it must have been deposited there; and non-detection may be read as evidence that contact did not occur. None of these conclusions follows automatically from the analytical result. Analyses of miscarriages of justice have shown how background DNA, secondary transfer, contamination, and inappropriate movement from sub-source statistics to activity-level claims can produce misleading investigative or legal conclusions [9]. The problem is therefore not the reliability of DNA profiling as a method of biological attribution, but the attribution of a historical meaning that the analytical result itself does not establish.

The problem spans the entire evidential pathway. Crime-scene personnel determine which items and locations are sampled and which handling details are preserved; investigators establish ownership, relationships, prior use, access, and alternative transfer opportunities; laboratory scientists recover, profile, and evaluate biological material; lawyers formulate the propositions placed before the court; and judges or juries decide what the evidence proves. Information omitted at one stage may be impossible to reconstruct later. International implementation of activity-level DNA evaluation also remains uneven. A survey of 162 forensic practitioners from multiple regions identified substantial variation in knowledge and practice, with recurring concerns about limited realistic transfer, persistence, prevalence/background and recovery data, insufficient education among forensic and legal professionals, lack of standardized reporting frameworks, and uncertainty regarding legal acceptance [10]. Analytical sensitivity alone cannot resolve these interpretive limitations.

This review is organized around that inferential boundary. It synthesizes evidence on direct and indirect transfer, subsequent transfer, biological reservoirs, persistence, background DNA, contamination, exhibit handling and packaging, recovery, and activity-level evaluation, with emphasis on how those mechanisms change the meaning of a DNA finding. The intended readership includes forensic scientists, investigators, lawyers, prosecutors, judges, students, and other justice-system professionals who may need to interpret or challenge DNA evidence without specialist training in forensic genetics. The aim is not to diminish the probative value of DNA, but to preserve it by matching each conclusion to the question the science can support. The review therefore moves from DNA detection and contributor attribution to transfer history, timing, activity, and crime-level inference. The central question is deliberately narrow: when a person's DNA is found on an exhibit or at a scene, what has been established, and what additional information is required before that finding can be attributed to the alleged crime?

2 REVIEW APPROACH

2.1 Strategic concept and positioning

The review is positioned as a focused critical narrative review of the evidential meaning of trace DNA rather than as a survey of touch DNA laboratory methods. Its organizing problem is inferential: when a person's DNA is recovered from an exhibit or scene, what has been established, and what remains uncertain? Empirical forensic genetics and legal reasoning are therefore treated within the same framework. Transfer, persistence, prevalence, recovery, contamination, and contributor composition are considered as processes that can generate competing histories for the same observed result, not as isolated laboratory phenomena. The central distinction is between biological attribution and evaluation of the activity or sequence of events responsible for deposition.

The structure follows the progression from laboratory observation to case-level inference. Evidence is considered according to the question it can answer: whether DNA was detected; whether a person is supported as a contributor; how the material could have reached the sampled location; whether it may pre-date the alleged event; whether post-event handling could have altered its distribution; and whether the complete findings discriminate between competing activities. This question-led structure retains the necessary forensic genetics detail while making the inferential boundaries explicit for investigators, lawyers, judges, prosecutors, students, and other non-specialist readers.

2.2 Scope and boundaries

The scope is limited to mechanisms and contextual factors that materially affect interpretation of DNA findings. It includes direct transfer; person- and object-mediated indirect transfer; tertiary or subsequent transfer; background and non-self DNA; persistence and prevalence; DNA already present on hands, clothing, shared objects, and routinely occupied environments; glove- and handler-mediated transfer; packaging-associated relocation; crime-scene, police, examiner, and laboratory contamination; and human-factor or implementation failures where these alter contamination risk or evidential reliability. Particular emphasis is placed on the distinction between source/sub-source and activity-level propositions, the interpretation of positive and negative findings, and the consequences for investigative and legal decision-making.

Detailed comparison of swab types, extraction kits, amplification chemistries, capillary-electrophoresis systems, STR marker biology, and probabilistic-genotyping software falls outside this review unless a methodological choice changes recovery probability, apparent contributor composition, contamination risk, spatial distribution, or interpretation of competing activities. Familial searching, forensic genetic genealogy, phenotype prediction, and detailed jurisdiction-specific legal doctrine are also outside scope. Body-fluid identification is considered only where biological-source information changes activity-level evaluation. Environmental or household DNA is discussed selectively as background or contextual evidence rather than as a separate environmental-DNA topic.

2.3 Evidence selection and weighting

Literature selection was purposive and directed by the predefined interpretive questions of the review. The work was not designed as a systematic review or quantitative meta-analysis, and no claim of exhaustive coverage is made. Priority was given to peer-reviewed empirical studies with known or well-characterized ground truth, realistic transfer scenarios, operational and casework datasets, studies examining contamination or packaging pathways, activity-level evaluations, and authoritative guidance on proposition formulation and evaluative reporting. Foundational reviews and methodological papers were retained when they clarified terminology, identified limitations in the evidence base, or materially affected interpretation of transfer, persistence, prevalence, and recovery.

Studies were weighted by inferential relevance rather than publication type alone. Operational datasets and realistic scenario studies anchored statements about casework occurrence and plausibility; controlled experiments were used mainly to isolate mechanisms and causal factors under defined conditions. Greater weight was placed on explicit ground truth, transparent sampling and analytical conditions, adequate replication, clearly defined transfer sequences, relevant comparators, and outcomes that could be linked to competing propositions. Demonstrating that a transfer route can occur was not treated as an estimate of how often it will occur in casework. This distinction between possibility and probability is central to the synthesis: experimental demonstration of secondary or tertiary transfer establishes a mechanism, not its probability in a different case context.

2.4 Synthesis and interpretive strategy

The synthesis is organized by inferential function rather than laboratory technique. Studies are compared according to how DNA can reach an exhibit, how time and prior use shape persistence and background, how contamination and post-event handling create alternative histories, and how those observations should be evaluated when the disputed question moves from contributor identity to activity. Quantitative findings are reported when they provide case-

relevant context, but results are not pooled across experiments that differ materially in substrate, contact sequence, donor characteristics, sampling area, environmental exposure, analytical workflow, or outcome definition. That heterogeneity is itself interpretively important because it limits transport of a probability estimated under one set of conditions to another.

Transfer, persistence, prevalence/background, and recovery are therefore treated as interdependent stages of the evidential pathway rather than as interchangeable explanatory labels. Empirical observations are separated from broader inference, and limitations on extrapolation are stated where the data are sparse or narrowly conditioned. The relevant question is not simply whether a mechanism is scientifically possible, but whether available data are sufficiently comparable to discriminate explicit competing histories. This principle also defines the practical framework developed later: strong source-level support may identify whose DNA was recovered, whereas conclusions about contact, timing, activity, or offence involvement require a separate proposition-based evaluation.

3 WHAT A DNA RESULT CAN—AND CANNOT—ESTABLISH

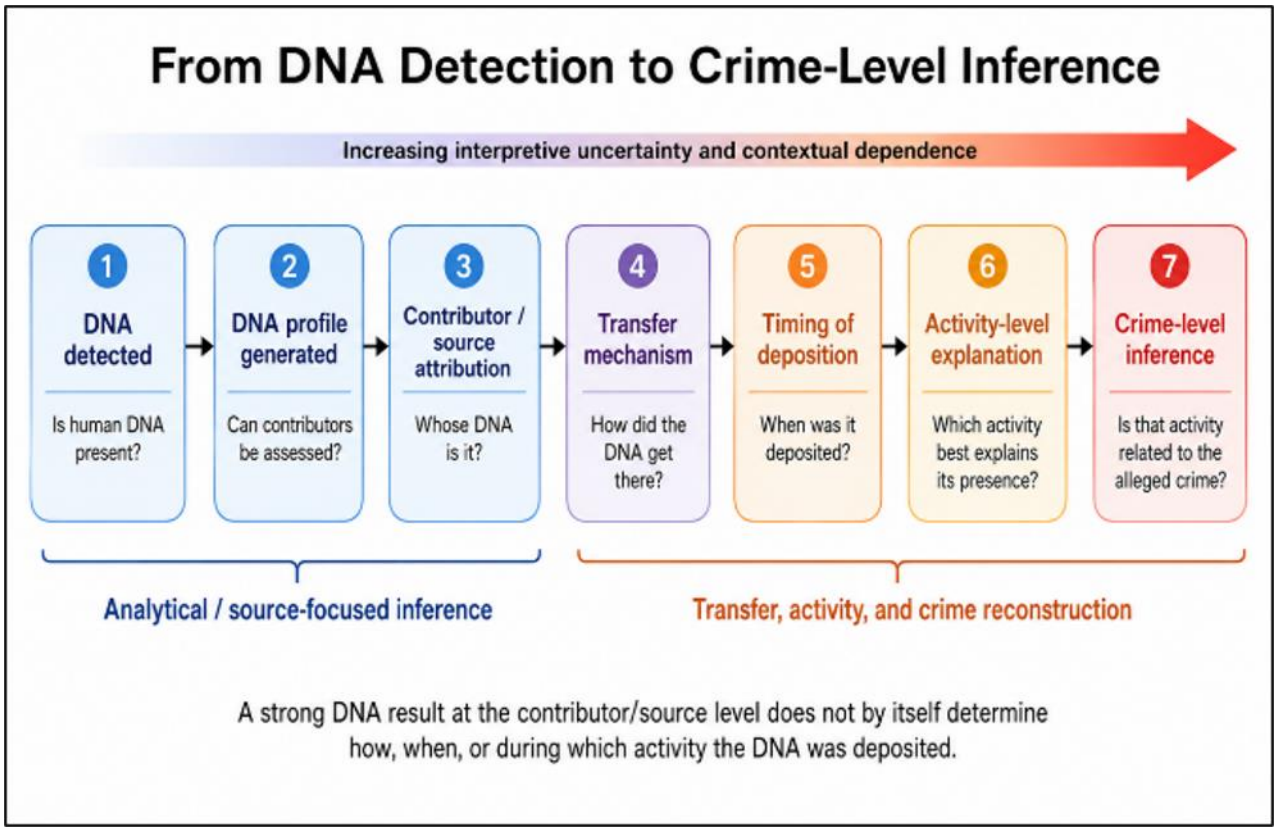

Figure 1: From DNA detection to crime-level inference. Conceptual framework illustrating the progressive transition from laboratory observation to increasingly context-dependent forensic interpretation. The first stages address whether human DNA is detected, whether a DNA profile can be generated, and whether one or more contributors can be associated with the recovered material. These analytical and source-focused conclusions do not, by themselves, establish how the DNA was deposited. Subsequent interpretation requires consideration of the transfer mechanism, the timing of deposition, and the competing activities that could explain the observed DNA findings before any inference is made about their relationship to the alleged crime. The increasing gradient reflects the greater interpretive uncertainty and dependence on case circumstances, transfer, persistence, prevalence/background DNA, recovery, contamination, and alternative activity propositions as the inference moves from DNA detection toward crime reconstruction. A strong contributor- or source-level result therefore should not be interpreted automatically as evidence that the person directly contacted the item, deposited the DNA during the relevant event, or participated in the alleged activity.

Table 1: From Laboratory Observation to Legal Question: Key Terms in DNA Evidence Interpretation. Definitions distinguish analytical observations from higher-level forensic inferences and identify both the question each term can address and the principal interpretive boundary that should not be crossed without additional evidence.

Term / concept	Technical meaning	Plain-language meaning	Question it appropriately helps answer	What it does not establish / key interpretive caution
A. Laboratory observation and analytical description				
DNA detection / biological material recovered	Detection means that DNA above the laboratory's relevant analytical criteria was recovered from the sampled material. It is an observation about the sample processed, not a reconstruction of the event that produced it.	DNA was recovered from the area that was sampled.	"Was detectable DNA present in this sample?"	Detection alone does not establish whose DNA it is, what biological material carried it, whether the person touched the item, when deposition occurred, or whether deposition was related to the alleged offence. [2,14]
DNA quantity	The amount or concentration of human DNA estimated in an extract, usually by quantitative PCR before STR amplification. It reflects both biological deposition and the efficiency/losses of sampling, extraction, storage, and measurement.	How much DNA was measured in the laboratory extract.	"How much human DNA was available for downstream profiling?"	Quantity is not a direct measure of contact duration, force, recency, culpability, or direct versus indirect transfer. Different deposition and recovery histories can produce overlapping quantities. [14–16]
STR DNA profile and profile quality	A pattern of alleles generated at short tandem repeat loci. Profile quality may be described by completeness, signal intensity, balance, degradation, dropout, or other validated laboratory criteria.	The laboratory obtained genetic information that can be compared with known samples.	"What genetic information was recovered, and how informative is it for comparison?"	A complete or high-quality profile does not by itself establish how the DNA arrived, when it was deposited, or whether it resulted from the alleged activity. [2,14,17]
Single-source profile	A profile whose observed data are adequately explained by one contributor under the laboratory's validated interpretation framework.	The DNA data appear to come predominantly from one person.	"How many contributors are needed to explain the observed profile?"	It does not prove that only one person ever contacted the item or that only one person contributed biological material to the broader scene; other contributors may have deposited no recoverable DNA or may be below detection. [14,17]
DNA mixture	A DNA profile containing genetic information from two or more contributors. Mixture interpretation may involve contributor-number assessment, allele sharing, dropout/drop-in, degradation, peak-height information, and probabilistic modelling.	DNA from more than one person is present in the tested sample.	"Can the observed profile be explained by multiple contributors, and what is the evidential value of including a person of interest under specified propositions?"	The number of contributors to a DNA profile is not necessarily the number of people involved in the alleged event, and mixture proportions do not identify who performed which activity. [14,17]

Contributor / number of contributors	A contributor is a person whose DNA is represented in the profile. The estimated number of contributors is a modelling/interpretation decision based on the observed data and validated laboratory procedures.	One or more people contributed DNA to the tested sample.	"How many DNA contributors are needed to explain the profile?"	Contributor number does not establish the number of people who handled the item, were present at the scene, or participated in the offence. [14,17]
Major / minor contributor	Relative descriptors sometimes used for contributors who account for more or less of the observed DNA signal in a mixture.	One person's DNA signal may be stronger than another's.	"Which contributor contributes more of the observed signal?"	"Major" does not mean primary offender, most recent handler, direct depositor, or person who had greatest contact. NIST specifically cautions that such terminology may be misunderstood as implying how or by whom DNA was deposited. [14]
Low-level / trace DNA and stochastic effects	Trace DNA generally refers to small amounts of DNA, often with no visible biological stain and potentially subject to stochastic effects such as allele or locus dropout, peak imbalance, degradation, and occasional drop-in. Terminology and thresholds vary by laboratory.	Very small amounts of DNA can be informative, but the profile may be more variable and complex.	"Is the amount and quality of DNA sufficient for reliable interpretation under validated procedures?"	"Trace" does not identify the biological source or transfer mechanism. Low-level results require careful consideration of analytical uncertainty, background DNA, and transfer history. [14,16,17]
Probabilistic genotyping	Statistical modelling software that evaluates complex DNA profile data, commonly by comparing the probability of the observed DNA findings under competing sub-source propositions while accounting for features such as peak heights, dropout, drop-in, and mixture proportions.	A statistical model helps assess how strongly the DNA profile supports one contributor hypothesis over another.	"How much more probable are these DNA profile data if the person of interest contributed than if an alternative person contributed?"	A sub-source probabilistic-genotyping LR does not, by itself, answer how or when DNA was deposited or whether the person performed the alleged activity. [2,14,17]
Reference sample / known profile	A DNA profile from a known individual used for comparison with an evidential profile. Depending on the case, known contributors may also be conditioned upon in statistical evaluation.	A known person's DNA is used as a comparison profile.	"Is the evidential profile more probable if this known person contributed DNA?"	A comparison association is not evidence that the person was present at the crime scene at the relevant time or performed the alleged activity. [2,14]
Association, "match," inclusion and exclusion terminology	Historically, terms such as "match," "included," "consistent with," or "cannot be excluded" have been used to describe profile comparisons. Contemporary guidance favours an explicit weight-of-evidence statement, commonly a likelihood ratio, because categorical terms can be misunderstood.	The profile may be compatible with a person, but compatibility alone does not quantify evidential strength.	"What is the strength of the DNA findings under the relevant competing propositions?"	Avoid treating "match" or "cannot be excluded" as identification, guilt, or proof of activity. NIST recommends reporting LR values rather than qualitative comparison labels where applicable. [2,14,18,19]

Negative result / non-detection	No reportable DNA profile or no detectable DNA from a particular person was obtained under the sampling and analytical conditions used.	The laboratory did not recover reportable DNA of the type being sought.	"Was DNA from this person detected in the tested sample?"	Non-detection does not prove that contact did not occur. Deposition may have been low, DNA may have been lost or degraded, the sampled area may not contain the trace, or recovery/analysis may have failed to detect it. [3,14–16]
B. Hierarchy of propositions and evidential value				
Proposition	A case-specific statement describing a disputed explanation to be considered when evaluating forensic findings. Evaluative reporting generally compares at least two mutually relevant propositions representing competing positions.	A proposition is a clearly stated version of "what happened" that the scientist uses as a condition for evaluating the findings.	"How probable are the findings if proposition A is true, compared with proposition B?"	The forensic scientist evaluates the probability of the findings given the propositions; the scientist does not determine which proposition is true. [2,3,18,19]
Sub-source-level proposition	A proposition concerned with the donor of the DNA itself, without specifying the cellular material or the activity that led to deposition; for example, whether DNA originated from the person of interest rather than an unknown individual.	It addresses "Whose DNA is this?"	"Did the DNA originate from the person of interest or from another person?"	It does not address whether the person touched the item, how the DNA arrived, when it was deposited, or whether it was associated with the alleged offence. [2,3]
Source-level proposition	A proposition concerning the source of a specified biological material or cellular material where that source is relevant and can be meaningfully addressed; for example, whether a bloodstain originated from a particular person.	It links a specified biological material to a person.	"Did this specified biological material come from the person of interest or from another person?"	Even when the biological source is established, the result does not automatically identify the activity that deposited the material. [2,3]
Activity-level proposition	A proposition concerning an activity that could explain the biological findings, such as competing accounts of contact, assault, prior legitimate interaction, or other events. Evaluation normally requires consideration of transfer, persistence, prevalence/background, and recovery.	It addresses "How or during what activity did the DNA get there?"	"Are the findings more probable if the alleged activity occurred than if the alternative activity occurred?"	Activity-level evaluation does not decide whether the offence legally occurred or whether a defendant is guilty. The proposition wording should describe activities rather than embed untested transfer mechanisms as facts. [3,8,15,16]
Offence-level proposition	A proposition addressing legal responsibility or whether the offence was committed by a person. It incorporates evidence beyond forensic DNA and is ordinarily for the fact-finder rather than the forensic scientist.	It addresses the ultimate legal question, such as guilt or responsibility.	"Did the defendant commit the offence?"	DNA evidence alone generally cannot answer an offence-level question. Scientific conclusions should not be converted into probabilities of guilt. [14,18]

Conditioning information	Information accepted or assumed as part of the evaluation, such as an undisputed contributor, relationship, or case circumstance. The LR is conditional on this information.	Some facts are treated as given so the scientist can evaluate the remaining disputed issue.	"What facts are being assumed when the evidence is evaluated?"	If material conditioning information changes, the evaluation may need to be redone; an LR is not independent of the assumptions on which it was based. [14,18,19]
Likelihood ratio (LR)	The ratio of the probability of the observed findings under one proposition to the probability of the same findings under an alternative proposition, given relevant conditioning information.	It measures how much more (or less) the findings support one stated proposition relative to another.	"Which of the two propositions makes these findings more probable, and by how much?"	The LR is not the probability that a proposition is true, not the probability that the person is the source, and not the probability of guilt. It applies only to the propositions and assumptions actually evaluated. [2,3,14,18,19]
Weight / value of evidence	The evidential value is the degree to which the findings discriminate between the competing propositions. Under the likelihood-ratio framework, this is represented by the LR rather than by the rarity or impressive appearance of the findings alone.	It tells the court how strongly the scientific findings favour one explanation over another.	"How informative are these findings for distinguishing the competing propositions?"	Strong sub-source evidence can coexist with weak, neutral, or different activity-level evidence. Evidential value cannot simply be carried from a lower proposition level to a higher one. [3,18]
Random match probability (RMP)	For an appropriate single-source comparison, the RMP estimates the probability that a randomly selected unrelated person from a specified population would coincidentally have a profile matching the evidential profile, subject to the model assumptions.	It describes how rare a matching profile would be in a specified population.	"How common would this profile be among unrelated people in the relevant population?"	The RMP is not the probability that the person of interest is innocent, not the probability that the DNA came from someone else, and not a probability of guilt. It should not be confused with an LR. [2,14]
Transposed conditional / prosecutor's fallacy	An inferential error in which the probability of the evidence given a proposition is incorrectly treated as the probability of the proposition given the evidence.	It confuses "How likely is this DNA result if X is the source?" with "How likely is X to be the source given this DNA result?"	"Are the expert and legal decision-maker keeping P(findings | proposition) separate from P(proposition | findings)?"	Forensic scientists should report the value of the findings; the fact-finder combines that evidence with all other case information when deciding the proposition or guilt. [14,18]
C. Transfer, persistence, prevalence/background and recovery (TPPR)				
Direct transfer	Transfer of DNA from a person or biological source to the sampled item or area without an intermediate carrier. Direct transfer may occur through touch or through deposition of cellular/body-fluid material.	DNA moves from a person directly onto the item.	"Could direct interaction with the item explain the DNA finding?"	A DNA profile that is consistent with direct transfer does not prove direct transfer occurred, nor does it establish the timing, purpose, duration, or legality of the contact. [3,8,16]
Secondary transfer	Transfer in which DNA reaches the sampled item through at least one intermediary person,	Someone's DNA can reach an object even if that	"Could an intermediary realistically have	Demonstrating that secondary transfer is possible does not establish

	object, surface, glove, or material rather than directly from the original donor.	person did not directly touch it.	transferred the donor's DNA to this item?"	that it occurred in the case. Its probability is highly dependent on the specific sequence of contacts and conditions. [3,8,16]
Subsequent / tertiary transfer	Onward movement of DNA through multiple contacts or after initial deposition, including person-to-object-to-object or person-to-person-to-object pathways. Terminology is not completely uniform across the literature.	DNA may be moved more than once after the original person deposited it.	"Could the trace have been redistributed through additional contacts after initial deposition?"	Multiple-step transfer generally introduces additional uncertainty and is strongly scenario dependent; it should not be inferred solely from a low DNA quantity or partial profile. [8,16]
Persistence	The retention, loss, or continued recoverability of DNA on a person, object, or surface over time and after intervening events such as handling, movement, wearing, washing, cleaning, exposure, or storage.	DNA can remain recoverable after the original contact, sometimes despite later activity.	"Could DNA from an earlier event still be recoverable under these conditions?"	Persistence is not a universal clock. Recovery after a given interval does not allow a precise deposition time to be inferred without highly relevant case-specific data. [3,8,15,16]
Prevalence / background DNA	The presence or expected occurrence of DNA on a person, object, surface, or environment that is not necessarily related to the activity being evaluated. Background DNA may arise from routine use, prior contacts, indirect transfer, shared environments, or unknown contributors.	DNA may already be present before the event under investigation.	"How likely is this DNA or this type of profile to be present even if the alleged activity did not occur?"	Background DNA is not synonymous with laboratory contamination. Its existence means that presence alone may have limited activity-level significance, particularly on shared or frequently handled items. [3,8,14,16]
Recovery	The probability that DNA present on an item is successfully collected, retained through processing, detected, and reported under the laboratory workflow. Recovery is influenced by substrate, sampled area, collection technique, extraction/lysis, storage, analytical sensitivity, thresholds, and stochastic effects.	Even if DNA is present, the laboratory may or may not recover and detect it.	"If DNA is present under this scenario, how likely is the sampling and analytical process to detect it?"	A negative result cannot be interpreted without considering recovery. Conversely, high recovery does not identify the transfer mechanism or activity. [8,14–16]
TPPR framework	A collective framework considering Transfer, Persistence, Prevalence and Recovery when evaluating biological findings given activities. These components influence the probability of obtaining the observed DNA results under each competing activity proposition.	TPPR asks what had to happen for this DNA to be deposited, remain, already be present, and finally be recovered.	"What processes determine whether these findings would be expected under each activity proposition?"	TPPR is not a fixed formula or universal database. The usefulness of published data depends on how closely the experimental conditions match the case circumstances. [3,8,15,16]
Shedder status / deposition variability	Individuals and individual events differ in the amount and composition of DNA deposited. Deposition can vary with biological, behavioural, physiological, environmental, and	Some people or situations leave more recoverable DNA than others, and the same person may not	"How variable is DNA deposition under comparable contact conditions?"	A person should not be treated as having a fixed "shedder type" that predicts every event. Deposition variability limits attempts to infer

	contact-related factors and may change over time within the same person.	deposit the same amount every time.		contact intensity or chronology from DNA quantity alone. [8,16]
DNA quantity / profile quality as transfer indicators	DNA amount, contributor proportion, allele recovery, and profile quality may differ on average between transfer conditions and can be informative within well-designed activity-level models.	More DNA or a better profile may sometimes be more expected after certain contacts, but the distributions overlap.	"Do the observed quantity and profile characteristics change the relative probability of the competing activities?"	There is no universal threshold at which a quantity, RFU level, contributor proportion, or profile completeness proves direct contact, excludes secondary transfer, or establishes recency. [3,8,15,16]
Time since deposition	The elapsed time between DNA deposition and collection. Its effect is mediated by substrate, environment, use, cleaning, movement, biological material, and recovery conditions.	Older DNA may still be detected, and newer DNA may be lost or not recovered.	"Are the findings compatible with deposition at the proposed time under relevant conditions?"	Routine STR results do not provide a validated universal "timestamp." Time-related interpretation should be framed probabilistically and only where relevant data exist. [3,8,16]
Spatial location of DNA on an exhibit	The precise sampling location and distribution of DNA on an item can be relevant to competing activities, particularly when different activities predict different contact areas.	Where the DNA was found can matter, not just whether it was found.	"Would this location be more expected under one activity than the alternative?"	Location is not immutable: DNA can relocate through use, folding, rubbing, handling, packaging, transport, or other site-to-site transfer. A "relevant" location does not automatically prove direct deposition there. [3,15,16]
D. Contamination, evidence integrity and practical legal interpretation				
Contamination	Introduction of DNA or biological material into an evidential sample through investigative, collection, packaging, transport, laboratory, analytical, or other handling processes rather than through the evidential events being evaluated.	DNA may be added to evidence during the investigation or laboratory process.	"Could the DNA finding have been introduced after the evidential event?"	Contamination can mimic a genuine contributor and may not always be identifiable from the profile alone. It should be assessed using handling history, controls, elimination profiles, quality records, and case context. [14,19]
Cross-contamination	Transfer of DNA between exhibits, samples, work areas, tools, personnel, or containers during collection or processing.	DNA from one piece of evidence can be moved to another.	"Were there opportunities for DNA to move between items or samples during handling?"	Separate packaging and controlled workflows reduce risk but do not make cross-contamination impossible. A negative control does not exclude every item-specific transfer event. [14,19]
Glove-mediated transfer	DNA acquired by gloves from a person, surface, or item can potentially be carried and transferred to another location if gloves are not	Gloves protect evidence only when their use is controlled; a	"Could a glove have acquired DNA earlier and redistributed it to the evidence?"	The use of gloves is not proof that contamination could not occur. Glove-changing sequence, contact

	changed appropriately or if contaminated outer surfaces contact evidence.	contaminated glove can itself become a carrier.		history, and handling practices remain relevant. [14,16,19]
Packaging / exhibit-to-exhibit transfer	DNA may be lost, redistributed within an item, transferred to packaging, or transferred between items if contact or movement occurs after collection. Site-to-site transfer can also alter the apparent location of DNA on a single exhibit.	DNA can move after the evidence has been collected.	"Could packaging, movement, or contact after collection have changed where the DNA was recovered?"	The sampled location at laboratory examination may not be identical to the original deposition location. Packaging history can therefore matter to activity-level interpretation. [3,15,16]
Negative controls / blanks	Control samples are processed to detect contamination introduced by reagents, collection materials, extraction, amplification, or laboratory processes, depending on the control type and workflow.	Controls help reveal whether contamination entered through parts of the testing process.	"Did the quality controls show evidence of contamination during the monitored process?"	A clean control supports process integrity but cannot prove that no contamination occurred on the specific exhibit at another time or location. [14,19]
Elimination profiles / staff elimination database	Known DNA profiles from personnel or others with legitimate access to evidence may be compared with unexpected casework profiles to identify potential contamination sources.	Known staff DNA can help identify accidental contamination.	"Could an unexpected profile originate from a person who legitimately handled the evidence?"	Failure to match an elimination profile does not rule out contamination from unprofiled persons or other sources. Policies and legal authority for such databases vary by jurisdiction. [14]
Chain of custody	The documented chronological record of collection, possession, transfer, storage, and handling of an exhibit or sample.	It records who had the evidence, when, where, and under what documented transfer history.	"Can the handling history of the exhibit be reconstructed?"	A complete chain-of-custody record supports traceability but is not itself proof that contamination, transfer, or handling error did not occur. [14,19]
Contextual information and human factors	Case information, workload, fatigue, expectations, communication, workflow design, and other human/system factors can affect discretionary decisions in forensic analysis and interpretation. Good practice manages task-irrelevant information and documents decision points.	People and systems influence how evidence is handled and interpreted, even when analytical methods are validated.	"Was the analyst exposed only to information needed for the task, and were key decisions made under controlled, reviewable conditions?"	The presence of contextual information does not automatically invalidate a result; the concern is whether avoidable information or system pressures could influence discretionary judgments and whether safeguards were in place. [14]
Investigative use versus evaluative use	Investigative use helps generate or prioritize leads; evaluative use assesses the strength of findings given explicit competing propositions, usually through a likelihood-ratio framework.	A DNA result can be useful for finding people to investigate without yet answering what the DNA proves in court.	"Is this result being used to generate a lead, or to assess evidential support between competing explanations?"	An investigative association should not automatically be presented as evaluative proof. The purpose, assumptions, and level of proposition should be explicit. [14,18]

Bayesian network	A graphical probabilistic model representing dependencies among propositions, activities, transfer/persistence events, contributor states, and observed findings. It can structure complex activity-level evaluations and make assumptions explicit.	A Bayesian network is a structured map of how different possible events could lead to the DNA findings.	"What causal and probabilistic pathways connect the competing activities to the observed DNA results?"	The network is only as defensible as its structure, assumptions, and probability assignments. It does not replace case-specific propositions or relevant empirical data. [3,8]
Association with an object or scene	A DNA association establishes that the recovered profile data are more or less probable under specified contributor propositions. The biological material itself was recovered from the sampled location at the time of collection.	The person's DNA can be associated with the sampled evidence; that is not the same as proving the person was physically present there during the crime.	"What does this DNA association establish about the sampled item, and what further inference is being proposed?"	DNA may reach an object through direct contact, indirect transfer, background presence, legitimate prior contact, or contamination. Presence of DNA on an item does not automatically prove presence at the crime scene or participation in the offence. [3,14,16]
Alternative explanation / competing activity history	A scientifically relevant alternative account that could plausibly generate the findings, such as prior legitimate contact, secondary transfer, background DNA, contamination, or a different sequence of activities.	The same DNA result may be compatible with more than one history.	"What realistic alternative activity could also explain these findings, and how probable would the findings be under that alternative?"	The existence of an alternative mechanism does not mean it occurred. The scientific task is to compare the probability of the findings under clearly specified competing propositions, not merely list possibilities. [3,8,16,18]
Expert–fact-finder boundary	The forensic scientist evaluates the scientific findings given propositions and relevant information; the judge or jury evaluates the propositions themselves in light of the totality of the evidence and the applicable legal standard.	The expert explains what the DNA evidence supports; the court decides what actually happened and whether the legal test is met.	"Is the expert reporting the value of the findings rather than deciding guilt or the truth of the proposition?"	Experts should avoid giving a probability of guilt, deciding the ultimate legal issue, or presenting a source-level LR as though it were the probability that the alleged activity occurred. [3,14,18,19]

Note. The hierarchy of propositions does not impose rigid boundaries in every case, and terminology may vary between jurisdictions and laboratories. Transfer, persistence, prevalence/background, and recovery are factors used to evaluate findings under activity propositions; the propositions themselves should describe the competing activities rather than assume a transfer mechanism. The table is an interpretive aid and does not replace case-specific expert evaluation.

A DNA result has no fixed evidential meaning outside the proposition it addresses. Modern forensic profiling can provide extremely strong support for an association between recovered biological material and a person, but that strength should not be transferred automatically to conclusions about contact, deposition, activity, or involvement in an offence. These questions occupy different levels of the hierarchy of propositions [1,2,4,8]. As shown in **Fig. 1**, movement from DNA detection to crime-level inference is a movement from analytical observation toward increasingly context-dependent reconstruction. Establishing whose DNA is present is therefore not equivalent to establishing how, when, or why it became present.

The first inferential boundary arises at the level of the sample itself. A positive result establishes that detectable human DNA was recovered from a defined sampling area under a particular collection and analytical workflow and, when sufficient genetic information is obtained, may permit assessment of contributor number and comparison with reference profiles. A negative result establishes only that DNA attributable to a particular person was not detected under those conditions. It does not demonstrate that the person never contacted the item. Transfer may have been limited; DNA may have been lost, degraded, redistributed, or masked in a mixture; the relevant area may not have been sampled; or the workflow may have failed to recover sufficient material. Recovery is affected by substrate, sampling location, collection method, extraction strategy, environmental exposure, and time [4,11–13]. Positive and negative results are therefore conditional on the pathway from deposition to recovery, not direct records of the event. **Table 1** summarizes the terminology and inferential boundaries used throughout this review.

3.1 From contributor attribution to transfer history

Where a DNA profile provides strong support for the person of interest as a contributor, the appropriate conclusion remains proposition-specific. Under a sub-source proposition, the question is typically whether the DNA originated from the person of interest rather than from an unknown unrelated individual. A likelihood ratio at this level may provide very strong support for contributor attribution. It does not, however, identify the biological or behavioural process by which that person's DNA reached the sampled location [2,8]. A separate source-level question may concern the biological material from which the DNA originated, where this has been independently assessed. Even identification of the biological source does not necessarily determine the activity responsible for its deposition.

This distinction becomes particularly important for trace DNA, where the cellular or fluid origin and the deposition mechanism are often unknown. DNA associated with a person can reach an item through direct contact, one or more indirect transfer steps, previous legitimate use, persistence from an earlier event, deposition by another person carrying that individual's DNA, movement between areas of the same exhibit, packaging-mediated transfer, or contamination during investigation and examination [4,20–25]. Several of these histories can produce an apparently indistinguishable source-level observation. The detection of Person A's DNA on an object is therefore compatible with the proposition that Person A handled the object, but it is not synonymous with proof of handling, still less proof that handling occurred during the alleged offence.

Terminology can itself import an activity assumption into what should remain an observation. Terms such as touch DNA, handler DNA, and wearer DNA may imply a known deposition mechanism even when the cellular or fluid origin and the transfer route are unresolved. A profile recovered from an area expected to have been touched may include DNA deposited during the questioned contact, DNA already present on the surface, DNA transferred indirectly during the same interaction, or contributions from earlier or later contacts. The term touch DNA is therefore potentially misleading when the mechanism is unknown; the more neutral term trace DNA is preferable unless contact is independently established or forms part of a controlled experimental design [4]. The same caution applies to wearer and handler DNA, because recovery from clothing or a handled object does not independently establish who wore or handled it.

3.2 DNA quantity, profile quality and contributor position are not provenance markers

The amount and quality of DNA recovered can contain useful information, but neither provides a unique signature of transfer mechanism. Controlled studies often demonstrate, on average, greater DNA recovery or more complete profiles after direct than indirect transfer. Such group-level differences are important for activity-level modelling, but their distributions overlap and are affected by numerous interacting variables. Substrate type, moisture, pressure and friction, duration and frequency of contact, the biological material involved, donor-specific deposition propensity, previous activities, environmental exposure, cleaning, persistence and recovery efficiency can all alter the quantity and composition of the final sample [4,12,20,21,26]. The individual depositing the most DNA is therefore not necessarily the individual who contacted the exhibit most recently, most extensively, or during the activity of interest. Variation between individuals can substantially alter contributor proportions. Experimental studies involving hand contact have shown that individuals differ in their propensity to deposit recoverable DNA and that a comparatively high depositor can dominate a profile over another person involved in the same or a subsequent contact [4,21]. DNA on hands is also not composed exclusively of material originating from the hands themselves: self-DNA transferred from other body regions and non-self DNA acquired from people, objects and the surrounding environment may subsequently be

deposited during contact. Short-term physiological and behavioural conditions may further influence the quantity and profile quality of touch DNA deposited during otherwise similar periods of interaction [27]. Consequently, labels such as “major contributor”, “high shedder”, or a relatively high DNA quantity should not be converted into an unsupported narrative of recent or direct contact.

Profile completeness is subject to the same limitation. A complete profile from a person of interest may be entirely compatible with direct transfer, but completeness alone does not establish directness. Conversely, a partial profile following genuine direct contact is plausible where transfer was limited or subsequent persistence and recovery were unfavourable. A mixed profile does not necessarily indicate simultaneous contact by the contributors, because components may have accumulated at different times and through different routes. Background DNA and use history can additionally alter both the detectability and relative representation of a target contributor. For these reasons, quantity, RFU, allele count, profile completeness and mixture position are observations that may inform a probabilistic comparison of competing activities; they should not be used as stand-alone classifiers of primary versus secondary transfer.

3.3 Location is informative, but it is not self-interpreting

The spatial location of DNA on an exhibit can carry substantial evidential information where competing activities predict different patterns of deposition. DNA recovered from a grip surface, an interior garment region, beneath fingernails or from another activity-specific location may therefore be more informative than DNA detected indiscriminately somewhere on the exhibit. However, spatial relevance should not be confused with proof of deposition at that location during the alleged event. DNA may persist from previous use, move between adjacent areas, be transferred through repeated handling, or relocate during packaging, transportation and examination [22,23]. The sampled location is thus the endpoint of a transfer–persistence–recovery history, not necessarily the site of the original deposit.

This distinction is especially important where the prosecution or defence narrative depends heavily on DNA being recovered from a particular region. The location should be interpreted in conjunction with the item's ownership and use history, accessibility of the sampled area, expected background DNA, opportunities for direct and indirect transfer, the time between the alleged event and collection, intervening activities, packaging and handling history, and the recovery protocol. A biologically or behaviourally relevant location may increase the discriminating value of the findings between competing propositions, but only when the alternative mechanisms capable of producing the same spatial observation are incorporated into the evaluation.

3.4 Evidential strength is specific to the level of proposition

The principal safeguard against overinterpretation is to maintain the distinction between the probability of the findings given competing propositions and the probability that a proposition is true given the findings. At activity level, the forensic scientist evaluates the observations E under at least two competing activity propositions, for example:

$$LR = P(E \mid H_p, I) / P(E \mid H\_d, I)$$

where H_p and H_d represent competing propositions and I denotes relevant conditioning information. The likelihood ratio describes how much more probable the observed findings would be under one proposition than under the alternative; it does not give the probability that either activity occurred [1,2,8]. This direction of reasoning is fundamental. Statements such as “direct transfer is more likely because the DNA profile is strong” move from the observation to the truth of an activity and risk transposing the conditional. The appropriate question is instead whether the observed DNA quantity, profile composition, location and other findings would be more probable if one proposed activity had occurred than if the competing activity had occurred.

Activity-level assessment consequently requires information that is largely unnecessary for sub-source attribution. Relevant considerations include the proposed sequence of contacts, transfer opportunities, biological material, persistence interval, expected prevalence of the person's DNA, background contributors, item use and ownership, cleaning, movement and packaging, recovery efficiency and any potential contamination pathway. These elements are commonly considered collectively within the transfer, persistence, prevalence and recovery (TPPR) framework [4,8]. The importance of each component is case-dependent, and interactions between them may be substantial. The available empirical data may also be only partially comparable with the circumstances under examination. Activity-level evaluation should therefore be balanced between competing propositions, logically correct, transparent about the data and assumptions used, and sufficiently robust that modest changes in uncertain parameter values do not reverse the conclusion [4,8,28].

A further consequence is that evidential strength does not automatically propagate upward through the hierarchy of propositions. A DNA profile may provide overwhelming support that Person A contributed DNA while providing little discrimination between two activities that both readily predict Person A's DNA on the exhibit. For example, if an owner

acknowledges regular prior use of an item but disputes using it during an offence, the sub-source issue may effectively be uncontested; the relevant question becomes whether the observed quantity, distribution and contributor composition are more probable under recent crime-related handling than under prior legitimate use and persistence. The source-level likelihood ratio cannot answer that question. The same principle applies where the disputed alternative is indirect transfer, contamination, or another legitimate activity.

Ultimately, DNA evidence is one component of reconstruction rather than a substitute for reconstruction. It may establish a strong association between biological material and an individual, and when appropriate TPPR data and well-formulated competing propositions are available it may also contribute substantially to evaluating activities. It cannot, in isolation, determine when the DNA was deposited, identify a unique transfer pathway, establish that a particular contact occurred, or determine whether the person committed the alleged offence. Those higher-level conclusions require integration of the DNA findings with the circumstances of the case and the remaining evidence by the fact-finder. The distinction between DNA attribution and activity attribution therefore provides the conceptual foundation for the sections that follow: the scientific problem is no longer simply whether a person's DNA is present, but which of the plausible histories of transfer, persistence, background deposition and contamination best explains the observations.

4 HOW DNA CAN REACH AN EXHIBIT OR SCENE

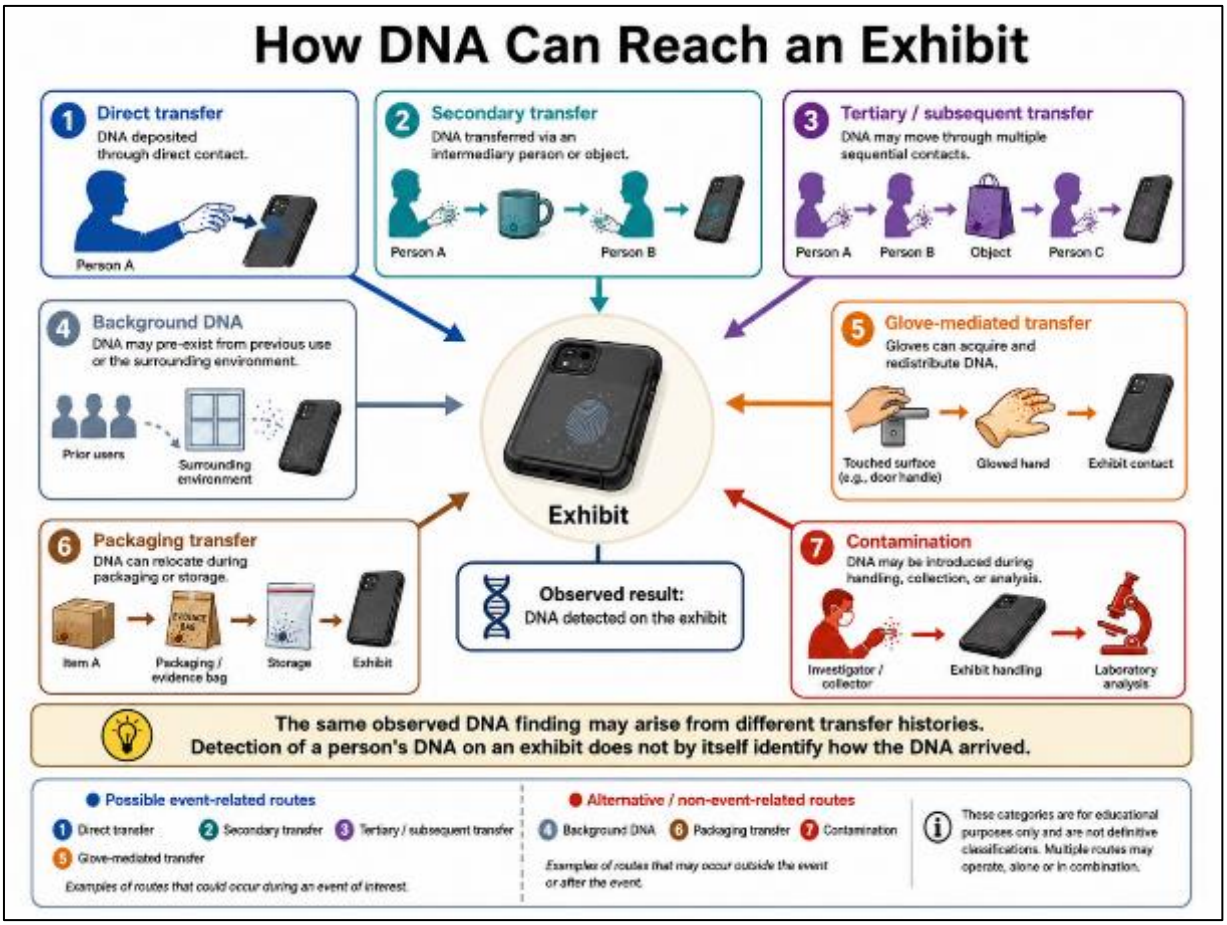

Figure 2: How DNA can reach an exhibit. Conceptual overview of the principal pathways by which a person's DNA may become detectable on an evidential item. DNA may be deposited through direct contact, transferred indirectly through an intermediary person or object, or redistributed through tertiary or subsequent contacts. DNA already present from previous users or the surrounding environment may contribute to the background DNA associated with an exhibit, while gloves can acquire DNA from one surface and subsequently transfer it during later handling. DNA may also relocate between items or sampling areas during packaging, transport, or storage, and contamination may be introduced during crime-scene collection, evidence handling, laboratory processing, or other investigative procedures. These pathways are not mutually exclusive and may operate sequentially or simultaneously. Consequently, the observation that a person's DNA is present on an exhibit does not, by itself, identify the route of transfer, establish direct contact, determine when deposition occurred, or demonstrate that the DNA was deposited during the alleged criminal activity. The distinction between potentially event-related and alternative or non-event-related pathways is illustrative rather than absolute and must be evaluated in the context of the competing case propositions, transfer opportunities, persistence, background DNA, recovery conditions, and handling history.

Table 2: Routes to a DNA Finding and Their Interpretive Consequences. Plausible pre- and post-event pathways by which DNA may reach an exhibit, the principal factors known to modify those pathways, and the inferential limits of the resulting finding. Several pathways may operate sequentially or simultaneously, and the same observed profile may be compatible with more than one history.

Route / pathway	Mechanism and realistic example	Evidence base and key determinants	What the finding may support	What it cannot establish	Interpretive consequence / question to ask
A. Contact-based and indirect transfer before evidence collection					
Direct transfer	DNA passes from the donor directly to the sampled item or area without an intermediary. Example: a person grips a phone, knife handle, steering wheel, garment, or skin surface.	Direct deposition is common but not inevitable and varies markedly among donors, substrates, contact conditions, and prior activity. In one paired experimental design, detectable primary transfer occurred in 71% of trials; direct-transfer studies consistently show strong between-person variability. [4,16,29]	The finding can be consistent with direct contact and, where appropriate empirical data exist, direct contact may be more probable than specified indirect alternatives.	It does not prove that direct contact occurred, identify when the contact occurred, determine why the item was touched, or show that contact took place during the alleged offence. A full profile or high DNA quantity is not unique to direct transfer.	Ask: What competing non-crime-related opportunities for deposition existed, and are the data sufficiently case-relevant to compare direct with indirect transfer?
Secondary transfer — person mediated	DNA first transfers from the donor to another person and is then deposited by that intermediary onto the exhibit. Example: Person A shakes hands with Person B; Person B later handles an axe, phone, or door handle.	Secondary transfer is empirically demonstrated and can remain possible after substantial delay. Non-self DNA acquired by handshaking has been recovered from a later-contacted object after 40 min and 5 h. Probability depends on donor shedding, amount initially acquired, sequence and duration of contacts, intervening activity, substrate, and background DNA. [20,21,24,30]	It provides a scientifically credible alternative when the donor had contact with an intermediary but no proven direct contact with the final exhibit.	Possibility alone does not establish that secondary transfer occurred in the case. Conversely, an informative or even complete profile cannot by itself exclude an indirect route.	Ask: Who could have acted as an intermediary, what was the contact sequence, and how closely does the experimental evidence match the case circumstances?
Secondary transfer — object/surface mediated	DNA passes through an intermediate object or surface before reaching the exhibit. Example: DNA deposited on a shared mug, table, tool, clothing item, or	Object-mediated transfer has been repeatedly demonstrated under controlled and realistic conditions. Transfer efficiency depends strongly on whether DNA is wet/dry, the donor and	It can explain DNA on an exhibit despite absence of direct donor–exhibit contact.	Profile quantity, completeness, or contributor rank generally cannot identify the intermediate object	Ask: What shared objects or surfaces connected the donor, other people, and the exhibit before collection?

	work surface is later picked up and redeposited elsewhere.	recipient substrate, friction/pressure, surface porosity, contact sequence, and pre-existing DNA. [4,30,31]		or distinguish this route uniquely from direct or person-mediated transfer.	
Tertiary / subsequent transfer	DNA is redistributed through two or more sequential transfer events after the original deposition. Example: Person A → Person B → object → Person C → exhibit.	Multiple-step transfer is experimentally documented. In the McCrane–Mulligan design, detectable tertiary transfer occurred in 27% of trials, compared with 71% primary and 50% secondary transfer under that specific experimental framework. Investigator-mediated experiments also demonstrate onward movement through sequential contacts. [29,31,32]	It supports the proposition that an apparently remote donor may reach an exhibit through a multi-step contact chain when a plausible sequence exists.	The number of transfer steps cannot be inferred simply from low DNA quantity, a partial profile, or contributor status. Multi-step transfer rates are highly scenario dependent.	Ask: Is there a realistic contact chain, and does each required step have empirical support under sufficiently similar conditions?
Biological carrier / reservoir transfer	Hands, sleeve cuffs, fingernails, clothing, and other body-associated surfaces can accumulate self- and non-self DNA and later act as carriers. DNA deposited during a later touch may therefore include material acquired earlier from people, objects, or the donor's own body.	Hands are dynamic reservoirs rather than clean transfer sources. Non-self DNA was detected in 95% of hand/sleeve-cuff samples in one workplace study; active hands deposited more DNA than hands prevented from normal touching, and DNA reaccumulates after handwashing. Fingernails can also retain mixed foreign DNA in non-criminal settings. [33–36]	It provides a biological explanation for unexpected contributors and for indirect transfer through routine human activity.	A contributor detected on a hand, cuff, or fingernail does not establish recent direct contact, assault, defensive interaction, or the activity in which the DNA was acquired.	Ask: What reservoirs could have carried the DNA, what activities occurred before the alleged event, and what background prevalence should be expected?
B. Pre-existing DNA, habitual use, and temporal persistence					
Background / pre-existing DNA	DNA is already present on the exhibit or in the surrounding environment before the questioned event because of routine use, prior visitors, shared spaces, indirect transfer, or unknown contributors.	Background DNA is common on real objects and shared environments. In co-working experiments, non-prevalent DNA was detected in 20/22 traces (91%), including DNA attributable to co-workers or cohabitants. Background DNA can also alter the detectability	It supports an alternative explanation in which DNA presence reflects ordinary historical contact or the normal biological background of the item/environment.	The presence of a named person's DNA does not establish recent contact or event involvement; conversely, calling a profile "background" requires case-specific support	Ask: Who routinely uses, lives with, works with, stores, cleans, or shares the item or location, and what DNA would reasonably be expected before the event?

		and apparent contribution of a target donor. [4,26,37]		rather than assumption.	
Habitual-use accumulation and contributor dominance	Repeated use can build a persistent DNA reservoir from an owner or regular user, while DNA from a one-time event may be lower, transient, masked, or mixed with habitual-user DNA.	Realistic office and regularly used object studies show that the habitual user can dominate DNA profiles even after another person has recently handled or occupied the space. In an office-reuse study, 98% of samples yielded profiles and 90% were mixtures; owner DNA could remain dominant after intruder contact and subsequent owner reuse. [25,38,39]	A dominant profile may be consistent with habitual or repeated use and can help explain why an expected event-related contributor is minor or absent.	The major contributor is not automatically the most recent handler, the person with the longest single contact, or the person involved in the alleged crime.	Ask: Is the item personal or routinely used, and could repeated historical deposition explain contributor proportions better than the alleged event?
Persistence of earlier deposition	DNA deposited before the questioned event remains recoverable at collection. Persistence is influenced by substrate, time, environment, cleaning, washing, wearing/use, friction, storage, and subsequent handling.	Persistence can extend well beyond the original contact and varies markedly by matrix and activity. DNA from earlier users has been observed after later reuse of items/spaces. On skin, mixed perpetrator profiles in one simulated study remained recoverable up to 48 h but were strongly affected by washing and physical activity. [4,25,38,40]	It supports the possibility that an older, innocent or unrelated deposition remains detectable during investigation.	Persistence is not a validated universal clock. DNA quantity, profile completeness, or mere survival does not provide a precise time-since-deposition estimate without highly relevant case-specific data.	Ask: What happened between possible deposition and sampling—use, washing, cleaning, movement, weather, storage, or additional contacts?
C. Redistribution after contact, during handling, or during evidence packaging					
Glove-mediated transfer	A glove acquires DNA from a person, surface, or exhibit and later deposits that DNA onto another area or item. The original donor need not touch the final exhibit.	DNA is frequently recovered from the exterior of gloves used in casework, but transfer probability varies with glove type, contamination level, contact history, and conditions. Working-glove experiments show that gloves can carry DNA over time, while another realistic study observed secondary transfer in only 1/81 transfer trials—illustrating strong scenario dependence. A recent	It provides a credible alternative route during scene examination, laboratory handling, burglary-type scenarios, or any activity involving reused/contaminated gloves.	Wearing gloves does not make a contact DNA-neutral; however, the mere existence of glove contamination does not prove that a particular transfer occurred.	Ask: Were gloves changed at appropriate transitions, what did each glove contact before the exhibit, and were glove practices documented?

		comparative study also found recoverable DNA and high profile completeness on contaminated gloves. [41–44]			
Laundering / cleaning / environmental redistribution	Washing, cleaning, wiping, or environmental movement can remove DNA from one location while transferring or redistributing it to another item or area.	Laundering studies demonstrate that biological material can move between garments; in one study, spermatozoa, vaginal epithelial DNA, and household-member DNA were transferred during washing, and some experimental conditions yielded complete genetic profiles on previously clean underwear. Cleaning may likewise reduce, smear, or redistribute traces rather than simply erase them. [4,45]	It can explain DNA on an item that the donor did not directly handle during the questioned event and can also explain loss of expected DNA.	A post-wash or post-cleaning profile does not by itself reveal whether the original deposition was direct, when it occurred, or which item was the source of redistributed DNA.	Ask: Was the item washed, wiped, cleaned, worn with other items, or exposed to processes capable of relocating biological material?
Within-item / site-to-site relocation	DNA initially deposited on one region of an exhibit is transferred to another region of the same item through folding, rubbing, movement, packaging, transport, or repeated handling.	Activity-level modelling has shown that site-to-site transfer can materially change interpretation when the location of DNA is central to the allegation. A packaged-underwear model explicitly incorporated cross-transfer between waistband and groin areas; published packaging data included detectable site-to-site transfer in 1/19 tests under one set of conditions. [4,46]	It supports the possibility that DNA detected in a highly relevant anatomical or functional area was deposited elsewhere first and subsequently relocated.	The recovery location cannot automatically be treated as the original deposition location, particularly after movement or packaging.	Ask: Was the exhibit folded, compressed, rubbed, transported, or otherwise manipulated in a way that could relocate DNA between areas?
Packaging / exhibit-to-exhibit transfer	DNA moves from an exhibit to the packaging, from packaging back to the exhibit, or between co-located items during storage and transport. Packaging can therefore become an intermediate transfer surface.	Police and laboratory studies identify evidence bags and high-contact handling environments as potential transfer routes. Packaging experiments show that DNA can be lost from the original deposition site, transferred to the package interior, and relocated to other parts of an exhibit. [23,46,47]	It provides an alternative explanation for DNA appearing at a new location after collection and highlights the evidential importance of separate, appropriate packaging.	DNA found after packaging does not necessarily reflect the spatial pattern present at the crime scene; package-associated transfer cannot be excluded simply because	Ask: How was each item packaged, moved, reopened, stored, and examined, and what surfaces or items shared a package or handling sequence?

				items were collected separately in time.	
D. Contamination introduced by investigative or laboratory processes					
Crime-scene / investigator-mediated contamination	DNA from investigators, police personnel, medical staff, shared tools, PPE, work surfaces, or previously handled items is introduced to or redistributed on evidence during search, collection, documentation, transport, or examination.	Operational datasets confirm that this is a measurable pathway. Austrian monitoring identified 347 police-attributable contamination incidents among ~46,000 crime-scene samples (0.75%). Swiss national data identified 709 contamination events, ~86% attributed to police personnel. Routine-search experiments also demonstrate investigator-mediated sequential transfer. [32,48–50]	It can explain unexpected DNA that is unrelated to the crime and supports the need for elimination databases, controlled workflows, PPE, documented glove changes, and contamination review.	Absence of a staff match does not prove absence of contamination: the source may be an unknown person, object, prior case, shared environment, or indirect chain.	Ask: Who handled the scene/exhibit, in what order, with what PPE/tools, and were staff/elimination profiles and contamination events reviewed?
Laboratory / pre-analytical contamination	DNA is introduced during evidence receipt, opening, sub-sampling, examination, extraction, amplification setup, equipment use, or laboratory surface contact. Contamination may be staff-derived, sample-to-sample, reagent-associated, or environmentally mediated.	Long-term operational studies document laboratory-origin contamination and show that targeted controls can reduce it. In one Swiss laboratory series, 260 contaminated traces were found among 77,962 trace samples (~0.3%); enhanced procedures reduced staff-related contamination by >70%. Laboratory surfaces and equipment can also act as DNA reservoirs. [48,49,51,52]	It provides a recognized alternative explanation for low-level, unexpected, or mixed DNA and justifies negative controls, cleaning, workflow separation, staff elimination databases, and incident investigation.	A negative blank does not rule out every contamination pathway, and contamination cannot be excluded solely because laboratory procedures were compliant on paper.	Ask: Were controls satisfactory, were staff/elimination comparisons performed, were concurrent cases/reagents/surfaces reviewed, and were any quality incidents recorded?
Human-factor / implementation failure as a contamination amplifier	A technical safeguard exists but is inconsistently implemented because of workload, interruption, glove-change behaviour, communication, handover, layout, training, or other human/organizational conditions.	Contamination prevention depends on reliable implementation of PPE, workflow separation, cleaning, environmental monitoring, negative controls, elimination databases, and chain-of-custody documentation. Human-factor reviews emphasize that written procedures do not eliminate risk	It supports examination of the entire handling system when an unexpected profile is found, rather than restricting the inquiry to analytical instrumentation or reagents.	A quality-certified process cannot be assumed to be contamination-free in every instance; conversely, a procedural deviation does not prove that a particular profile arose from contamination.	Ask: Were safeguards actually implemented at the relevant time, and is there contemporaneous documentation sufficient to reconstruct the handling pathway?

		if routine practice is unreliable. [50,53]			
E. Integrated interpretation of the observed DNA finding					
Multiple concurrent pathways / mixed transfer history	Two or more mechanisms operate together—for example, background DNA plus direct contact, glove transfer plus packaging relocation, or prior persistence plus investigator-mediated redistribution.	Modern TPPR literature shows that transfer, persistence, prevalence/background, recovery, and contamination are interdependent rather than isolated variables. Activity-level evaluation therefore requires explicit competing propositions and data relevant to the actual contact chain and evidence history. [4,9,15,16,54]	It supports a case-specific comparison of alternative histories rather than a binary assumption that DNA either arrived directly during the crime or is irrelevant.	The observed profile alone usually cannot identify a unique history. Strong source/sub-source support must not be carried automatically into a conclusion about activity, timing, or crime involvement.	Ask: Which complete histories—not isolated mechanisms—are genuinely disputed, what observations would be expected under each, and how relevant are the available TPPR data?

Note. Pathways are not mutually exclusive or ranked by probability. Their relevance depends on the competing propositions and case circumstances. "Possible" denotes scientific plausibility under some conditions, not that the mechanism occurred in the case. DNA quantity, profile completeness, contributor rank, and recovery location should not be used as stand-alone indicators of directness, recency, or crime-related deposition. TPPR = transfer, persistence, prevalence/background, and recovery.

Once contributor attribution is separated from activity inference, the critical question is how the biological material reached the sampled location. The alternatives extend well beyond a binary choice between 'direct' and 'secondary' transfer. DNA can move through people, objects, clothing, gloves, tools, packaging, and other surfaces; it can be acquired, lost, redistributed, retained temporarily, and transferred again. Different contributors within one trace may also have arrived by different routes and at different times. Transfer is therefore better represented as a set of contributor-specific histories than as a single property of the sample [4]. **Fig. 2** summarizes the principal routes, **Table 2** sets out their interpretive consequences, and **Table 3** collates representative evidence.

Transfer terminology should reflect what is known rather than imply an unobserved sequence. Direct or primary transfer describes deposition from the person or biological source to the sampled item without an intermediate transfer surface. Indirect transfer describes movement through at least one intermediary. 'Secondary transfer' is often used for the first indirect step but is also used more broadly for transfer after the initial deposit; tertiary and subsequent transfer describe additional sequential steps [4,29]. When the number of intermediaries is not established by the case information, 'indirect transfer' is the more defensible description because assigning a transfer generation can imply a history that the DNA result itself does not establish.

4.1 Direct transfer is a pathway, not a guaranteed outcome

Direct contact is an obvious route by which DNA may reach an exhibit, particularly when hands, skin, saliva, blood, or other biological material contact a surface. The amount transferred, however, is highly variable and a contact event does not guarantee detectable deposition. Transfer depends on the biological material, donor-related deposition propensity, substrate properties, moisture, pressure and friction, contact duration and sequence, and subsequent recovery [4,20,21]. These factors interact rather than operating independently. The same person may therefore leave markedly different quantities on different surfaces or during different contacts, and two people performing nominally similar actions may generate different profile outcomes.

Paired and scenario-based studies show why direct contact cannot be treated as synonymous with detectable deposition. McCrane and Mulligan detected primary transfer in 71% of 22 trials, secondary transfer in 50%, and tertiary transfer in 27% within the same paired experimental framework [29]. These are study-conditioned frequencies, not general transfer probabilities. Their value is that direct deposition sometimes failed to produce a detectable result while indirect and multi-step transfer remained detectable. In a video-recorded one-hour social interaction, direct contact resulted in detectable transfer in 87% of non-intimate samples and clothing, yet the most recent toucher was not invariably detected and surfaces contacted by all four participants did not yield all four profiles [55]. The recovered profile is therefore a selective product of transfer and recovery, not a complete record of everyone who contacted the surface.

Deposition propensity can also change within the same person over short intervals. DNA on hands reaccumulates after washing and varies with daily activity [33,34]. In a paired crossover study, competitive gaming produced greater DNA recovery and STR profile quality on keyboards and mice than routine browsing, alongside increased palmar moisture and heart rate [27]. The study does not establish physiological activation as a casework classifier of transfer; it shows that deposition is dynamic even within an individual. A weak profile therefore does not uniquely indicate brief or indirect contact, and a strong profile does not uniquely indicate forceful, recent, or crime-related handling.

4.2 Person-mediated indirect transfer

Hands are especially important intermediaries because they continuously acquire biological material from the body, other people and the surrounding environment. Following contact between two individuals, DNA from one may be carried on the other person’s hand and deposited during a later interaction with an exhibit. Controlled handshake studies have repeatedly demonstrated this route. Szkuta et al. detected non-self DNA acquired by handshaking on subsequently contacted surfaces, with detectability decreasing as additional contacts and delays intervened; everyday activities could either reduce the transferred component or, through repeated interaction with previously contacted objects, permit retention and re-transfer [56]. In a separate activity-level study, handshake-acquired non-self DNA was detected on an axe handle after delays of 40 min and 5 h, but not after an 8-h delay under the tested conditions [24]. These observations show both the plausibility of delayed person-mediated transfer and its dependence on the intervening history.

Secondary transfer can, under some conditions, challenge intuitive assumptions about contributor position. Cale et al. detected secondary transfer in 85% of samples after two minutes of hand-to-hand contact followed by immediate knife handling; in five samples, the secondary contributor was the only or major contributor despite never touching the knife [57]. The study is important because it demonstrates a possible outcome under a transfer-favouring design, not because it establishes that secondary transfer commonly produces major profiles. Other experimental systems have produced much lower frequencies. Contributor position and profile strength therefore cannot determine transfer route without scenario-relevant data [4,20,29].

4.3 Object-mediated, tertiary and subsequent transfer

An intermediary need not be a person. DNA deposited on a phone, cup, table, garment, tool, vehicle surface or other object may be acquired during later contact and moved to a new location. Contact between two DNA-bearing surfaces may also be bidirectional: each can lose some material while acquiring material from the other [4,30]. The resulting trace can therefore contain DNA that was already present on the recipient surface, DNA directly deposited during the current contact, and DNA that the contacting person or object had acquired elsewhere. In routine environments, these routes are superimposed on repeated use rather than occurring as isolated laboratory events.

With each additional transfer step, the quantity of the original deposit available for onward movement would generally be expected to diminish, but the composition of the final trace need not change monotonically. At each contact, other DNA can be added, dominant contributors can mask minor ones, and a previously transferred component can be reacquired. The "DNA parking" concept describes one such pathway: DNA is secondarily deposited onto an intermediate object, remains there for a period, is later picked up again, and is then transferred to another surface [4,56]. Studies on regularly used knives likewise show that direct and indirectly transferred components can persist across repeated handling and contribute to later samples [25]. This provides a mechanistic explanation for why the temporal gap between an original interpersonal contact and final deposition need not correspond simply to continuous persistence on the intermediary's hand. Multi-step pathways can branch, intersect, or be interrupted by washing, cleaning and unrelated contacts, producing histories that are difficult to infer from the terminal profile alone.

Realistic social settings show how quickly direct, indirect, and background contributions become entangled. Cahill et al. followed four participants during a recorded residential interaction and recovered profiles ranging from single-source to four-person mixtures. Unknown contributors were detected in 34% of all samples and 41% of non-intimate samples, and DNA from cohabiting partners who were not present at the study location was also recovered [55]. Pre-existing background DNA can also alter both transfer and subsequent detection of a target contributor [26]. These observations go beyond demonstrating that indirect transfer is possible: they show that indirect and background contributions can coexist with genuine direct contacts in ordinary environments. Contributor history must therefore be reconstructed within the contact network of the scene rather than inferred from presence or mixture proportion alone.

4.4 A single contact can produce simultaneous direct and indirect transfer

Classifying an entire trace as "primary" or "secondary" can be conceptually wrong when different contributors within the same sample arrived by different routes. During a single hand contact, the person making the contact may directly deposit their own biological material while simultaneously depositing non-self DNA previously acquired from another person, object or body site [4]. The same event may therefore contain both direct and indirect transfer. Moreover, a person can deposit DNA and acquire DNA from the recipient surface during the same contact, creating bidirectional exchange. Transfer route is consequently contributor-specific, and sometimes even component-specific, rather than sample-wide.

For mixtures, this contributor-specific view is essential. A profile containing the handler as a major contributor and another person as a minor contributor does not establish that both people touched the exhibit or did so at the same time. Conversely, the physical handler may be absent or weakly represented if little DNA was deposited or if pre-existing material from another individual dominates the recovered sample. In an office-use study, the owner could remain the sole or major contributor after subsequent contact by an intruder, while the later toucher could be excluded [38]. Contributor rank therefore cannot be read as a direct chronology of contact.

4.5 Biological reservoirs: hands, clothing and fingernails as mobile sources

The intermediary surface may be part of the person. Hands are not clean conveyors of self-DNA; they are dynamic reservoirs containing material derived from the individual and from recent interactions. Henry and Zieger detected non-self alleles in 95% of hand and sleeve-cuff samples collected under everyday conditions, with more non-self than self-DNA in 10.5% of hand samples and 26% of sleeve-cuff samples [33]. The composition also changed during the working day, and one participant showed more than a sixfold increase in hand DNA between morning and afternoon. These data support a critical interpretive point: when a person touches an exhibit, the contact can simultaneously deposit DNA from the toucher and biological material they acquired elsewhere.

The amount and composition of hand DNA are also influenced by individual and temporal factors. Studies of shedder behaviour show reproducible between-person differences, but also substantial within-person variation across conditions and time [35,58,59]. Following handwashing, Alketbi and Goodwin observed progressive DNA reaccumulation, with significantly greater recovery at 30 min than at 5 min post-wash [34]. Thus, handwashing may alter the available reservoir without resetting it to a DNA-free state. The relevant question is not simply whether an individual is a "good" or "poor" shedder, but what DNA was available on the relevant body surface at the time of the contact and how subsequent activities modified that reservoir.

Fingernails provide another biologically plausible reservoir. Subungual material can accumulate through self-contact, grooming, cohabitation, handling, scratching and indirect transfer, while the protected nail environment can retain mixed and foreign DNA [36]. Treating foreign DNA beneath fingernails as intrinsically indicative of recent aggressive contact therefore overlooks alternative acquisition pathways. The same principle extends to sleeve cuffs, clothing and other frequently contacted body-adjacent surfaces: they can receive DNA during routine activity and later participate in transfer without the original donor being present at the final location [33].

4.6 Gloves, tools and packaging are active transfer vectors

Forensic and non-forensic intermediaries can extend the transfer chain after an event. Gloves are particularly important because they are often assumed to prevent contamination, yet their outer surfaces can acquire DNA from every item they contact. Casework observations found DNA on the majority of examined gloves and identified exhibit removal and repackaging as periods of elevated transfer risk [41]. Experimental burglary models further show that contaminated working gloves can transfer a previous wearer's DNA to an object that person never handled: Otten et al. recovered the first wearer's profile from the final screwdriver in 6 of 19 scenarios, all involving high shedders [42]. In contrast, Tanzhaus et al. observed only one successful secondary transfer among 81 glove-to-surface experiments under their tested conditions [43]. The disparity is informative rather than contradictory; glove-mediated transfer is strongly dependent on glove material, donor deposition, prior use, contact history, recipient substrate and the sensitivity of the workflow.

Recent experimental work has also demonstrated substantial transfer from deliberately contaminated forensic gloves under favourable contact conditions, with glove type and decontamination procedure affecting both retained DNA and subsequent profile recovery [44]. Such data are useful for mechanism and mitigation, but should not be converted into universal transfer probabilities. The same reasoning applies to examination tools. Forceps, fingerprint brushes and other implements can acquire DNA from one item and redistribute it if they are reused without adequate decontamination [31,60]. Thus, PPE and tools reduce risk only when the handling sequence and replacement or decontamination practices interrupt the transfer pathway.

Packaging creates an additional post-collection transfer environment. Earlier work demonstrated loss of DNA from the original deposit to the inside of packaging and relocation to other regions of the same exhibit or to co-packaged items [22]. Fonnelop et al. further showed that DNA on the exterior of evidence bags could be transferred during examination [23]. More recent packaging experiments confirm that movement is strongly dependent on the biological material and the degree of exhibit-package contact. In unsecured packaging, touch DNA transferred from the exhibit to the directly contacted side of the package in all four tested replicates, whereas suspending and securing the exhibit prevented detectable touch DNA and saliva transfer under the tested conditions; blood behaved differently because flaking permitted movement even when direct contact was reduced [47]. Packaging is therefore not a neutral interval between scene and laboratory. It can alter both the amount and spatial distribution of DNA before the exhibit is sampled.

4.7 Transfer history is scenario-dependent, not profile-determined

The transfer literature supports two distinct conclusions. Direct, indirect, and multi-step transfer are all empirically established mechanisms, but demonstration of a mechanism does not identify the probability that it produced a particular case finding. Reported frequencies vary widely because studies differ in donor combinations, biological material, contact sequence, substrates, delay, intervening activities, background DNA, sampling strategy, analytical sensitivity, and interpretation thresholds [4,20,29,31,42,43,57]. Frequent secondary transfer in one experimental system and rare transfer in another are not necessarily contradictory; they estimate different conditional probabilities.

The forensic question is therefore not 'Can secondary transfer occur?' but 'How probable are the observed findings if the DNA arrived by the proposed direct route rather than the specified alternative route?' The same discipline applies to gloves, tools, packaging, and biological reservoirs. Mechanistic plausibility is the basis for formulating propositions, not the endpoint of evaluation. **Fig. 2** makes this multiplicity explicit: several histories can converge on the same terminal observation—a person's DNA detected on an exhibit. Sections 5 and 6 examine the two major modifiers of those histories: persistence and background DNA before collection, and contamination or relocation introduced through investigative and laboratory processes after the event.

5 TIME, PERSISTENCE, PREVALENCE AND BACKGROUND DNA

A DNA profile recovered from an exhibit is an observation at the time of sampling, not a timestamp of deposition. Before collection, biological material may persist, decline, move, accumulate through repeated use, or become obscured by later deposits; the sampled surface may also contain DNA from routine users, close associates, previous visitors, or the wider environment. The DNA detected after an alleged offence may therefore have been deposited during that event, before it, after it, or through several episodes of contact.

Table 3: Key Evidence from the Literature. Representative empirical, operational, methodological, and evaluative evidence relevant to transfer, persistence, background DNA, redistribution, contamination, recovery, and activity-level interpretation. Studies are grouped by the forensic question they inform rather than by laboratory technique so that experimental findings can be read alongside casework and quality-system evidence.

Evidence domain / phenomenon	Representative studies	Key evidence from the literature	Interpretive significance and boundary
A. Transfer mechanisms and sequential movement of DNA			
Direct, secondary, and tertiary transfer can all occur	McCrane SM et al. (2024) [29] van Oorschot RAH et al. (2019) [4] Fonneløp AE et al. (2015) [31]	Controlled and scenario-based studies demonstrate a progressive transfer chain rather than a simple direct/indirect dichotomy. McCrane and Mulligan detected primary, secondary, and tertiary transfer in 71%, 50%, and 27% of 22 paired transfer trials, respectively. Fonneløp et al. additionally showed primary-to-glove-to-secondary-surface transfer during simulated investigative handling, with transfer strongly affected by the original substrate and subsequent contact sequence. [4,29,31]	DNA on an exhibit can be compatible with more than one transfer generation. The presence or quality of a profile cannot, by itself, identify whether the donor directly contacted the final exhibit or whether DNA passed through one or more intermediaries; transfer probabilities remain scenario-specific.
Substrate morphology and contact mechanics modify transfer efficiency	Goray M et al. (2010) [30] Zoppis S et al. (2014) [61] Alketbi SK et al. (2019) [12] Singh HP et al. (2026) [62]	Experimental work shows that transfer/recovery depends strongly on the combination of primary substrate, recipient substrate, friction or pressure, skin area, and surface morphology. Goray et al. found greater transfer from non-porous primary substrates and to porous secondary substrates, with friction increasing transfer. Alketbi and co-workers likewise demonstrated significant effects of surface type, extraction method, and non-porous surface morphology on recovered DNA and STR profile quality. [12,30,61,62]	A DNA result is partly shaped by physical contact mechanics and the surfaces involved. Data from one substrate/contact system should not be treated as a universal transfer probability for another material or contact history.
Delayed person-mediated secondary transfer remains possible	Taylor D et al. (2017) [20] Szkuta B et al. (2018) [24] Onofri M et al. (2023) [54]	Bayesian and empirical studies demonstrate that secondary transfer can remain plausible after an interval between the initial donor-intermediary contact and final deposition. Controlled experiments have recovered non-self DNA on a later-contacted object after delays of 40 min and 5 h. In a credit-card study, direct transfer produced more DNA (mean 1.60 ng) and greater POI profile completeness (~90–91%) than secondary transfer (0.657 ng; ~68–72%), but informative secondary-transfer profiles still occurred. [20,24,54]	Higher DNA quantity or profile completeness may shift probabilities in a defined model, but neither metric uniquely identifies direct contact. The appropriate question is comparative: how well do the findings fit specified direct and indirect propositions under relevant conditions?
Shedder status and pre-existing DNA alter transfer outcomes	Fonneløp AE et al. (2017) [21] Jansson L et al. (2024) [58]	Experimental studies consistently show substantial between-person variability in deposition. In one longitudinal study, low shedders produced <0.2 ng in 67.5% of samples, whereas high shedders produced >0.5 ng in 80%. Jansson et al. found	Contributor abundance is influenced by donor biology and prior hand activity as well as the questioned event. A major contributor or high DNA quantity should not automatically be equated with

	Jansson L et al. (2022) [35]	active hands deposited significantly more DNA than hands prevented from touching objects (2.1 ± 2.7 ng vs 0.83 ± 1.1 ng), supporting acquisition of DNA through routine contact with the body and environment. Attack-scenario research further showed interaction between shedder status and background DNA. [21,35,58]	the most recent toucher or the person responsible for the alleged activity.
Shared environments generate complex, distributed transfer histories	Cahill A et al. (2024) [55] Onofri M et al. (2024) [37] Henry L et al. (2024) [33]	Realistic social and workplace studies show that DNA from participants and non-participants can move across people, objects, hands, and clothing. In a co-working study, non-prevalent DNA occurred in 20/22 (91%) traces, and known co-workers or co-inhabitants were identifiable as additional contributors in some samples. Repeated hand/sleeve sampling also demonstrated routine self- and non-self DNA carriage. [33,37,55]	Shared spaces can create plausible non-crime-related pathways to an evidential item. Background and associate DNA should therefore be considered when reconstructing transfer opportunities rather than treated automatically as unexpected or incriminating.
B. Biological deposition variability and endogenous DNA reservoirs			
Hands rapidly reacquire DNA after washing	Alketbi SK et al. (2024) [34] Jansson L et al. (2022) [35] Kanokwongnuwut P et al. (2018) [59]	Temporal hand studies show that washing does not create a stable DNA-free baseline. Alketbi and Goodwin observed significantly greater DNA recovery at 30 min than at 5 min after handwashing ($p<0.01$), with strong inter-individual differences. Complementary work found increasing cellular material within minutes after washing and evidence that ordinary hand activity increases deposited DNA. [34,35,59]	Hand DNA is dynamic. The amount available for transfer at any moment depends on time since washing, subsequent touching, and individual shedding behaviour; it cannot be inferred solely from whether hands were recently washed.
Short-term physiological and behavioural state can change deposition	Alketbi SK et al. (2027) [27] Alketbi SK (2018) [11]	A randomized paired crossover study of 24 adults (96 touch DNA samples) found competitive gaming produced greater physiological activation and substantially higher DNA recovery than routine browsing. Mean recovery increased from 0.18/0.21 ng on browsing keyboard/mouse samples to 0.40/0.60 ng during gaming; profile completeness and RFU also increased significantly ($p<0.001$). Broader reviews identify pressure, moisture, behaviour, substrate, and donor characteristics as interacting determinants of touch DNA success. [11,27]	Deposition is not a fixed personal trait. The same person can leave materially different DNA quantities and profile qualities under different physiological and behavioural conditions. Such differences do not permit retrospective identification of a specific activity from DNA quantity alone.
Fingernails can act as semi-enclosed DNA reservoirs	Alketbi SK (2026) [36] Henry L et al. (2024) [33]	The fingernail literature shows accumulation through direct contact, secondary/tertiary transfer, grooming, and environmental exposure. Foreign DNA is detectable beneath fingernails in non-criminal contexts, while studies of hands and sleeve cuffs show that non-self DNA is commonly carried during routine activity. [33,36]	Foreign DNA beneath fingernails may be highly relevant in assault investigations, but its presence requires an activity-level assessment of contact, grooming, persistence, background prevalence, and alternative transfer routes; it is not synonymous with a recent struggle.

Shedder classifications are useful but imperfect	Jansson L et al. (2024) [58] Kanokwongnuwut P et al. (2018) [59] Fonneløp AE et al. (2017) [21]	Repeated-deposition studies demonstrate reproducible high/low tendencies for some donors, yet intermediate donors can fluctuate and experimental condition, activity history, and background DNA affect observed results. Studies therefore support a continuum of deposition propensity more than an immutable binary classification. [21,58,59]	"Good" and "poor" shedder labels should be treated as contextual descriptors, not deterministic explanations for a case result. Case interpretation should retain uncertainty about within-person and between-event variability.
C. Background DNA, persistence, and context of prior use			
Worn clothing carries wearer, associate, and background DNA	Szkuta B et al. (2019) [39] Lehmann VJ et al. (2015) [26] Onofri M et al. (2024) [37] Zacher M et al. (2024) [38]	An inter-laboratory study generated 448 profiles from worn upper garments and found substantial variation by wearer, garment area, wearing occasion, and laboratory. Other studies show that background DNA can modify detection of a target contributor and that intruder DNA can persist in an office after the owner returns and reuses the space. Co-working experiments further demonstrate frequent non-prevalent DNA. [26,37–39]	DNA on clothing or in a repeatedly occupied environment may reflect cumulative histories rather than one event. Interpretation should consider ordinary use, close associates, site-specific background, later reuse, and the location sampled.
Deposition location and sampled area matter on fabric	Alketbi SK et al. (2022) [63] Alketbi SK et al. (2022) [64] Alketbi SK (2022) [65] Alketbi SK et al. (2026) [66]	Alketbi studies show that fabric type, deposition area, sampled area, collection method, and swab wetting volume materially affect recovery. One study reported mean recovery of 0.80 ng/µL from a polyester/cotton blend versus 0.14 ng/µL from woven cotton; another found significantly greater recovery from the chest of a T-shirt than from the buttocks of trousers, with time and deposition-area interactions. Minitapes can outperform swabs on some fabrics, while greater wetting volume can improve recovery from absorbent materials. [63–66]	Spatial differences on clothing can reflect substrate and sampling behaviour as well as the underlying activity. A weak/negative result from one fabric area does not exclude contact, and a strong result from another area does not prove that deposition occurred there during the alleged event.
DNA can persist on human skin after contact	Alketbi SK et al. (2025) [40] Alketbi SK (2023) [67]	A simulated skin-persistence study collected 168 samples across 1–72 h plus washing/activity conditions; DNA remained recoverable over extended intervals, while allele recovery changed with time and intervening activity. A strangulation-scenario study also showed that swabbing technique significantly altered recovery from neck skin, with different optimal approaches for cotton and nylon swabs. [40,67]	DNA recovered from skin can support contact-related hypotheses but is influenced by time, washing, activity, anatomy, and collection technique. Presence on a body site does not by itself date the contact or establish the alleged assault mechanism.
Environmental conditions and surface structure alter persistence	Alketbi SK et al. (2019) [68] Chahal RB et al. (2026) [69]	At room conditions, one study found no significant decline in recovered touch DNA from 3 h to 1 week, whereas high-temperature and cold/high-humidity conditions produced significant time effects. On wood, rough unfinished surfaces yielded more DNA than smooth sealed surfaces (0.052 vs	Persistence is substrate- and environment-dependent; there is no universal decay curve. Time-since-deposition inference from DNA amount or profile completeness should therefore be avoided unless supported by highly relevant empirical data.

		0.022 ng/μL; p<0.001), and humidity/environmental exposure altered recovery over time. [68,69]	
Sand and outdoor contamination can substantially change recoverability	Alketbi SK et al. (2019) [70] Alketbi SK et al. (2025) [71]	Controlled sandy-surface experiments found strong effects of collection and extraction method, while casework-style wearable items exposed to sand showed that cotton swabs could outperform minitapes and that recovery differed by item type. These studies demonstrate that environmental material can modify adhesion, release, and sampling efficiency. [70,71]	Outdoor traces may be weak or altered because of substrate contamination rather than absence of contact. Environmental context must therefore be separated from assumptions about whether or when a person interacted with the item.
Unusual, perishable, and routinely cleaned surfaces can retain detectable DNA	Alketbi SK (2020) [72] Salleh HM et al. (2026) [73] Singh VS et al. (2025) [74]	touch DNA has been recovered from perishable food surfaces over multiple days, including full profiles from banana skin over a one-week room-temperature study. A 270-sample edible-surface study showed surface-dependent decline over 7 days. Door-handle research found 2–3-fold differences between swab types, higher recovery from wood/plastic than metal, and reduced recovery with more frequent cleaning. [72–74]	The forensic meaning of a result depends on the history and physical properties of the item. Persistence on an unusual substrate supports feasibility, not a precise deposition time or proof of crime-related contact.
D. Gloves, packaging, and contamination pathways			
Gloves are DNA carriers, but onward transfer is scenario-dependent	Goray M et al. (2019) [41] Otten L et al. (2019) [42] Tanzhaus K et al. (2021) [43] Mehta AA et al. (2025) [44]	Casework observations show DNA is commonly recoverable from glove exteriors. Working-glove experiments demonstrate persistence of wearer DNA and occasional transfer to tools or surfaces, but a realistic burglary study detected only 1 secondary transfer among 81 trials despite DNA on 92/98 glove exteriors. In a comparative study, uncleaned gloves transferred full STR profiles to mock evidence in ~80–83% of contact events; nitrile retained less DNA than latex/vinyl and hypochlorite substantially reduced recoverable DNA. [41–44]	Glove-mediated transfer is a credible mechanism, not an automatic explanation. Probability varies with glove material, contamination level, contact sequence, pressure/friction, and cleaning; glove use does not guarantee protection against DNA redistribution.
Packaging can relocate DNA within and between evidential surfaces	Fonneløp AE et al. (2016) [23] Stella CJ et al. (2026) [47] Taylor D et al. (2024) [46]	Police-unit investigations identified transfer from evidence-bag exteriors to exhibits. Controlled packaging studies using blood, saliva, and touch DNA showed loss from deposit sites and transfer to package interiors under transport/handling, with mitigation dependent on how the exhibit was secured. Activity-level modelling of packaged underwear demonstrated that site-to-site transfer can alter the evidential value of DNA recovered from anatomically relevant areas. [23,46,47]	The sampled location after transport may not be the original deposition location. Packaging history should be considered whenever spatial distribution is central to competing activity propositions.
Police and investigator contamination is a	Pickrahn I et al. (2017) [48]	Austrian monitoring identified 347 police-attributable contamination incidents among ~46,000 crime-scene	Unexpected DNA can arise before laboratory receipt. Staff elimination databases, documented

measurable operational pathway	Basset P et al. (2018) [49] Carson S et al. (2022) [32]	samples (0.75%). Swiss national data identified 709 contamination events; ~86% originated from police personnel, and 96% involved touch DNA. Experimental search activities show that movement, repeated handling, and sequential contacts can mediate investigator-to-object and object-to-object DNA transfer. [32,48,49]	handling sequences, scene discipline, glove-change practice, and contamination investigation are interpretive safeguards, not merely administrative quality measures.
Laboratory controls and PPE can materially reduce contamination risk	Basset P et al. (2019) [51] Alketbi SK et al. (2025) [75] Alketbi SK (2024) [76]	A Swiss laboratory identified 260 contaminated traces among 77,962 samples (~0.3%); additional controls reduced staff-related contamination by >70%. A multi-laboratory PPE study reported contamination rates of 5% under strict protocols versus 30% with inconsistent practice ($p<0.001$), with improper glove removal and contact with contaminated surfaces prominent error modes. Laboratory reviews emphasize physical separation, dedicated equipment, decontamination, and environmental monitoring. [51,75,76]	Contamination prevention is effective but not absolute. A negative blank or nominal SOP compliance does not exclude all pre-analytical or handling pathways; implementation evidence and incident records remain relevant to interpretation.
Chain of custody and human implementation affect evidential reliability	Alketbi SK (2023) [77] Alketbi SK (2024) [50] Abdullahi AA et al. (2026) [53] Kloosterman A et al. (2014) [78] Jeanguenat AM et al. (2017) [79] Dror IE et al. (2011) [80]	Reviews and operational error studies identify handling, packaging, training, PPE practice, interruptions, and human error as recurrent vulnerabilities. Quality-system analyses emphasize that safeguards depend on implementation under workload and routine conditions. Cognitive-bias research also shows that DNA mixture interpretation can vary among experienced examiners and may be influenced by context, supporting structured review and context management. [50,53,77–80]	Reliability is a pathway property extending from scene to report. Interpretation should distinguish biological transfer uncertainty from preventable process error and should avoid treating a technically valid DNA profile as automatically immune to handling, quality-system, or cognitive influences.
E. Recovery and detectability as modifiers of the observed DNA result			
Surface type and collection method influence whether DNA becomes observable	Alketbi SK et al. (2019) [12] Singh HP et al. (2026) [62] Alketbi SK (2018) [11]	Controlled studies demonstrate significant effects of surface type, extraction, morphology, and swabbing technique. Glass has produced higher yields than paper in comparative work; smooth glass yielded higher recovery/profile completeness than textured plastic in a 135-sample morphology study. Reviews also document substantial failure rates in routine touch DNA recovery. [11,12,62] Additional studies of cotton-swab validation, non-porous collection, trace DNA quantification, doctoral synthesis, microFLOQ direct sampling, post-PCR clean-up, and extraction/direct-amplification workflows further demonstrate that the	The laboratory observation is filtered through the recovery process. Low quantity, partial profiles, or non-detection may reflect collection/substrate limitations rather than absence of prior contact; recovery efficiency does not identify the transfer route.

		analytical pathway can materially change recoverability and profile quality. [81–87]	
Porous evidence requires substrate-specific recovery strategies	Alketbi SK (2022) [65] Alketbi SK et al. (2022) [64] Alketbi SK et al. (2025) [88] Alketbi SK et al. (2026) [66]	On fabric, minitapes can outperform cotton/nylon swabs, while fabric composition and sampled area substantially affect yield. A 100-sample face-mask study found higher mean DNA concentration with minitapes than cotton swabs (0.41 vs 0.17 ng/μL; $p<0.05$). A 270-sample wetting-volume study showed significantly improved recovery and profile completeness with increased wetting volume, particularly on highly absorbent fabrics. [64–66,88] Direct-amplification collection and dual DNA/fingerprint recovery studies similarly show that evidence-recovery strategy can alter the DNA information retained for analysis. [89–91]	Differences among collection methods can change whether a contributor becomes reportable. Interpretation of weak or absent DNA should therefore be grounded in the validated recovery method and substrate rather than treated as a direct measure of contact.
Large casework datasets show that analytical success is exhibit-dependent	Alketbi SK et al. (2025) [6] Aidarous NI et al. (2025) [92] Hoffmann R et al. (2026) [7]	Dubai Police casework included 14,513 collected samples; 8,592 were profiled and 7,003 were positive (81.5%), while trace samples achieved ~64% success. In 1,769 vehicle samples, 67.5% of targeted sites generated interpretable profiles, with steering wheels outperforming door handles. A 47,097-sample Australian dataset likewise found large recovery differences by exhibit type and showed that high recovery did not always correspond to high investigative added value. [6,7,92]	Recovery rate and investigative utility are different endpoints. Selection and interpretation should consider whether an item is likely to yield informative, non-redundant evidence, not merely whether DNA can be detected.
Outdoor, edible, and structured surfaces illustrate the breadth of recovery variability	Alketbi SK et al. (2019) [70] Alketbi SK et al. (2025) [71] Salleh HM et al. (2026) [73] Chahal RB et al. (2026) [69]	Studies of sand-contaminated items, edible surfaces, and wood consistently demonstrate interactions among substrate morphology, environmental exposure, time, and collection method. Rough wood retained more DNA than sealed wood, smooth fruits generally yielded more complete profiles than highly textured/fragile fruits, and sand changed optimal collection strategy. [69–71,73]	Methodological breadth is useful for scene planning, but such studies mainly inform recoverability. They should not be converted into claims about how, when, or during which activity the DNA was deposited.
F. Activity-level evaluation and legal meaning			
Activity-level evaluation requires explicit competing propositions	Kokshoorn B et al. (2017) [93] Onofri M et al. (2023) [54] Taylor D et al. (2017) [20]	Bayesian frameworks show that the same DNA findings can have different evidential value depending on whether the disputed issue concerns who acted, whether an activity occurred, or how DNA was deposited. Direct/secondary credit-card experiments demonstrate how empirical transfer data can inform such comparisons, while modular Bayesian networks separate transfer, persistence, and recovery components. [20,54,93]	The evidential question should be framed at the level actually disputed. A strong sub-source association cannot simply be carried upward as equally strong support for touching, timing, or the alleged criminal activity.

Site-to-site and packaging transfer must be represented when location matters	Taylor D et al. (2024) [46] Fonneløp AE et al. (2016) [23] Stella CJ et al. (2026) [47]	Activity-level modelling demonstrates that omitting within-item or package-mediated transfer can overstate support for an allegation when DNA is recovered from a location considered crime-specific. Empirical packaging studies provide data on movement, loss, and redistribution that can be incorporated into competing propositions. [23,46,47]	Spatial location is evidentially meaningful only after plausible post-deposition movement is considered. The original deposition site and the sampled site should not be assumed to be identical.
Transfer/recovery research used for evaluation requires transparent, standardized data	Gill P et al. (2026) [15] van Oorschot RAH et al. (2019) [4]	Current FSI: Genetics guidance requires sample-level transfer/recovery datasets, harmonized quantification, total and contributor-specific DNA recovery, mixture proportions from continuous probabilistic genotyping, and sufficient methodological detail for replication. Major reviews similarly emphasize TPPR variables and the limits of generalizing across conditions. [4,15]	Activity-level numbers are only as defensible as the relevance and transparency of the underlying data. Published frequencies should not be imported into casework when propositions, substrates, contact sequences, recovery methods, or environmental conditions differ materially.
Misinterpretation can convert a strong DNA result into an unsupported crime-level conclusion	Gill P (2019) [9] Hoffmann R et al. (2026) [7] Alketbi SK et al. (2025) [6]	Case-based analyses of miscarriages of justice show how background DNA, contamination, secondary transfer, and overreliance on sub-source statistics can mislead when the mechanism and timing of deposition are not evaluated. Operational studies also show that a recovered profile may be analytically successful but add little new investigative information, depending on exhibit type and expected users. [6,7,9]	The appropriate endpoint is not “DNA found = crime proven.” DNA evidence should be integrated with transfer opportunities, persistence/background, handling history, competing propositions, and other case information while preserving the distinction between scientific evaluation and legal decision-making.

Note. This is an evidence synthesis rather than a ranking of studies or a set of universal transfer probabilities. Experimental frequencies depend on donor characteristics, substrate, biological material, contact sequence, time, environment, recovery method, analytical workflow, and study design. Numerical observations should be applied only to propositions and conditions sufficiently relevant to the case. TPPR = transfer, persistence, prevalence/background, and recovery.

Persistence and prevalence change the meaning of a finding even when contributor attribution is not disputed [4,26,39]. **Table 3** summarizes representative evidence relevant to these processes.

For interpretive purposes, persistence and prevalence should be kept conceptually distinct. Persistence concerns the probability that biological material deposited at an earlier time remains recoverable at the later sampling time. Prevalence concerns the probability that DNA from a specified person or class of individuals is already present at a relevant location under the circumstances being considered. "Background DNA" is used here for biological material present independently of the questioned deposition event, particularly material accumulated through prior use, ordinary social interaction, environmental exposure, or previous handling. These concepts overlap in practice: background DNA is often background precisely because an earlier deposit has persisted. Neither, however, supplies a simple measure of time since deposition [4,26].

5.1 Persistence is conditional and cannot be treated as a molecular clock

The intuitive expectation that more DNA, a more complete profile, or a higher contributor proportion indicates more recent deposition is not generally defensible. The amount recovered at time t is conditioned by the amount initially deposited, the biological form of that material, the receiving substrate, environmental exposure, subsequent contact, cleaning, movement and the efficiency of recovery and analysis. Initial deposition itself can vary by orders of magnitude between individuals and contact events [4,34,35,58,59,94]. A later sample containing more total DNA than an earlier sample can therefore reflect additional self- or background DNA, redistribution, differences in recovery, or mixture composition rather than preservation of the original deposit. Time may influence detectability, but it is only one component of the trajectory from deposition to observation.

Persistence experiments show why a universal decay model is not defensible. Raymond et al. followed deposited DNA on outdoor residential surfaces and laboratory-stored controls for up to six weeks. DNA on externally exposed window-frame and vinyl surfaces declined significantly, whereas comparable material stored on glass in a dark laboratory environment did not show the same decline [95]. Kaesler et al. later recovered informative STR profiles from fabric, steel, and rubber stored indoors for up to nine months; under semi-exposed outdoor conditions, informative profiles persisted to nine months on fabric, six months on steel, and three months on rubber [96]. These are not fixed persistence windows. They demonstrate that the same elapsed time can have very different consequences depending on substrate and environment.

Shorter-term studies show the same interaction between time and environment. Alketbi and Goodwin found no significant time effect on recovered touch DNA over 3 h to 1 week under room conditions, whereas time, environmental condition, and surface interactions were significant under high-temperature and high-humidity conditions [68]. Large-scale proxy-DNA experiments have likewise shown strong surface-specific behaviour and differences between cellular and cell-free DNA persistence [97]. Such studies identify mechanisms and relative trends, but their numerical results remain conditioned on the deposited material and experimental system. Proxy deposits, controlled laboratory surfaces, and known high shedders are not numerically interchangeable with unknown casework traces.

Human skin presents an even more dynamic substrate because the receiving surface is biologically active and subject to washing, friction, clothing contact, perspiration and continual shedding. In simulated skin-to-skin assault experiments, Bowman et al. found offender DNA most readily after immediate collection, with substantially reduced recovery at 3 h and 24 h [98]. A later simulated violent-contact study reported mixed profiles containing perpetrator alleles up to 48 h under the tested conditions, but no detectable perpetrator alleles at 72 h; washing and physical activity also affected recovery [40]. These studies support prompt sampling of relevant skin sites, but they do not establish a maximum evidential interval. Detection after many hours does not prove recent contact, while failure to detect after a shorter interval does not exclude genuine contact.

5.2 Habitual use creates a persistent DNA history that later contact may not erase

Many evidential items are not clean surfaces awaiting a single crime-related touch. Knives, tools, phones, clothing, vehicles, office equipment and household objects often carry DNA accumulated during repeated use. When a second person interacts with such an item, the resulting profile reflects competition between an established reservoir and the new deposit. The relative contribution of the regular and subsequent user depends on their deposition propensities, the nature and duration of each contact, substrate, intervening activity and recovery method. The last person to touch an item is therefore not necessarily the major contributor, and the major contributor is not necessarily the person who used it during the alleged offence [4,25,38,99,100].

Regularly used knives provide a useful model. Meakin et al. observed marked inter-individual differences in DNA accumulated during simulated regular use, and DNA from the regular user persisted for at least one week. DNA acquired from a brief handshake and transferred indirectly to the same knives could also persist, but generally as a minor component under the tested conditions [25]. In burglary-tool experiments, Pfeifer and Wiegand found that after a

second user performed a simulated burglary bare-handed, the first user could be attributed to the handle profile in only 1 of 40 cases; when the second user wore gloves, first-user DNA was detected more frequently, consistent with reduced replacement or masking by the second user [99]. These contrasting outcomes illustrate why persistence cannot be separated from subsequent use: a later user may add DNA, remove earlier DNA, redistribute it, or leave the pre-existing profile largely dominant.

Studies specifically comparing habitual and brief use reach the same broader conclusion. Atkinson et al. found substantial variation among common household items and users, but regular-user DNA frequently remained prominent after short-duration use by another person [100]. In a realistic office-occupation study, Zacher et al. generated profiles from 98% of 196 samples, 90% of which were mixtures. The office owner was the sole, major or majority contributor in 77% of samples, compared with 14% for the temporary intruder; intruder DNA nevertheless remained detectable after subsequent owner contact, and indirect or contactless transfer was also observed [38]. The study is particularly instructive for burglary-type propositions because it demonstrates that the DNA composition of a location reflects occupancy history rather than simply the identity of the most recent visitor.

For casework, prior legitimate use is an empirically testable alternative history rather than an abstract explanation. Its plausibility depends on the object, the duration and recency of prior use, the extent of later handling, and the expected background contribution of habitual users. A regular user's persistent DNA may be unsurprising on a personal object but potentially discriminating on a rarely accessed surface. Conversely, a temporary user may remain detectable after the owner resumes use. Temporal interpretation should therefore begin with the item's documented history rather than an assumed relationship between contributor rank and recency.

5.3 Background DNA and prevalence are structured features of the environment

Background DNA should not be treated as random analytical noise. It arises from the use history and ecology of a surface. Most routinely handled items are not DNA-free, and contact commonly occurs between two DNA-bearing surfaces [101]. The probability and composition of background DNA therefore depend on who occupies the environment, how often the item is handled, whether it is shared, how often it is cleaned, its exposure to public contact, and how much time has elapsed since previous use. These factors determine which alternative contributors are plausible before any crime-related activity is considered.

Empirical studies demonstrate that recoverable human DNA can be present even on objects for which no recent identified handler is known. Sorg et al. detected human DNA on 69% of 108 stones collected from an urban environment; 6.5% yielded a single or major profile meeting Swiss database-entry criteria [102]. This does not mean that DNA recovered from a stone lacks evidential value. It means that presence alone must be interpreted against the prevalence expected on comparable stones and against the location and quality of the recovered profile. The same reasoning applies to windows, door handles, public objects and other surfaces that accumulate low-level DNA through ordinary environmental contact [4,95].

Background contributions become more structured in shared indoor spaces. Onofri et al. detected non-prevalent DNA in 20 of 22 trace samples re-evaluated from realistic credit-card transfer experiments; known co-worker or cohabiting-partner DNA was identified in eight traces [37]. In the video-recorded residential social-interaction study of Cahill et al., unknown contributors were common and indirect transfer occurred despite a fully documented one-hour interaction [55]. Henry and Zieger likewise detected non-self alleles in 95% of 300 samples from hands and sleeve cuffs collected during ordinary working days. In four samples, an unknown major profile was sufficiently informative to meet the study’s database-suitability threshold [33]. These data show why a foreign contributor is not necessarily foreign to the environment and why the biological background of people, clothing and shared spaces should be considered together.

Prevalence is most informative when defined for the actual forensic question. The relevant probability may concern detecting Person A's DNA somewhere in their own vehicle, on an office desk they use daily, on the exterior of a garment worn in a shared workplace, or on a surface they claim never to have contacted. These propositions are not equivalent. Where feasible, case-specific contextual samples, information on regular users, and reference profiles from plausible close associates may be more informative than a generic estimate of 'background DNA' [4,37,39]. The purpose is not to explain every unexpected profile as background, but to define which contributors and locations would reasonably be expected before the alleged activity is evaluated.

5.4 Hands, clothing, skin and fingernails are biological reservoirs, not neutral carriers

Hands continuously acquire and lose DNA. Their deposits may contain self-DNA originating from the hands or other body regions, non-self DNA acquired from people and objects, and material transferred from clothing or the surrounding environment [24,33,56]. Handwashing reduces this reservoir but does not create a lasting DNA-free state. Alketbi and Goodwin observed progressive reaccumulation after washing, with significantly greater recovery at 30 min than at 5 min [34]. Henry and Zieger further showed that the relative composition of hand DNA changed during the

working day and that co-resident DNA detected in morning samples could be replaced by workplace-associated contributors later in the day [33]. A hand should therefore be viewed as a transient sampling surface with a contact history, not as a direct proxy for the individual's own DNA alone.

Clothing provides an even more persistent and spatially heterogeneous reservoir. In a four-laboratory study generating 448 DNA profiles from worn upper garments, Szkuta et al. observed substantial variation in DNA quantity and profile composition among garment areas, wearing occasions, participants and laboratories; the wearer was frequently, but not invariably, detected, and DNA from close associates was common [39]. Experimental handling studies also show that non-wearer DNA can become prominent after comparatively brief contact [103]. On fabric, deposition area and elapsed time affect recovery: Alketbi and Goodwin reported higher mean DNA quantities from the chest area of a T-shirt than from the buttocks area of trousers (0.28 versus 0.05 ng/μL), with significant effects of deposition area, time and their interaction [63]. These findings reinforce that "DNA from clothing" is not a single evidential category. Internal wearer-contact zones, external grab areas, cuffs, collars and exposed fabric regions have different use histories and transfer opportunities.

Laundering further complicates the assumption that washing resets clothing to a clean baseline. Noël et al. demonstrated transfer of semen- and vaginal-secretion-derived DNA between garments during machine washing, in some experimental conditions producing complete genetic profiles on previously pristine items [45]. DNA from household members was also detected on control children's underwear in the absence of alleged sexual abuse. Washing can therefore both remove and redistribute biological material. A profile recovered after laundering cannot be interpreted simply as evidence that the contributing material survived on the same location where it was originally deposited.

Body sites present comparable interpretive challenges. Foreign DNA beneath fingernails is a well-established finding in both casework and the general population. Matte et al. detected foreign DNA in 33% of 265 forensic casework fingernail samples and 19% of 178 general-population samples; controlled scratching produced foreign DNA in approximately one-third of participants immediately after contact, falling markedly after several hours [104]. Fingernails are physically protected reservoirs in which self- and non-self material may accumulate through grooming, cohabitation, social contact and scratching [36,104]. The evidential value of a foreign profile therefore depends on its quality, quantity, contributor proportions, timing, relationship between the individuals and the competing activities. The mere presence of foreign DNA beneath a fingernail is not synonymous with a recent struggle.

5.5 Cleaning, shared objects and environmental exposure alter both persistence and interpretation

Cleaning is best understood as another intervention in the DNA history of an item rather than a binary clean/dirty state. It may reduce DNA, redistribute residual material, expose protected deposits, or introduce new material from cloths, gloves or surrounding surfaces. In a simulated study of entrance door handles, daily cleaning reduced recovered DNA by approximately half and weekly cleaning by approximately one quarter under the tested conditions; the most recent handler was still not invariably the major contributor, with contributor dominance varying by surface material [74]. These results are scenario-specific, but the principle is general: knowledge that an item was cleaned changes the expected persistence distribution; it does not justify assuming that all earlier DNA was removed.

Vehicles illustrate the same problem on a larger scale. Steering wheels, gear shifts and interior handles are frequently contacted by regular users and can accumulate substantial owner or passenger DNA before an incident. In 359 hit-and-run vehicles, Aidarous et al. found significant site-to-site differences in DNA recovery, with the steering wheel producing the highest profile success rate (42%), followed by the gear shift (28%), interior door handle (19%) and exterior door handle (11%) [92]. These are operational recovery data rather than measurements of background prevalence, but they show that vehicle surfaces have markedly different DNA histories and detectability. A strong profile on a steering wheel may be highly useful for identifying an unknown driver; where ownership or prior legitimate use is conceded, however, the same finding may contribute little to establishing when the person drove the vehicle.

The interpretive distinction between analytical productivity and temporal relevance is important across all shared objects. A surface that yields abundant DNA is not necessarily the surface that best discriminates competing activities. Frequently used areas may have high recovery rates but also high expected background prevalence; rarely touched or activity-specific locations may yield less DNA but potentially greater discriminating value. Sampling strategy should therefore consider both the likelihood of recovering DNA and the expected meaning of a profile from that location.

5.6 Recovery is the final filter through which persistence and prevalence become observable

Persistence is often discussed as if the deposited DNA either remains or disappears, yet forensic laboratories observe only the fraction that is successfully collected, extracted, amplified and interpreted. Surface topography, porosity, sampling area and collection method affect how much of the retained biological material enters the analytical workflow [12,13,39,63,94]. A low-yield result may therefore reflect poor initial deposition, substantial post-deposition loss,

inefficient sampling, or some combination of these. Conversely, a highly efficient collection method may reveal older or background contributors that a less sensitive workflow would not detect. Increased analytical sensitivity can consequently improve source detection while simultaneously increasing the number of plausible deposition histories that require consideration.

This is why time since deposition cannot be inferred from DNA quantity or profile completeness alone. The observed result is conditioned on an unknown initial deposit and an only partially known sequence of persistence, transfer, environmental exposure and recovery. Studies using different substrates, sampling methods, extraction systems, amplification kits and interpretation thresholds are therefore not directly interchangeable simply because they report "persistence" [4,39,94,97]. For activity-level evaluation, the most relevant data are those that approximate the item, biological material, contact history, time interval, environment and analytical workflow of the case. Where those data are unavailable, the uncertainty should be made explicit rather than replaced by an unsupported temporal conclusion.

Collectively, these studies challenge the assumption that DNA recovered after an incident necessarily originated during that incident. Habitual users can remain dominant after later contact; temporary users can persist after the owner resumes use; non-self DNA is common on hands, clothing, and shared surfaces; laundering and cleaning can redistribute rather than eliminate material; and environmental persistence varies substantially across substrates. Background DNA is therefore part of the expected biological history of many exhibits, not a peripheral complication. The relevant question is whether the quantity, composition, and location of a person's DNA are more probable under the alleged event than under realistic histories of prior use, persistence, and background deposition. Section 6 extends that reasoning to DNA introduced or relocated after the event through investigative and laboratory processes.

6 CONTAMINATION AS AN ALTERNATIVE TRANSFER HISTORY

Contamination is often treated as a quality-control problem separate from DNA transfer, but the underlying physical process is the same: DNA-containing material moves from one person, object, or environment to another. What differs is the point in the evidential history at which that movement occurs. After a scene or exhibit enters investigative control, DNA can be introduced, removed, or relocated through post-event contacts that are unrelated to the alleged criminal activity yet remain analytically detectable [4]. In trace DNA work, the contaminating material need not be abundant, visible, or introduced by bare-hand contact. Personnel, gloves, tools, packaging, work surfaces, and storage environments can all act as intermediaries. Contamination is therefore best evaluated as a specific alternative transfer history, not merely as a laboratory defect.

The interpretive consequence is broader than the appearance of an unexpected allele. Post-event handling can add a new contributor, increase or decrease an existing contributor's relative representation, relocate DNA from one region of an exhibit to another, move DNA between exhibits, or remove material that was originally present. The final profile is consequently a product not only of the event under investigation but also of every subsequent contact capable of altering the biological trace. **Fig. 2** and **Table 2** place contamination within this wider transfer framework. The relevant question is not simply whether anti-contamination procedures existed, but whether the handling history makes a particular contamination pathway sufficiently plausible to require consideration when evaluating the evidence.

6.1 Contamination begins at scene control, not at the laboratory door

Operational datasets demonstrate that contamination is not confined to rare laboratory accidents. Pickrahn et al. reviewed approximately 46,000 crime-scene trace samples over 17 years and identified 347 contamination incidents attributable to police officers, corresponding to a detected frequency of 0.75% [48]. This value should not be treated as a universal contamination probability: detection depended on the availability of staff profiles, comparison practices and the monitoring system in place. Indeed, expansion of the Austrian Police Elimination Database increased the ability to recognize events that would otherwise have remained unexplained. The study is nevertheless important because it shows that contamination can be measured in routine forensic operations and that its apparent frequency is partly a function of how actively a system looks for it.

A national Swiss analysis provides complementary evidence on where contamination arises and how the mechanism differs across the forensic pathway. Basset and Castella identified 709 contaminations between 2011 and 2015, equivalent to a mean of 11.5 (9.6–13.4) events per 1,000 profiles submitted annually to the national database; detailed information was available for 552 events [49]. Approximately 86% were attributed to police personnel, 11% to forensic laboratory employees and 3% to other sources. Direct contact between the contaminant and the trace was reported in 91% of police contaminations but only 51% of laboratory contaminations, indicating a much larger indirect-transfer component within the laboratory environment [49]. The same investigation found that most police contamination occurred at the crime scene and was commonly associated with the person collecting the sample. Thus, the pre-analytical phase is not merely a precursor to DNA analysis: it is part of the transfer history that determines what is ultimately analysed.

Fonneløp et al. reached a similar conclusion through environmental monitoring and retrospective casework comparison. DNA was recovered from high-contact surfaces, tools and equipment within police forensic units, and comparison of staff profiles with casework samples identified 16 previously undetected contamination incidents [23]. In six cases, the matching officer reported no involvement with the case, making a simple direct officer-to-exhibit explanation insufficient and implicating indirect pathways. DNA quantities in wipe samples ranged from undetectable to 51.5 ng, illustrating that operational environments can contain substantial reservoirs of human DNA. These findings are particularly relevant to highly sensitive trace DNA workflows because an analytically valid profile can originate from a post-event pathway that is invisible in the final electropherogram.

This does not justify presuming that every low-level profile is contaminated. Contamination becomes interpretively relevant when chronology, access history, staff comparisons, environmental findings, or procedural records provide a scientifically credible route. Nor does failure to identify a contaminant prove that contamination did not occur: elimination databases are incomplete, visitors or unprofiled personnel may contribute DNA, and indirect transfer can obscure the immediate donor-to-exhibit pathway. The strongest contamination assessment reconstructs a specific route and tests it against the DNA findings rather than invoking contamination as a generic possibility.

6.2 Crime-scene personnel and PPE: barriers are only as reliable as their use

Crime-scene personnel can contribute DNA directly through unprotected contact and indirectly through respiratory droplets, clothing, gloves, equipment and movement between contaminated and nominally clean areas. Experimental work established early that investigators can deposit detectable DNA during simulated scene activities and that protective clothing can reduce this risk [105]. The principle remains important as analytical sensitivity increases: protective clothing, masks and gloves are not simply occupational equipment but controls intended to limit the introduction and redistribution of biological material after scene control.

PPE, however, does not create a binary boundary between contaminated and uncontaminated evidence. Its effectiveness depends on selection, donning, removal, replacement and the sequence of contacts made while it is worn. In a six-month observational study involving 20 forensic DNA laboratories and 600 samples, Alketbi and Carta reported contamination in 5% of samples from laboratories using stringent PPE protocols compared with 30% where PPE practice was inconsistent [75]. Reported implementation errors included improper glove removal, contact with contaminated surfaces and reuse of disposable PPE. These findings support the general proposition that implementation matters, but the study's limited laboratory sample and reliance partly on reported practice constrain extrapolation of the numerical rates to other organizations. The more defensible lesson is that availability of PPE is not equivalent to reliable contamination control.

At activity level, PPE records are informative only when linked to the handling sequence. Documentation that personnel wore PPE does not by itself exclude an investigator-mediated route. More probative details include glove-change sequence, whether masks or protective garments were changed between relevant tasks, the surfaces and equipment contacted, scene access, and whether clean consumables remained protected. Conversely, a procedural deviation does not prove contamination; it identifies a transfer opportunity that must be evaluated with the DNA findings and the remaining handling history.

6.3 Gloves and tools can become active transfer vectors

Gloves illustrate the central paradox of contamination control: a barrier that protects an exhibit from direct skin contact can itself become a mobile DNA-bearing surface. During operational casework examinations, Goray et al. recovered DNA from the outer surfaces of most gloves examined and observed substantial variation in the areas touched, sequence of contacts and timing of glove changes [41]. Case-associated DNA as well as staff/examiner DNA could be detected on gloves, and handling associated with removing exhibits from packaging and repackaging them represented particularly important transfer opportunities. The study therefore reframed glove use from a passive yes/no control to a dynamic component of the transfer pathway.

Controlled studies reinforce this mechanism. Mehta and Alketbi examined nitrile, latex and vinyl gloves under defined contamination and cleaning conditions and found material-dependent differences in DNA retention [44]. Uncleaned gloves transferred full STR profiles to contacted cloth in 8 of 10 transfer events, whereas chemical treatment reduced transfer to varying degrees. Sodium hypochlorite reduced recoverable glove DNA by up to 94%, while 70% ethanol was substantially less effective under the tested conditions [44]. These values are experiment-specific and should not be generalized into universal decontamination efficiencies: only three glove types were assessed and environmental variables such as humidity, temperature and contact pressure were not comprehensively modelled. Their interpretive significance lies in demonstrating that a glove can retain sufficient DNA for onward transfer even after some cleaning treatments.

From a contamination-prevention perspective, changing gloves at defined transition points is therefore generally more reliable than assuming that a worn glove remains "clean" because it has not visibly contacted biological material. DNA may be acquired from packaging, pens, cameras, benches, door handles or other equipment and then deposited on an exhibit during subsequent manipulation. The same logic applies to forceps, scissors, fingerprint brushes and other examination tools. Szkuta et al. demonstrated that examination tools can transfer DNA between substrates, while studies of fingerprint brushes and residual DNA have similarly shown that apparently routine equipment can act as an intermediary [60]. The transfer chain may consequently involve several innocuous actions, none of which is memorable in isolation, before DNA reaches the evidential surface.

This has two interpretive implications. First, contamination cannot always be reconstructed from the identity of the person who physically handled the exhibit at the final step; the immediate handler may simply be the vector for DNA acquired elsewhere. Second, the absence of the handler's own profile does not exclude the pathway. A glove or tool can preferentially acquire, retain and transfer DNA from another source, and contributor proportions can change at each step. Where gloves or shared equipment form part of a plausible alternative history, the relevant information includes the sequence of use, replacement or cleaning points, prior contacts, and whether the same equipment was used across exhibits or cases.

6.4 Packaging, transport and storage can alter DNA after collection

Collection does not freeze the spatial distribution of DNA on an exhibit. Once an item is packaged, movement and contact within the package can relocate DNA from one region to another or transfer it between co-packaged items. Goray et al. demonstrated loss and relocation of DNA within forensic exhibit packaging [22], and subsequent studies have confirmed that packaging material, movement and contact geometry influence post-collection redistribution [47]. This is especially important where interpretation relies on the precise location of DNA—such as a handle, garment region or other activity-specific site—because the sampled position may not be identical to the original deposition site.

Evidence packaging can also become a bridge between the external environment and the exhibit. Fonneløp et al. experimentally demonstrated transfer of DNA from the exterior of evidence packaging to an exhibit during examination [23]. The finding is conceptually important because the outside of a package is routinely handled by personnel who may never touch the internal item directly. Opening, unpacking, repositioning and repackaging can therefore connect environmental or staff DNA with the exhibit through a sequence of indirect contacts. This route also explains why chain-of-custody documentation has interpretive value beyond administrative continuity: records of who packaged, transported, opened, examined and repackaged an item help reconstruct post-event opportunities for DNA movement [77].

Storage environments add another layer. Mercer et al. followed cleaned shelves in an operational forensic exhibit storeroom for 14 weeks, collecting 147 shelf samples while 445 exhibits were stored in the monitored area [106]. DNA quantity and contributor number increased with time, and DNA detection was associated with both elapsed time and the presence of exhibits. Staff DNA was detected frequently on shelving, whereas comparison of 258 exhibit profiles with shelf samples identified only three common contributors across more than 32,000 comparisons [106]. The results should not be read as evidence that exhibit-to-shelf-to-exhibit transfer is common; rather, they demonstrate that operational storage environments progressively acquire complex DNA backgrounds and that the probability of a particular transfer route must be distinguished from the mere existence of a DNA reservoir.

Packaging and storage therefore raise three separate questions: whether DNA could move, how often a relevant movement is expected under comparable conditions, and whether the case findings are more probable under that route than under the competing history. Demonstrating physical possibility answers only the first.

6.5 Laboratory handling and environmental DNA reservoirs

The accredited laboratory is often perceived as the point at which contamination risk becomes controlled. In reality, control changes the probability and detectability of contamination; it does not eliminate the underlying transfer processes. Laboratory staff move between workstations, handle packaging and consumables, manipulate multiple samples and use equipment that can accumulate trace biological material. Environmental surfaces can consequently function as DNA reservoirs from which material is redistributed indirectly. The Swiss contamination study is instructive: although laboratory personnel accounted for a smaller proportion of detected contaminations than police personnel, nearly half of laboratory events were compatible with indirect rather than direct contact [49]. This pattern is consistent with transfer through surfaces, equipment or other intermediate reservoirs rather than simple analyst-to-sample deposition.

Contamination in this phase can also be analytically subtle. A staff-derived allele may appear as a minor component, may be masked by a stronger contributor, or may alter mixture complexity without being recognized immediately as foreign. Conversely, a contaminating profile may be sufficiently complete to resemble an evidential contributor.

Analytical validity is therefore not the same as historical validity: the STR profile can be generated correctly even though the DNA entered the sample after the event of interest. Negative extraction and amplification controls remain essential for detecting some forms of process contamination, but they cannot reconstruct every exhibit-specific event occurring before the control shares the relevant pathway.

For this reason, contamination surveillance requires complementary layers: controlled workflow separation, validated cleaning, environmental monitoring, contemporaneous records, negative controls, staff and relevant personnel elimination databases, and investigation of unexpected matches or recurrent profiles [4,48,49,53]. Elimination databases are particularly valuable because they convert otherwise unexplained contributors into identifiable post-event sources. Yet a staff match should be interpreted carefully. It establishes contributor identity, not necessarily the exact mechanism, timing or direction of transfer. Reconstruction may still require determining whether the person contacted the exhibit, packaging, shared equipment or a contaminated intermediate surface.

6.6 Human factors and implementation reliability are part of the transfer pathway

Contamination-control systems are commonly described through their technical components—PPE, cleaning, spatial separation, monitoring, controls and elimination databases—but each control is implemented through repeated human actions. The relevant vulnerability is therefore not simply whether a procedure exists, but whether it is performed at the correct point in the workflow, in the correct sequence and with sufficient consistency to preserve the intended barrier. Abdullahi and Alketbi framed this as implementation reliability: glove-change behaviour, cleaning records, handovers, documentation corrections, near-misses, environmental monitoring results, staff matches and corrective actions can be treated as observable quality-system indicators rather than as peripheral administrative data [53].

This framing is particularly useful because it avoids attributing contamination automatically to individual negligence. Workload, time pressure, interruptions, fatigue, room layout, staffing, task design and communication may influence whether low-visibility contamination-control steps are performed consistently, but current evidence does not justify treating any one of these conditions as a direct cause of a particular contamination event [53]. They are contextual risk indicators. A delayed glove change, interrupted exhibit sequence or incomplete handover becomes evidentially relevant only when it creates a plausible route by which DNA could have been introduced or relocated. Root-cause analysis should therefore ask how the system permitted or failed to detect the opportunity rather than infer causation from workload or human error alone.

Documentation is central to this approach. A defensible chain of custody should preserve not only possession of the exhibit but also the handling information needed to evaluate its biological history: collection and packaging sequence, transfers between units, access, opening and repackaging, relevant personnel, deviations, cleaning or equipment issues, and unusual events [77]. Where these records are incomplete, the analytical result is not necessarily invalid; rather, the range of post-event transfer histories that can be excluded with confidence becomes narrower. For low-level, mixed or unexpected profiles, implementation records may therefore have direct interpretive significance.

6.7 Contamination should be evaluated as a specific competing history

Contamination is over-interpreted in two opposite directions when it is treated as impossible because procedures were followed or as probable merely because contamination is known to occur. A contamination proposition becomes informative only when it specifies a history with identifiable transfer opportunities. Relevant information includes who accessed the exhibit and packaging; which gloves, tools, and surfaces were contacted; whether items were processed together; whether packaging was reused or opened; whether environmental or staff profiles were detected; whether a relevant elimination match exists; whether negative controls address the suspected stage; and whether any deviation, unusual handling event, or shared equipment provides a route compatible with the DNA location and mixture composition.

The strength of such an explanation depends on more than physical possibility. Operational contamination rates cannot be transferred directly between organizations or cases because monitoring sensitivity, elimination-database coverage, sampling practice, analytical methods and reporting thresholds differ [48,49]. Experimental glove or packaging studies likewise establish mechanisms under defined conditions, not universal probabilities for a particular case [22,44,47]. When quantitative activity-level evaluation is attempted, the data should be matched as closely as possible to the relevant handling scenario and uncertainty in poorly characterized parameters should be made explicit.

Contamination also interacts with the other histories discussed in this review. An exhibit may already contain background DNA before the crime, acquire crime-related DNA during the event, lose or redistribute material during subsequent handling, and then acquire additional DNA during collection or examination. These processes can operate concurrently rather than as mutually exclusive alternatives. A profile obtained at the end of the workflow may therefore contain biological information from several time periods and activities. The role of contamination analysis is to

reconstruct which post-event processes remain plausible and how they alter the probability of the observed findings—not to label an unexpected contributor as artefactual.

Contamination control and evidence interpretation are therefore parts of the same evidential problem. Effective controls reduce the number of plausible post-event histories; contemporaneous documentation makes remaining histories testable; environmental monitoring and elimination databases can identify sources; and activity-level evaluation determines whether the DNA findings discriminate between competing accounts. Section 7 develops that evaluative step: once more than one transfer history remains scientifically plausible, the task is to compare the observed findings under explicit activity propositions rather than to ask only whether each mechanism can occur.

7 FROM SOURCE-LEVEL EVIDENCE TO ACTIVITY-LEVEL EVALUATION

Forensic DNA evidence is strongest when it answers a source question and most vulnerable to overstatement when that answer is carried into an activity question. A highly discriminating profile may provide overwhelming support that a person contributed DNA to a sample while providing limited discrimination between competing accounts of how the DNA arrived. Activity-level evaluation is therefore not a higher-resolution form of source attribution; it is a different inferential task requiring different propositions, different data, and explicit modelling of the processes connecting an alleged activity to the laboratory result [3,4,8]. The question changes from whose DNA is present to how probable the complete DNA findings would be if one specified activity occurred rather than its competitor.

This distinction matters particularly for trace DNA because several histories may predict the same contributor. Direct handling during the alleged offence, prior legitimate use, indirect transfer, persistence from an earlier encounter, site-to-site redistribution, background DNA, and post-event contamination can all be compatible with a source-level association. The evidential task is not to select the most intuitive history, but to compare the probability of the observations under propositions that represent the material dispute. ISFG guidance accordingly places proposition formulation, relevant conditioning information, and transfer-persistence-prevalence-recovery (TPPR) data at the centre of activity-level evaluation [3].

7.1 The proposition pair defines the scientific question

Activity-level propositions should be formulated before the DNA findings are assigned evidential value. They should address the same level of the hierarchy, reflect the actual dispute, and be specific enough that expected findings under each can be considered. A proposition that the person of interest handled an item during an alleged assault cannot be meaningfully compared with a proposition that the DNA came from another person; the first concerns activity and the second source. Likewise, a defence account based on previous legitimate use is scientifically different from an account based on secondary transfer through another person. Combining distinct histories into an undefined alternative obscures the mechanisms that determine the probability of the evidence [3,8,93].

Kokshoorn et al. showed that activity-level evaluation changes materially depending on whether the dispute concerns the identity of the actor, whether the criminal activity occurred, or whether the person of interest performed an alternative legitimate activity [93]. Identical DNA observations can therefore have different evidential values under different, legally plausible proposition sets. That dependence is intrinsic to probabilistic evaluation: evidential value is conditional on the question asked. Activity propositions should consequently be developed from case information supplied independently of the DNA result rather than reverse-engineered to fit the profile. The expert evaluates the findings under the specified propositions; the expert does not decide which proposition is true.

7.2 TPPR is the causal bridge from activity to observation

Between an activity and an electropherogram lies a sequence of contingent events. DNA must first be transferred, then remain available long enough to persist, compete with DNA already present or commonly encountered at the relevant location, and finally be recovered and detected by the chosen analytical workflow. TPPR provides a practical structure for separating these stages [3,4,8]. Transfer concerns how biological material moves during the proposed contacts; persistence concerns loss, redistribution or survival over the relevant interval; prevalence concerns the probability that target or non-target DNA may already be present in the relevant context; and recovery encompasses sampling, extraction, amplification, detection and interpretation. In this setting, prevalence is not an allele-frequency concept. It concerns contextual background and the expected presence of DNA before or independently of the questioned activity.

Separating these processes is important because the same final result can arise through different combinations of them. A small quantity of a person's DNA may reflect limited direct deposition, efficient secondary transfer followed by loss, substantial earlier deposition with poor persistence, or a larger surviving deposit sampled inefficiently. Conversely, a complete profile does not require that every step was highly efficient. Experimental studies of non-self DNA on hands, background DNA and repeated-use objects demonstrate that the material available for transfer at the start of a

questioned event is rarely biologically pristine [24,33]. TPPR evaluation must therefore consider not only the person of interest but also expected wearer, owner, household, co-worker, investigator and unknown contributions where these are relevant to the scenario.

The observation set should also extend beyond a binary statement that a profile was present. Depending on the validated model and available data, informative features may include DNA quantity, allele or locus recovery, contributor number, relative contribution, profile quality, distribution across sampled sites, the presence of expected background contributors, and negative or no-profile results. Unsuccessful observations are not merely laboratory failures to be discarded: where sampling and analytical performance are understood, non-detection can alter the relative probability of competing activities. The evidential model should therefore represent the pathway that generated all relevant observations, not only the result most favourable to one proposition.

7.3 Bayesian reasoning evaluates the findings given the activities

The logic of activity-level evaluation is expressed by the likelihood ratio. Let E denote the relevant DNA findings, H_p and H_d the competing activity propositions, and I the conditioning information accepted for the evaluation. The activity-level likelihood ratio is:

$$LR_{activity} = P(E \mid H_p, I) \,/\, P(E \mid H_d, I)$$

An LR greater than one indicates that the observed findings are more probable under H_p than under H_d; an LR below one indicates the reverse. It does not state the probability that H_p occurred, the probability that H_d occurred, or the probability that the person committed the offence [3,8]. Those posterior questions require prior odds and the non-DNA evidence and ultimately belong to the fact-finder. This distinction prevents a transposed conditional from reappearing at the activity level in a more subtle form.

Bayesian networks are useful because they expose the assumed causal structure. Separate nodes can represent direct or indirect contact, the amount available for transfer, persistence, background DNA, recovery, multiple contributors, and multiple sampling sites, while conditional relationships identify which observations are linked [20,107]. A network does not discover the historical truth from the profile. It provides a transparent accounting framework for asking what findings are expected under each proposition and for testing how the evaluation changes when uncertain parameters or model structures are varied.

The statement that 'direct transfer is more likely' is therefore not, by itself, an appropriate evidential conclusion. It reverses the direction of conditioning and usually leaves the competing activity undefined. An experiment may legitimately show that a particular outcome occurred more frequently, or that more DNA was recovered, after direct than secondary transfer under the tested conditions. A case evaluation may conclude that the observed findings are several times more probable if the person directly used the item than if the person's DNA reached it through a specified secondary-transfer pathway. Neither statement establishes that direct transfer itself is more probable. The probability of the activity and the probability of the evidence given the activity are different quantities.

7.4 A strong source-level result can have modest activity-level value

Empirical activity studies illustrate how sharply source-level and activity-level strength can diverge. In a credit-card study comprising 11 direct- and 11 secondary-transfer experiments, Onofri et al. obtained a reportable sub-source LR greater than 10^6 in 9/11 direct-transfer samples but also in 4/11 secondary-transfer samples [54]. Direct transfer produced a greater mean DNA yield (1.60 ng versus 0.657 ng) and more often placed the person of interest as the major contributor, yet background DNA was detected in 19/22 samples. When the experimental observations were incorporated into a Bayesian network, an observation containing only the person of interest produced an activity-level LR of approximately 10.6 for the direct-use proposition; inclusion of an unknown contributor reduced the LR to approximately 3.5 [54]. Thus, a source association capable of being reported as extremely strong did not translate into comparably extreme discrimination between activities.

Drug-packaging experiments show the same divergence. Fonnelop et al. generated empirical data for direct handling of zip-lock bags, indirect transfer through personal bags, and persistence from previous tape users [108]. In one Bayesian-network example, detection of contributor A alone gave an LR of approximately 11 in favour of the proposition that A packed the drugs, whereas observing A together with an unknown contributor produced an LR of approximately 0.1, favouring the alternative proposition under that model. In the tape scenario, detection of the previous handler's DNA provided only limited activity-level discrimination; even continuous RFU-based modelling produced LRs of modest magnitude under the tested conditions [108]. The additional contributor was not incidental noise: it changed which history better predicted the complete observation.

DNA quantity should be treated similarly. Taylor et al. demonstrated through a Bayesian-network framework that the relationship between recovered quantity and support for primary rather than secondary transfer need not be monotonic [20]. Under their model assumptions, increasing DNA quantity initially increased support for primary transfer, but at sufficiently high quantities the evidential pattern could become less compatible with the modelled primary pathway. The numerical turning points are scenario- and model-specific; the broader lesson is more important. Quantity is evidence to be conditioned on competing transfer histories, not a universal scale on which 'more DNA' means 'more direct,' 'more recent,' or 'more criminal.'

7.5 Evidential dependence must be modelled, not multiplied away

Activity-level cases often contain several DNA results from the same item, multiple related items, or repeated observations generated by a common handling history. These findings may be statistically dependent. Two samples from adjacent regions of one garment may share DNA because material relocated between sites; several packaged items may share contributors because they contacted the same surface or handler; and the same unknown contributor on multiple objects may originate from a common background source rather than repeated independent contacts. Treating such results as independent and multiplying their likelihood ratios can materially overstate evidential strength.

Taylor et al. emphasised this issue when modelling common unknown DNA across multiple items, showing that plausible sources include background DNA on the objects, non-self DNA carried by a handler, an alternative actor, or combinations of these routes [109]. A later study on packaged exhibits demonstrated the same principle within a single item: DNA recovered from one location may have moved to another location during packaging and transport, so spatial observations cannot automatically be treated as independent deposits [46]. The presence of wearer or background contributors can itself provide information about whether such relocation occurred. Dependence is therefore not a purely statistical technicality; it reflects the physical history of the evidence.

Dependence also arises in the experimental data used to populate activity models. Repeated deposits from the same donor, multiple samples derived from one transfer chain, several sites from the same exhibit and repeated measurements from the same laboratory do not provide the same information as an equal number of independent donors or events. Failure to preserve that structure can produce over-precise transfer frequencies and unrealistically narrow uncertainty. This is especially consequential in trace DNA research, where sample sizes are often modest and donor effects can be large.

7.6 Data relevance and transportability determine how much can be quantified

An activity-level LR is only as defensible as the data used to assign its conditional probabilities. Ideally, empirical data should approximate the case in the dimensions most likely to influence the findings: the biological material, donor population, contact sequence, substrate, time interval, environmental exposure, background conditions, packaging, sampling method, analytical workflow and outcome definition [3,4,8]. Exact replication of a case is neither possible nor necessarily desirable, but differences between study and case conditions must be identified and their likely impact examined. A transfer percentage from one donor, one surface and one deliberately optimised contact is not a population probability for all secondary-transfer allegations.

Recent inter-laboratory work makes the recovery component particularly important. The ReAct project found substantial differences in DNA recovery distributions and dropout among 23 laboratories examining activity-level scenarios, demonstrating that pooled data can obscure laboratory-specific behaviour [110]. Companion Bayesian-network analyses showed that evidential values can change with the choice of pooled, hierarchical or laboratory-specific data [111], while subsequent work explicitly accounting for inter-laboratory recovery variability generally reduced apparent discrimination and increased uncertainty compared with naive pooling [112]. These findings caution against importing a published probability table into another laboratory's casework model without examining differences in recovery and analytical performance.

Contextual background data require the same scrutiny. Samples from comparable locations or items may inform prevalent DNA and expected background contributors, but their value depends on when, where, and how they were sampled, the number of samples collected, and their relationship to the questioned item [113]. They are most useful when they address a defined uncertainty in the propositions. Poorly matched contextual samples can create an appearance of case specificity without providing relevant probability estimates.

Publication quality has direct evidential consequences when experimental data are intended for activity-level use. Recent minimum requirements for transfer and recovery studies emphasize explicit scenario definition, defensible experimental units and denominators, appropriate controls, complete outcome reporting, and characterization of uncertainty [15]. These requirements address a recurring limitation: a study may demonstrate that a pathway can occur while lacking the donor structure, replication, independence, or reporting needed to estimate a transportable

probability. Possibility evidence should not be upgraded silently into frequency evidence, and narrowly conditioned frequencies should not be treated as universal activity-level parameters.

7.7 Numerical activity-level evaluation is useful, but not automatically objective

A numerical LR can make assumptions auditable and force explicit comparison of the competing propositions, but a number does not remove judgment from the evaluation. Model structure, data selection, parameter estimation, treatment of unknown contributors, dependence assumptions and the representation of non-detection all require scientific choices. Sparse data can make several different parameter values defensible, and structural uncertainty may be more important than sampling error. Sensitivity analysis is therefore integral rather than optional when plausible changes in transfer, persistence or recovery probabilities could materially change the LR [114].

Contemporary hierarchical approaches attempt to represent some of this uncertainty more explicitly. The ReAct analyses and the HaloGen framework incorporate laboratory or population heterogeneity, non-detection and uncertainty in transfer-recovery data rather than assuming one fixed probability applies universally [15,110–112,115,116]. Simulation studies using these frameworks show that laboratory effects and data-selection strategies can change activity-level LRs by orders of magnitude in some settings [111,116]. The appropriate response is not to abandon numerical evaluation, but to report how robust the conclusion is to reasonable alternatives and to distinguish uncertainty in the model from uncertainty about the ultimate facts of the case.

When proposition-relevant data are too sparse or poorly matched to support a defensible numerical LR, precision should not be manufactured through subjective point estimates. The expert can still identify scientifically plausible transfer histories, explain which variables are expected to increase or decrease the probability of the observations, and state why reliable quantification is not possible. A transparent limitation is preferable to a precise-looking LR whose denominator, dependence structure, or data relevance cannot be defended [3,15,117].

7.8 Reporting should describe the value of the findings, not decide the activity

The final activity-level opinion should remain tied to the proposition pair and the observations evaluated. Appropriate wording describes how much more or less probable the DNA findings are under one specified activity than under the competing activity, together with the principal assumptions and limitations. It should not convert a likelihood ratio into a statement that the person probably performed the activity, that a transfer mechanism probably occurred, or that the DNA was deposited during the crime. Likewise, qualitative expressions such as 'consistent with direct transfer' have little evaluative content unless the competing explanation is considered, because many trace DNA observations are simultaneously consistent with several transfer histories.

Activity-level DNA evidence is therefore comparative rather than reconstructive in isolation. It can show that one proposed history predicts the observations better than another, sometimes by a substantial factor, but it does not determine which history occurred. Preserving that boundary explains why apparently conclusive source-level evidence may become far less discriminating when the dispute concerns contact, timing, or activity. Section 8 examines the legal and investigative errors that arise when this boundary is lost.

8 WHY DNA FINDINGS CAN BE LEGALLY MISLEADING

A DNA result can be analytically correct yet legally misleading when the conclusion presented to the court exceeds the question actually answered by the science. The principal risk is inferential escalation rather than an erroneous STR profile or contributor comparison. A laboratory observation such as 'DNA attributable to Person A was recovered from the exhibit' can acquire a progressively stronger narrative: Person A's DNA was on the item, therefore Person A touched it, therefore the contact was recent, therefore Person A used it during the offence. Each step introduces a new proposition requiring additional information about transfer, persistence, prevalence, recovery, and case circumstances [3,4]. **Fig. 3** illustrates the problem: materially different histories can converge on the same source-level observation. The uniqueness of a DNA profile should not be mistaken for uniqueness of the history that produced it.

Increasing analytical sensitivity makes this boundary more important, not less. Improved recovery and interpretation extend the range of useful evidence while also increasing detection of low-level material from ordinary prior use, secondary or subsequent transfer, environmental background, and post-event contamination [4,9]. Trace DNA is not therefore inherently unreliable; its evidential meaning is conditional. The errors considered below arise when that condition is lost and a conclusion is stated at a higher inferential level than the analysis supports.

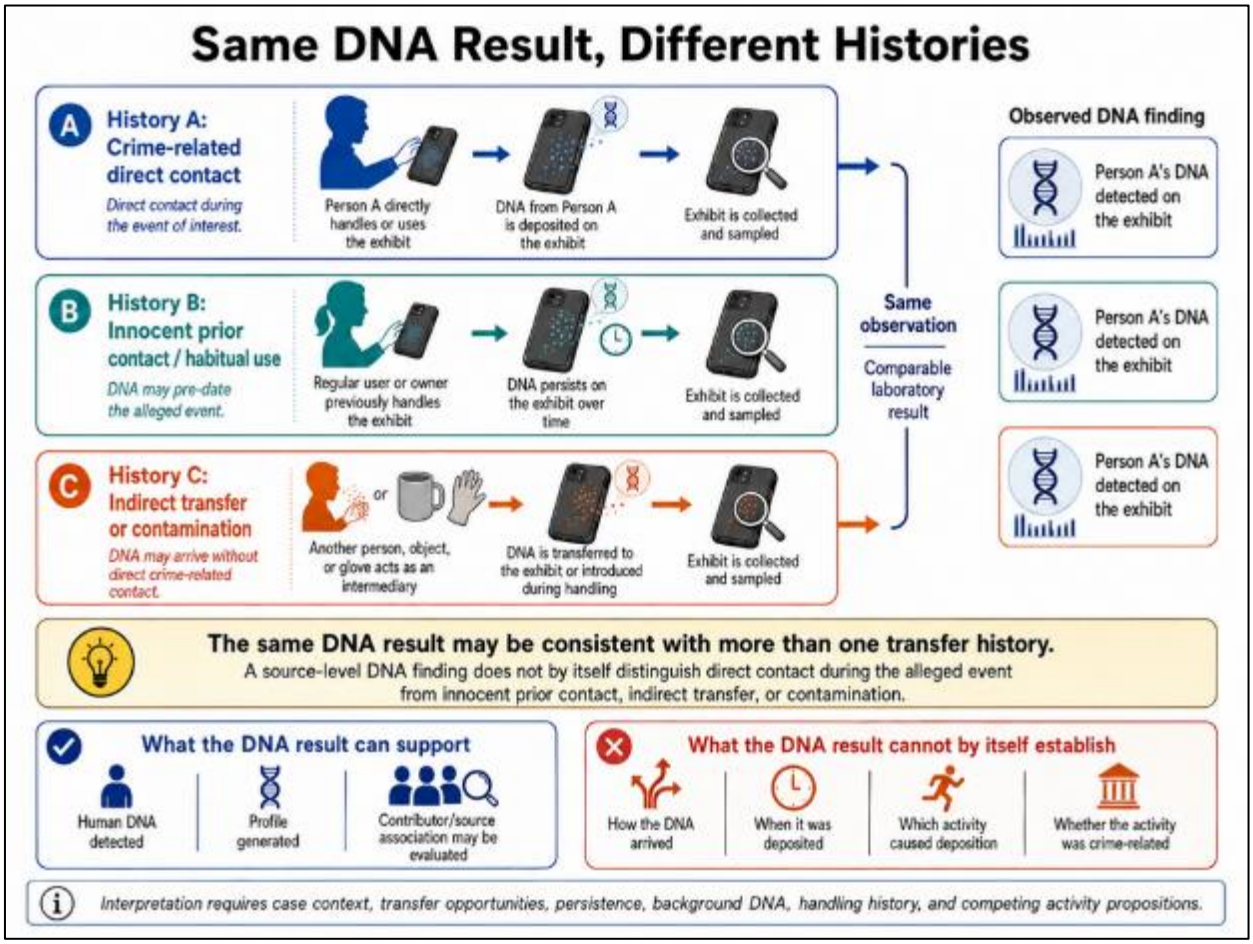

Figure 3: Same DNA result, different histories. Conceptual illustration showing how an identical source-level DNA observation may arise from substantially different transfer histories. In History A, Person A directly contacts the exhibit during the event of interest and deposits DNA through crime-related handling. In History B, Person A is a legitimate or habitual user whose DNA was deposited before the alleged event and persisted until collection. In History C, Person A's DNA reaches the exhibit indirectly through another person, object, glove, handling step, or contamination pathway without direct crime-related contact. Although the underlying histories differ, each can produce the same laboratory observation: detection of Person A's DNA on the exhibit. The figure therefore distinguishes what the DNA result may support—such as the presence of human DNA, generation of a profile, and evaluation of contributor/source association—from what it cannot establish by itself, including the transfer route, timing of deposition, activity responsible for deposition, or whether that activity was related to the alleged offence. Interpretation requires consideration of case circumstances, transfer opportunities, persistence, background DNA, handling and packaging history, contamination pathways, and competing activity-level propositions.

8.1 A DNA association is not a record of touch

The most persistent interpretive shortcut is to equate a strong DNA association with direct physical contact. At sub-source level, a likelihood ratio may strongly support the proposition that the DNA originated from Person A rather than an unknown unrelated person. That result addresses contributor identity. It does not determine whether Person A directly touched the exhibit, whether DNA was transferred through another person or object, whether it persisted from earlier legitimate use, or whether it was introduced during later handling [3,4,8]. The phrase 'DNA match' can be especially problematic in non-specialist communication because its apparent certainty concerns the contributor comparison, while the disputed legal question often concerns the mechanism or activity.

Empirical activity studies show why the distinction is substantive rather than semantic. In the credit-card study of Onofri et al., a reportable sub-source LR greater than 10^6 was obtained in 9/11 direct-transfer samples, but also in 4/11 secondary-transfer samples [54]. The indirectly transferred person could therefore be associated very strongly with DNA recovered from an item that they had not directly used in the tested scenario. Direct transfer produced more DNA on average and more often resulted in the person of interest being the major contributor, but those group tendencies did not convert the source-level result into proof of direct contact. A strong association can identify whose DNA contributed to the sample while leaving the route by which it arrived unresolved.

The careful legal formulation is consequently not 'the DNA proves that A touched the item' but, where supported, 'the DNA findings strongly support A as a contributor to the sampled DNA.' Whether direct contact is better supported than a specified indirect route is a separate activity-level question. This distinction is particularly important where direct contact itself supplies an element of the prosecution narrative, for example handling a weapon, packaging drugs, restraining a complainant or accessing a restricted surface.

8.2 The major contributor is not necessarily the most recent handler

Contributor position is another feature that is easily converted into chronology. A major contributor is the person whose DNA accounts for a relatively large component of the recovered mixture under the analytical interpretation; the label does not encode when that DNA was deposited. The observed proportion at collection is the product of initial deposition, donor-specific shedding, accumulated prior use, subsequent contacts, persistence, loss, redistribution and recovery. The last handler may become dominant, remain minor, or be undetectable, while an earlier habitual user can remain the major contributor [4,25,38,100].

Repeated-use experiments make this especially clear. On regularly used knives, established user DNA can persist despite subsequent handling, and indirectly transferred DNA may remain as a minor component [25]. In a realistic office-occupation study, the office owner was the sole, major or majority contributor in 77% of samples, compared with 14% for the temporary intruder, even though the study specifically included an intervening period of temporary occupation [38]. Studies of routinely used household items likewise show that a habitual user's contribution can remain prominent after shorter use by another person [100]. These observations do not establish that habitual users will always dominate. They demonstrate that contributor rank cannot be read as a simple contact sequence.

The reverse error is also possible. A recent handler may deposit sufficient DNA to dominate a mixture despite brief contact, particularly when the pre-existing reservoir is weak or the later handler deposits comparatively large amounts. Accordingly, statements such as 'the major profile is most consistent with the last person who handled the item' require proposition-relevant data rather than intuition. Contributor dominance may be evidentially informative, but only as one observation within a defined transfer history.

8.3 DNA quantity and profile completeness are not clocks

Courts and investigators may understandably attach temporal meaning to abundance: more DNA can appear to imply more recent, more forceful or more direct contact, while a low-level partial profile can appear old or indirectly transferred. These inferences are not generally valid without conditioning on the relevant activity and recovery model. DNA quantity at analysis does not begin from a known baseline. The initial amount deposited varies between people and contact events; subsequent material may be lost, added or redistributed; and the amount entering the analytical workflow depends on substrate, sampling area, collection method, extraction, amplification and interpretation [4,68,95,96]. A profile therefore has a history, not a single decay clock.

Even when controlled experiments show higher average quantities after direct than secondary transfer, the distributions can overlap. Taylor et al. demonstrated in a Bayesian-network framework that increasing DNA quantity did not produce a universally monotonic increase in support for primary transfer; the relationship depended on the modelled transfer, persistence and recovery processes [20]. Similarly, the Onofri et al. credit-card experiments produced a higher mean yield after direct transfer (1.60 ng) than after secondary transfer (0.657 ng), yet secondary-transfer samples still generated substantial profiles and, in some cases, very strong source-level associations [54]. The scientifically relevant question is therefore how probable the observed quantity or profile quality would be under each specified activity, not whether the amount appears 'high' or 'low' in isolation.

Temporal inference is even more constrained. Environmental and substrate studies show that equal elapsed times can produce very different recoverability, while earlier deposits may remain informative under favourable conditions [68,95,96]. Conversely, genuine recent contact can yield little or no reportable DNA. A statement that a profile 'must be recent because it is complete' or 'must be old because it is weak' overstates what STR quantity and profile quality can establish. Unless a validated time-since-deposition method applicable to the biological material, substrate, environment and case interval is used, conventional STR evidence should not be presented as a molecular timestamp.

8.4 Absence of DNA is not the inverse of presence

A related error is to interpret non-detection categorically: if Person A's DNA was not recovered, Person A did not touch the item. This treats transfer and recovery as deterministic. Direct contact does not invariably produce a detectable profile, and a deposited trace may subsequently be lost, masked by other contributors, missed by sampling or fall below analytical thresholds [3,4]. The absence of a detected profile is therefore an observation generated by the same transfer-persistence-recovery process as a positive result.

Non-detection can nevertheless have evidential value. If one proposition predicts a high probability of recovering Person A's DNA and the competing proposition predicts a much lower probability, failure to detect that DNA may support the latter. The distinction is between probabilistic evaluation and categorical exclusion. Negative results should be retained in the observation set and interpreted using proposition-relevant detection and dropout information where available [3,15]. This is particularly important when multiple sites or items are sampled: selectively discussing the positive sample while disregarding nearby negative samples can distort the pattern that the competing activities actually predict.

8.5 A source-level likelihood ratio cannot be promoted into activity support

Perhaps the most consequential statistical error is to transfer the magnitude of a source-level LR directly to an activity proposition. A source or sub-source LR compares explanations for contributor identity. An activity-level LR compares specified histories of conduct and must incorporate the processes by which those histories generate the complete DNA findings [3,93]. A source LR of millions or billions may therefore coexist with an activity LR close to one if both activities predict that the person's DNA would be present. The numerical strength at the lower proposition level does not 'carry upward.'

The empirical examples in Section 7 illustrate the scale of this divergence. In the Onofri et al. study, source-level LRs exceeding 10^6 were observed after both direct and secondary transfer, whereas the activity-level LR was approximately 10.6 when only the person of interest was observed and approximately 3.5 when an unknown contributor was also present [54]. In the drug-packaging study of Fonnelop et al., detection of contributor A alone produced an LR of approximately 11 for the proposition that A packed the drugs, while observing A together with an unknown contributor shifted the discrete-model LR to approximately 0.1 under the tested proposition set [108]. The additional DNA was not irrelevant background to be removed from the narrative; it changed the probability of the evidence under the competing histories.

The related linguistic error is to report that 'direct transfer is more likely' because the profile is strong. An evidential LR evaluates P(findings | activity), not P(activity | findings). Concluding that an activity itself is more probable requires prior information and the non-DNA evidence, which lie outside the DNA LR. The expert can state that the findings provide support for one specified activity relative to another; the fact-finder decides what probably occurred after considering the whole case [3,117].

8.6 Spatially persuasive DNA may have moved

The location of DNA can be highly relevant because competing activities may predict different spatial patterns. DNA recovered from the grip of a weapon, the inner region of clothing or another activity-specific area can therefore be more discriminating than DNA recovered from a generic external surface. The legal risk arises when the sampled location is treated as an immutable record of the original deposition site. DNA can move within an exhibit or package after the relevant event through folding, friction, handling, transport and contact between regions [22,46,47].

Taylor et al. demonstrated the interpretive consequence using a packaged-underwear model. If site-to-site movement was omitted, DNA detected in the inner groin region could be treated as arising only through the alleged activity, thereby overstating support for that proposition. Incorporating possible transfer from another region of the same exhibit changed the causal structure of the evaluation [46]. The presence of wearer or background contributors across locations may itself provide information about whether relocation occurred. Spatial evidence is therefore potentially powerful precisely because location matters, but its value depends on modelling how stable that location was from deposition to sampling.

Courtroom wording should preserve the distinction between observation and history. 'DNA was recovered from the inner surface' is an analytical observation; 'DNA was deposited on the inner surface during the alleged act' is a historical conclusion. Moving from the first statement to the second requires evaluation of competing deposition and relocation histories. **Fig. 3** generalizes this point: the laboratory endpoint may be identical even when the route to that endpoint differs.

8.7 Alternative histories must be evaluated, not merely imagined or dismissed

Recognizing transfer complexity does not mean that every alternative explanation deserves equal weight. Secondary transfer, background DNA and contamination are scientifically established processes, but the fact that a mechanism can occur does not establish that it probably occurred in a particular case. A generic assertion that 'the DNA could have been transferred' is no more evaluative than the opposing assertion that a match proves direct contact. The alternative should be formulated as a concrete history: who or what could have carried the DNA, what contacts were required, in what sequence, over what interval, under what persistence conditions, and through which recovery pathway. The observed

quantity, mixture composition, location, negative results and handling record can then be compared under that history and its competitor [3,15,93].

The same discipline applies to contamination. Evidence that personnel wore PPE or that a laboratory was accredited does not make contamination impossible; conversely, the existence of documented contamination incidents elsewhere does not make contamination a probable explanation for the case at hand. Section 6 showed that post-event transfer becomes evidentially meaningful when a specific route is supported by access, handling, packaging, staff comparisons, environmental data, process records or other case information [48,49]. Alternative-history reasoning is therefore a safeguard against both prosecution and defence overstatement: it requires competing explanations to be specified and tested rather than accepted or rejected by label.

8.8 When the science is right but the legal story is wrong

Case-based analyses demonstrate why these distinctions matter beyond laboratory terminology. Gill's discussion of miscarriages of justice describes several different ways in which scientifically detectable DNA was assigned an incorrect or overstated history: laboratory contamination in the Adam Scott case, low-level/background DNA and contextual interpretation in the Amanda Knox case, and secondary-transfer concerns in the David Butler case [9]. The cases differ materially and should not be collapsed into a single 'DNA error' category. Their common feature is that contributor detection was treated as more historically informative than the circumstances justified.

These cases should not be used to imply that low-level DNA is presumptively innocent, contaminated, or indirectly transferred. That would reproduce the same inferential error in the opposite direction. Analytical validity and historical relevance are separate questions: a profile may be correctly generated and correctly associated with a person while the proposed explanation for its presence remains unsupported. The safeguard is explicit proposition setting, investigation of realistic alternative histories, and reporting that preserves the direction and level of scientific inference [3,9].

This communication challenge remains operationally important. A global survey of 162 forensic DNA practitioners reported substantial variability in knowledge and implementation of activity-level evaluative reporting across jurisdictions, despite broad support for its development [10]. Such variability matters because courts may receive DNA evidence framed at different inferential levels even when the underlying laboratory observations are similar. Standardized terminology and reporting cannot replace case-specific data, but they can reduce the risk that source-level certainty is unintentionally converted into activity-level certainty through wording alone.

8.9 The legally relevant question is often narrower than the apparent power of the DNA result

The evidence supports a consistent set of inferential boundaries. A match does not establish touch; contributor dominance does not establish recency; quantity is not a universal clock; non-detection does not prove absence of contact; a source-level LR does not quantify activity-level support; and the sampled location is not necessarily the original deposition site. These limitations do not weaken DNA evidence. They define the conditions under which its strength is scientifically meaningful.

The most useful interpretation therefore begins by identifying what remains genuinely disputed. If the person accepts that an item is theirs or that they handled it previously, a very large source-level LR may resolve little of the contested issue. If the dispute concerns how DNA reached a surface, when it was deposited, whether it moved after collection, or whether it arose during the alleged offence, the evidential value lies in how well the complete observations discriminate the competing histories. In some cases that discrimination may be substantial; in others, the available TPPR data may support only a cautious qualitative assessment or may be insufficient for a reliable activity-level conclusion. The strength of the forensic opinion should follow the information available for the disputed question, not the numerical impressiveness of the contributor association.

For legal decision-makers, the central point is that DNA can be highly discriminating about biological source while remaining equivocal about criminal activity. Avoiding overinterpretation requires separation of observation from reconstruction and contributor attribution from activity attribution. Section 9 translates these distinctions into operational questions: what information should be preserved, what should be asked of the DNA evidence, and whether the reported conclusion actually addresses the proposition in dispute.

9 PRACTICAL FRAMEWORK FOR INVESTIGATORS AND LEGAL PROFESSIONALS

The evidential meaning of a DNA result depends not only on the analytical profile but also on the information preserved about the exhibit, the competing activities, and the route from deposition to sampling. This has an operational consequence: activity-level interpretation cannot be reconstructed reliably after the fact if item history, handling chronology, sampling location, or alternative transfer opportunities were never documented. The quality of the eventual

forensic opinion is therefore partly determined before the laboratory receives the exhibit [3,4,93]. **Fig. 4** and **Table 4** translate the preceding sections into a workflow that begins with the disputed question and follows the evidence through sampling, handling, evaluative reporting, and courtroom use.

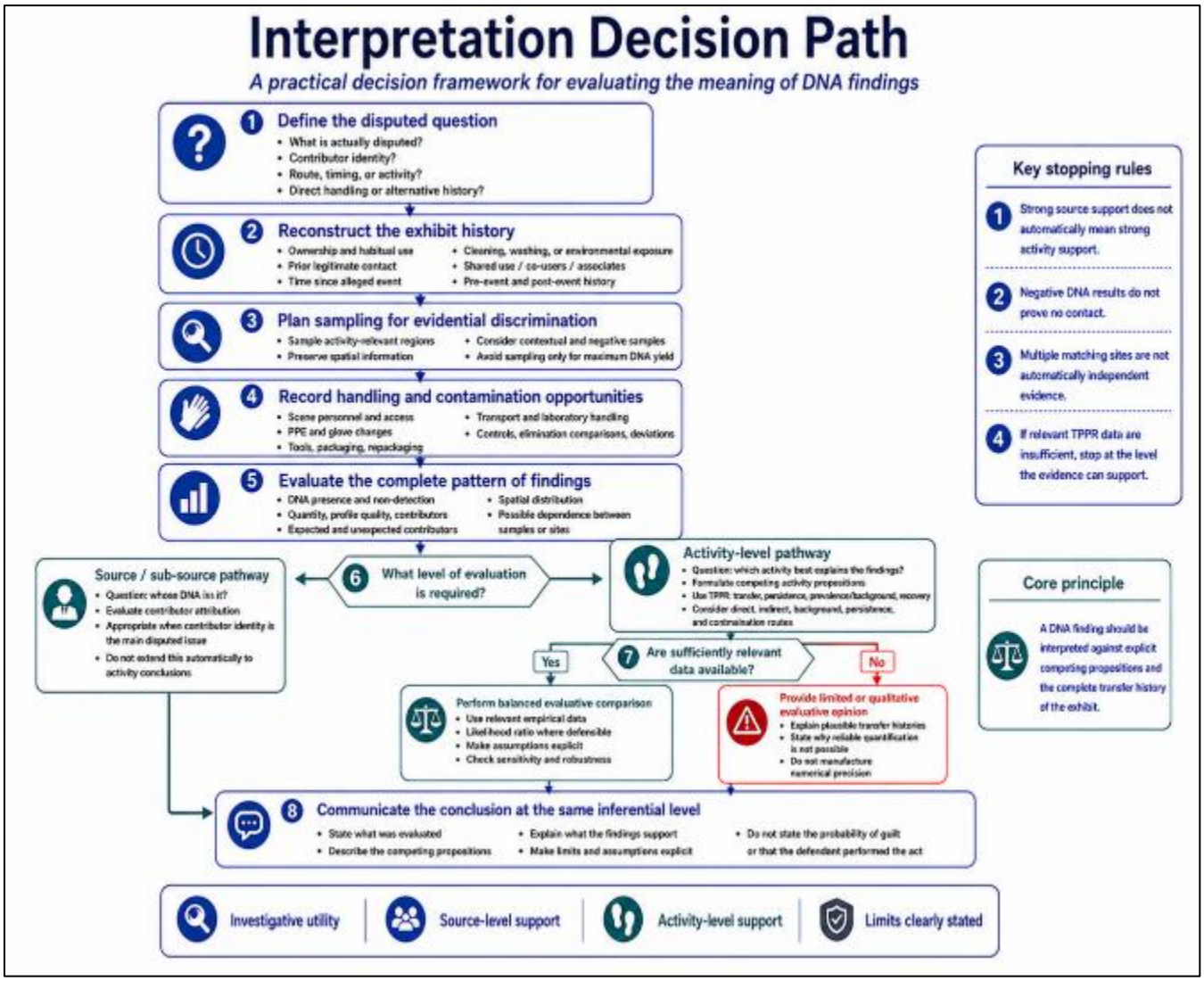

Figure 4: Interpretation decision path for evaluating the meaning of DNA findings. Practical framework integrating the principal interpretive steps discussed in this review. The pathway begins by defining the disputed question and reconstructing the pre-event and post-event history of the exhibit, including legitimate use, environmental exposure, sampling location, handling, packaging, and potential contamination opportunities. The complete pattern of DNA findings—including positive and negative results, quantity, profile quality, contributor composition, spatial distribution, and possible dependence between samples or sites—is then considered before determining the appropriate level of evaluation. Where contributor identity is the principal dispute, interpretation may appropriately remain at the source or sub-source level. Where the dispute concerns how, when, or during which activity the DNA was deposited, an activity-level evaluation requires explicit competing propositions and consideration of transfer, persistence, prevalence/background, and recovery (TPPR), together with direct, indirect, background, persistence, redistribution, and contamination pathways. Quantitative evaluative comparison should be undertaken only where sufficiently relevant empirical data and defensible model assumptions are available; otherwise, the opinion should remain qualitative or limited rather than introducing unsupported numerical precision. The final conclusion should be communicated at the same inferential level as the evaluation performed and should state the assumptions, limitations, and scope of the opinion without expressing the probability that an individual performed the alleged act or is guilty. The accompanying stopping rules emphasize that strong source-level support does not automatically imply strong activity-level support, negative DNA findings do not prove absence of contact, multiple matching results are not necessarily independent, and interpretation should stop at the highest level that the available evidence can scientifically support.

Table 4: Questions Investigators and Lawyers Should Ask. Case-focused questions for preserving the information required for later interpretation, testing whether a DNA conclusion addresses the proposition in dispute, and distinguishing strong contributor attribution from unsupported conclusions about contact, timing, activity, or offence involvement. The questions are prompts for case-specific reasoning rather than a mandatory checklist.

Stage / core question	Investigators should establish or document	Lawyers and legal professionals should ask or request	Why the answer matters for DNA interpretation
A. Define the disputed question and level of inference			
What is actually disputed?	Record whether contributor identity is disputed, admitted, or already explained by ownership or prior legitimate contact. Identify whether the live issue is contact, timing, route of deposition, actor identity, activity, or offence involvement.	Ask what proposition the reported statistic addresses: contributor identity, biological source, or activity. If prior contact is accepted, ask what additional issue the DNA result is said to resolve.	A highly discriminating source-level result may add little when the real dispute concerns how or when DNA was deposited. Evidential strength must be tied to the proposition actually in issue. [3,4,8,93]
Are the competing propositions at the same level?	Formulate realistic alternative histories from case information before interpreting the DNA result. Specify actors, activities, sequence of contacts, relevant time interval, and any legitimate prior use rather than recording a vague alternative.	Ask whether the propositions are mutually intelligible, address the same inferential level, and reflect the actual prosecution and defence accounts. Challenge comparisons such as an activity proposition versus a source proposition.	An LR is meaningful only for the proposition pair evaluated. Changing the proposition set can materially change evidential value without changing the laboratory observations. [3,8,93]
What information is being treated as given?	Separate observed facts from assumptions, admissions, and disputed statements when compiling the case circumstances for the laboratory. Update the laboratory if material facts change.	Ask which facts were used as conditioning information and whether any were subsequently withdrawn, disputed, or modified. Determine whether the evaluation should be revisited after a change in case information.	Activity-level probabilities are conditional on stated information. An opinion may cease to address the same question if material conditioning information changes. [3,8,93,117]
Does the DNA result answer the question the court must decide?	Use DNA initially as a lead where appropriate, but continue investigating factual components of the transfer history. Do not treat identification of a person as completion of the reconstruction.	Distinguish a source-level association from evidence that a person performed a particular act. Ask whether additional TPPR evaluation was actually performed before activity language was used.	The uniqueness of a profile concerns biological attribution; it does not create uniqueness of the historical route that produced the profile. [3,4,8,9]
B. Reconstruct the pre-event biological history of the exhibit			
Who owns, uses, wears, or routinely handles the item?	Document ownership, frequency and duration of use, habitual users, co-users, and recent legitimate handlers.	Ask whether the person of interest would be expected to contribute DNA before the alleged event.	Repeated use can create persistent DNA reservoirs; a habitual user may remain a major

	For clothing and personal items, record wearer history and whether areas differ in expected contact.	Request evidence of routine use rather than assuming that prior-use DNA would be absent or minor.	contributor after another person interacts with the item. [4,39]
Who else belongs to the item or environment?	Identify household members, co-workers, partners, passengers, carers, regular visitors, and other plausible close associates. Where justified, obtain elimination/reference profiles from relevant people under appropriate legal and ethical procedures.	Ask whether known associates or regular occupants were considered when unexpected contributors were interpreted. Distinguish an unknown contributor from a biologically unexpected contributor.	Background DNA is structured by occupancy and use. Foreign DNA can be ordinary to the environment even when it is foreign to the person of interest. [4,33,36,109]
What happened before the alleged event?	Establish the last known legitimate contact, intervals between uses, storage location, item sharing, and prior movement between people or environments. Record whether the object was recently purchased, cleaned, borrowed, repaired, transported, or left in a public/shared area.	Ask whether the alternative history has a factual time line and whether the relevant persistence interval was considered. Avoid treating "earlier contact" as either automatically plausible or automatically negligible without context.	Persistence is conditional on substrate, use, environment, subsequent contact, and recovery; elapsed time alone does not determine whether earlier DNA should remain detectable. [4,20]
Was the item cleaned, washed, laundered, or environmentally exposed?	Record cleaning agent, washing/laundering, water exposure, weather, friction, storage, and subsequent reuse where relevant. Preserve information about whether cleaning materials or other items could themselves redistribute DNA.	Ask whether cleaning was treated as complete removal rather than as a process that can reduce, redistribute, or leave protected DNA. Question temporal claims based only on survival after cleaning.	Cleaning changes recovery probabilities but does not reset the biological history of the item. Surviving DNA is not necessarily recent. [4,12]
Could a person, garment, or body site act as a DNA reservoir?	Consider non-self DNA on hands, sleeve cuffs, clothing, fingernails, gloves, and frequently contacted personal items when reconstructing indirect transfer. Document recent activities that may create plausible intermediary routes.	Ask whether the proposed transfer history assumes hands or clothing carried only self-DNA. For fingernail or skin findings, ask whether ordinary background, grooming, persistence, and indirect acquisition were considered.	People are themselves DNA-bearing environments. Biological reservoirs can carry non-self DNA forward into a later contact without the original donor touching the final exhibit. [33,36]
C. Design and interpret sampling in context			
Why was this location sampled?	Define the proposition-relevant reason for each sampled region before collection where possible.	Ask why the sampled area is informative for the disputed activity and what DNA would be expected there under each account. Distinguish analytical productivity from evidential discrimination.	Frequently touched areas may yield abundant DNA yet have high background prevalence; a lower-yield activity-specific area may be more discriminating. [3,4,7,8,12,92]

	Prioritize locations that may discriminate activities, not only those expected to maximize DNA yield.		
Were functionally distinct areas kept separate?	Record exact sampling boundaries and avoid unnecessary pooling where spatial distribution could distinguish activities. Photograph or map sampling locations when location is likely to be evidentially important.	Ask whether DNA from different regions was combined and, if so, what spatial information was lost. Where location is central, ask whether post-deposition movement could link the regions.	Pooling can erase spatial patterns. Conversely, separate samples are not automatically independent if DNA can relocate between nearby sites. [22,23,46,47]
Was the recovery method appropriate for the substrate?	Document surface type, morphology, sampled area, swab/tape method, wetting conditions, extraction route, and deviations from validated procedure. Preserve information needed to understand why a low or negative result may have occurred.	Ask whether the method is validated or supported for that substrate and whether recovery efficiency limits the inference being made. Do not interpret a weak result as a direct measure of weak contact without considering collection and recovery.	The observed DNA is filtered through sampling and analytical recovery. Surface and collection effects alter whether a prior deposit becomes reportable. [4,12,15,39]
Would contextual or comparison sampling answer a defined uncertainty?	Collect contextual samples only where they address a proposition-relevant question about background prevalence or spatial distribution. Match contextual sites, timing, exposure, and sampling method as closely as reasonably possible.	Ask why each contextual sample was collected and whether it is genuinely comparable to the questioned site. Avoid treating a convenient control location as representative background without a defensible relationship to the exhibit.	Contextual sampling can inform background prevalence, but poor matching may create an appearance of case specificity without relevant probability estimates. [113]
What do the negative samples show?	Retain and report relevant non-detections, failed profiles, adjacent negative areas, and control results rather than focusing only on positive swabs. Ensure sampling strategy allows negative observations to be linked to specific locations and methods.	Ask whether negative observations were included in the activity evaluation and whether dropout/recovery probabilities were considered. Question selective presentation of the strongest positive profile when nearby or related samples were negative.	Non-detection is probabilistic evidence, not categorical proof of no contact. Its value depends on how strongly each proposition predicts recovery. [3,15]
D. Preserve the post-event handling and contamination history			
Who had access to the scene and exhibit?	Record scene entry, collectors, medical personnel, photographers, fingerprint personnel, transport staff, laboratory handlers, and other relevant access. Preserve chronology rather than relying only on a final possession log.	Request the access/handling history where contamination or indirect transfer is a live issue. Ask whether any person whose DNA was detected had legitimate post-event access.	A chain of custody can establish possession while still omitting biologically important contacts. Access creates potential transfer routes that must be reconstructed, not presumed consequential. [48,49,53,77]

What did gloves, PPE, and tools contact before the exhibit?	Document glove-change points, reused equipment, forceps/scissors/brushes, cameras, pens, benches, packaging, and transitions between exhibits. Change gloves and clean tools at defined workflow transitions rather than only when visibly soiled.	Ask whether "gloves were worn" is being used as a complete answer to contamination risk. Request task sequence and equipment-use records when a glove- or tool-mediated route is plausible.	Gloves and tools can become intermediary DNA-bearing surfaces. Barrier use reduces direct contact but does not make the workflow DNA-neutral. [23,48,49,53,75,77]
How was the exhibit packaged?	Record packaging material, orientation, folding, restraints, internal movement, whether items shared a package, and whether the package exterior contacted the exhibit during opening. Package items separately where appropriate and preserve item position when location matters.	Ask whether the exhibit could move or rub within its package and whether co-packaging or package contact created a route for relocation. Where location is relied upon, request the packaging and transport history.	Collection does not freeze DNA location. Packaging can cause loss, site-to-site movement, and exhibit-package-exhibit transfer. [22,23,46,47]
What happened during transport, storage, opening, and repackaging?	Document transport conditions, storage location, package integrity, dates opened, persons present, repackaging, and shared work surfaces. Preserve any unusual event or damaged packaging.	Ask whether the sampled location necessarily reflects the scene location after movement, folding, transport, or re-examination. Examine whether repeated openings create additional transfer opportunities.	A biologically relevant location at analysis may not be the original deposition location if post-collection redistribution is plausible. [22,23,46,47]
What contamination controls and elimination comparisons were available?	Preserve negative collection/extraction/amplification controls, environmental monitoring, staff/police elimination data, incident logs, and relevant concurrent-case information. Investigate recurrent or unexpected profiles rather than treating them as unexplained noise.	Ask what stage each control actually monitors and which stages it cannot address. A negative blank should not be treated as excluding all scene- or exhibit-specific contamination routes.	Controls are pathway-specific. Elimination matches can identify contributors to post-event DNA but may not reveal the exact transfer route. [48,49,53,75,77,117]
Were there deviations or implementation vulnerabilities?	Record interruptions, glove-change failures, packaging errors, shared equipment, cleaning failures, unexpected access, near-misses, and corrective actions contemporaneously. Treat documentation quality as part of evidence integrity.	Ask whether a documented deviation creates a plausible route to the DNA finding, rather than assuming every deviation caused contamination. Conversely, ask whether nominal SOP compliance is being used to claim impossibility.	Contamination prevention depends on implementation reliability. Human-factor information identifies opportunities and barriers; it does not by itself prove causation. [53,75,77]
E. Reconstruct and compare complete transfer histories			

What is the proposed direct-transfer history?	Specify who contacted what, with which body part or biological material, for what activity, at what approximate time, and what subsequent events followed. Avoid reducing the history to "A touched the item" if the alleged activity is more specific.	Ask what observations the direct-contact account predicts beyond mere presence of A's DNA: quantity, location, mixture, other contributors, or non-detection elsewhere. Identify whether these predictions are supported by relevant data.	Direct transfer is a mechanism, not a crime label. The same direct contact can occur during innocent or alleged activity. [4,20,54,108]
What exact indirect-transfer route is proposed?	Identify the intermediary person/object, sequence of contacts, time intervals, intervening activities, and final recipient surface. Look for factual evidence supporting each required link.	Require a concrete causal chain rather than accepting or dismissing "secondary transfer" as a generic label. Ask whether each step has empirical support under sufficiently similar conditions.	Scientific possibility does not establish case probability. An indirect history gains evidential relevance when the necessary contacts and timing are plausible and testable. [4,20,54,108,109]
Could background, habitual use, or persistence explain the finding?	Model prior legitimate use as part of the case history where supported by ownership or routine access. Document time since last use, later users, cleaning, and whether the sampled site is one expected to carry habitual-user DNA.	Ask whether the observed contributor would already be expected on the item and whether that expectation is spatially specific. Do not treat "background" as an automatic explanation for every unexpected profile.	Background and persistence are competing causal histories, not labels for inconvenient findings. Their weight depends on item-specific prevalence and use history. [4,33,36,39,109]
Could DNA have moved after its original deposition?	Consider within-item movement, packaging transfer, laundering, repeated handling, and transfer between surfaces before and after collection. Preserve information on folds, contact surfaces, movement, and package configuration.	Where the location is incriminating, ask what evidence supports treating the sampled site as the original deposition site. Request evaluation of site-to-site movement if it could alter the activity comparison.	Spatially persuasive DNA can be historically misleading if relocation is omitted from the causal model. [22,23,46,47]
Is contamination a specific history or only a generic possibility?	Reconstruct who/what could have introduced the DNA, at which stage, through what contact, and what records or controls bear on that route. Compare the route with staff/elimination data and actual handling chronology.	Ask for the proposed mechanism and supporting case facts. Reject both categorical claims that compliance made contamination impossible and unsupported claims that contamination must have occurred.	Contamination becomes evaluative when linked to a plausible post-event transfer route; general contamination rates from other organisations are not case probabilities. [48,49,53,75,77,117]
Could several pathways have operated together?	Allow for pre-existing DNA plus crime-related deposition plus later redistribution or contamination.	Ask whether the model accommodates mixed histories and whether unknown contributors, background, and post-event transfer are represented when relevant.	Transfer, persistence, prevalence, recovery, and contamination can interact. The final profile may contain material from different times and activities. [3,4,8,46,108,109]

	Do not force mixtures into a single-route explanation if the chronology supports multiple episodes.	Check that one contributor is not interpreted in isolation from the biological history of the entire sample.	
F. Evaluate the complete pattern of DNA findings			
What is the complete observation set?	Compile all relevant DNA quantities, profile qualities, contributor numbers, contributor proportions, locations, unknown contributors, negative samples, and controls. Preserve links between observations and sampling sites.	Ask what observations were included in the evaluation and which were omitted. Where only the strongest positive result is discussed, ask whether excluded findings would be predicted differently by the competing histories.	Activity-level evaluation concerns the pattern generated by a history, not only the most incriminating profile. [3,8,46,54,108,109]
Are quantity and profile completeness being used as stand-alone classifiers?	Treat DNA amount, RFU, allele recovery, and profile completeness as observations to be interpreted under specified histories. Avoid operational labels such as "high DNA = direct" in case summaries.	Ask for the empirical basis for any claim that a quantity is typical of direct, recent, forceful, or crime-related deposition. Examine overlap between experimental distributions and differences in recovery method.	Direct transfer may produce more DNA on average in some experiments, but distributions overlap and are conditional on donor, substrate, contact, persistence, and recovery. [4,15,20,54,108]
Is the major contributor being treated as the last handler?	Document habitual use and repeated contact before inferring chronology from contributor rank. Consider whether later handlers may leave little DNA or earlier users may remain dominant.	Ask what data support any temporal meaning assigned to major/minor status. Separate contributor proportion at recovery from sequence of contact.	Major-contributor status is an analytical description of relative contribution, not a timestamp or direct indicator of the most recent contact. [4,39]
What do unknown contributors contribute to the interpretation?	Investigate whether additional profiles could represent associates, background users, intermediary handlers, investigators, or environmental contributors. Retain unknown components in the reconstruction where they may discriminate histories.	Ask whether unknown contributors were ignored, conditioned away, or explicitly modelled. Determine whether their presence is more expected under one proposition.	Additional contributors are not necessarily noise. In activity models, they can materially change the LR because they inform the plausibility of the transfer pathway. [54,108,109]
Are multiple samples statistically or causally dependent?	Identify shared deposits, common handlers, co-packaging, adjacent sampling sites, repeated sampling, and common transfer chains. Avoid describing related samples as independent events without justification.	Ask whether LRs from multiple samples were multiplied and, if so, what independence assumptions justify that operation. Consider common-source or site-to-site transfer explanations.	Dependence reflects physical evidence history. Ignoring it can materially overstate the combined evidential value. [46,109]

How should non-detection be interpreted?	Document analytical thresholds, sampling success, substrate and method limitations, and other reasons a genuine contact might not produce a reportable profile. Retain negative observations for comparison with the activity predictions.	Ask whether the absence of DNA was converted into categorical absence of contact. Where used evidentially, request the relevant detection/dropout basis under both propositions.	Absence is not the logical inverse of presence. A negative result can be informative only through proposition-relevant recovery probabilities. [3,15]
G. Scrutinize activity-level evaluation and the data behind it			
What exactly does the likelihood ratio compare?	Ensure reports label source/sub-source and activity-level LRs unambiguously and preserve the stated proposition pair in communications. Do not quote a source LR as if it measured activity.	Ask for the numerator and denominator propositions in plain language before considering the magnitude of the LR. Confirm that the statistic addresses the disputed issue.	A source LR and an activity LR can differ by many orders of magnitude because they answer different questions. [3,8,54,93,108]
How relevant are the TPPR data to this case?	Provide the laboratory with case information needed to assess donor, substrate, biological material, contact sequence, time, environment, background, packaging, and recovery. Avoid requesting numerical evaluation where the necessary history is unspecified.	Ask how closely the cited experiments match the case on the variables most likely to affect the findings. Identify important extrapolations rather than assuming that a published transfer percentage is universal.	Activity-level numbers are only as defensible as the transportability of the underlying transfer, persistence, prevalence/background, and recovery data. [3,4,8,15]
Are the experimental units, denominators, and outcomes suitable for probability estimation?	Where internal experiments are used, preserve participant structure, repeated measures, failures, controls, and complete outcome data. Avoid converting a convenience set of deposits into a population rate.	Ask how many independent donors/events generated the data, what counted as a success, how non-detections were handled, and whether repeated observations were treated appropriately. Distinguish possibility evidence from frequency evidence.	A study can demonstrate that a mechanism occurs while still being insufficient to estimate a transferable probability for casework. [15]
Does laboratory-specific recovery matter?	Use validated local recovery information where available and document material deviations from published workflows. Recognize that pooled external data may not represent local dropout or recovery behaviour.	Ask whether activity calculations use pooled, hierarchical, or laboratory-specific data and why that choice is appropriate. Request discussion of inter-laboratory variability where material.	Inter-laboratory studies show substantial recovery heterogeneity; naive pooling can make activity-level evidence appear more discriminating or more precise than warranted. [110,112]
Was uncertainty and sensitivity examined?	Where modelling is used, identify parameters that are weakly informed by data and test reasonable alternatives.	Ask whether plausible changes in transfer, persistence, background, recovery, or dependence assumptions would change the conclusion or verbal category.	A numerical LR does not remove scientific judgment. Sensitivity analysis reveals whether apparent precision is robust to plausible model uncertainty. [110,112,117]

	Document assumptions that materially drive the result.	Request sensitivity results for influential uncertain parameters.	
Is a numerical activity-level LR justified at all?	Do not force quantification when propositions are poorly specified or data are too remote from the case. Where appropriate, provide a transparent qualitative explanation of plausible routes and the limits of available evidence.	Ask whether the model is supported strongly enough for a numerical conclusion or whether the correct scientific result is an explicit limitation. Do not treat lack of a number as lack of scientific value.	A precise-looking number is not preferable to a transparent boundary. The analysis should stop at the highest inferential level supported by relevant data. [3,15,117]
H. Communicate and use the DNA conclusion correctly			
Is the conclusion stated at the same level as the evaluation?	Use source language for source evaluations and explicit comparative activity language for activity evaluations. Avoid shorthand in investigative briefings that turns contributor attribution into contact or crime involvement.	Compare the report wording with the proposition actually evaluated. Challenge phrases such as "the DNA proves touch" or "the DNA proves use" unless an activity-level comparison supports them.	Language can silently escalate inference even when the underlying laboratory analysis is correct. Reporting should preserve the scope of the scientific conclusion. [3,8,10,93,117]
Has the conditional been reversed?	Train case teams to distinguish P(findings | proposition) from P(proposition | findings). Avoid describing an LR as the probability that the proposition is true.	Ask whether the expert is evaluating how probable the findings are under each proposition, or stating which proposition probably occurred. Reserve the latter for the fact-finder after all evidence is considered.	The LR measures evidential value, not the probability of guilt, innocence, source, contact, or activity. [3,8,93,117]
Are possibility and probability being kept separate?	When an alternative route is raised, investigate its factual components instead of stopping at "it can happen." Similarly, do not dismiss a route merely because it is uncommon in a different experimental setting.	Ask whether the literature establishes only that a pathway is possible or provides sufficiently relevant frequency data for this case. Demand the same evidential discipline for prosecution and defence alternatives.	A demonstrated mechanism is not a case probability. Alternative histories become informative only when specified and compared against the complete findings. [4,15,20]
Is investigative utility being confused with evidential proof?	Use trace DNA to identify leads, associates, networks, or new sampling targets, then investigate the contact history independently. Record why a DNA hit changed investigative priorities.	At trial, ask what the DNA adds after identity, ownership, or legitimate contact is known. Do not present the fact that DNA generated a lead as proof that the lead performed the alleged activity.	A DNA result can be operationally valuable while having limited activity-level discrimination once the case circumstances are known. [7,92] DNA may also contribute alongside other forensic information in multimodal investigative strategies. [118]
Has the expert-fact-finder boundary been preserved?	Provide accurate case information without asking the scientist to determine guilt or credibility.	Ask whether the conclusion evaluates the evidence or decides the ultimate issue.	The expert evaluates the probability of the findings under stated propositions; the fact-finder determines what occurred using the

	Keep factual disputes distinct from scientific assumptions.	Integrate the DNA opinion with the remaining evidence rather than converting it into a posterior probability of guilt.	DNA evidence together with all other evidence. [3,8,93,117]
Have the evidential stopping rules been respected?	Stop at source level when activity is not disputed or activity data are inadequate. Escalate to activity level only when the proposition pair and data justify it.	Ask two final questions: Was an activity comparison actually performed? Are the available TPPR data sufficiently relevant to support the stated strength? If either answer is no, resist higher-level interpretation.	The safest practical rule is not to weaken DNA evidence, but to prevent its strength from being applied to a question the science has not evaluated. [3,9,15,117]

Note. Questions are not ranked and do not imply that every transfer route is equally plausible. A scientifically possible route becomes evidentially relevant when it can be formulated as a case-specific history and evaluated against the complete findings. Source/sub-source likelihood ratios are not activity-level likelihood ratios. DNA quantity, profile completeness, contributor rank, spatial location, and non-detection are observations to be evaluated under competing propositions, not stand-alone indicators of directness, recency, or crime-related deposition. TPPR = transfer, persistence, prevalence/background, and recovery.

The framework does not imply that every trace DNA result requires a numerical activity-level likelihood ratio. In many cases the relevant question remains source attribution; in others, available transfer, persistence, prevalence/background, and recovery (TPPR) data are too remote from the case circumstances to support defensible quantification [3,15,117]. The objective is to identify the inferential level genuinely in dispute, preserve the information needed to address it, and prevent a technically strong result at one level from being interpreted as stronger evidence at another.

9.1 Define the disputed question before deciding what the DNA can add

The first practical step is to identify what is actually disputed. A DNA case may concern contributor identity, the identity of the actor, whether a particular activity occurred, the timing or route of deposition, or some combination of these. These are not interchangeable questions. If a person denies ever having possessed or encountered an exhibit, a sub-source comparison may be central. If the person accepts ownership or previous legitimate use but disputes using the item during the offence, the same source-level result may add little to the contested issue and the relevant question moves to activity level [3,93].

Competing propositions should therefore be formulated from the case dispute rather than reverse-engineered after viewing the DNA result. They should be at the same level of the proposition hierarchy, sufficiently specific to generate different expectations for the findings, and anchored in histories that could realistically have occurred. A proposition that Person A handled a knife during an assault may appropriately be contrasted with a proposition that Person A handled the knife during earlier legitimate use and another person used it during the assault. It is not appropriately contrasted with a source proposition that the DNA came from an unknown person. Similarly, a defence suggestion that DNA was 'transferred somehow' is too vague for meaningful evaluation; the proposed intermediary, sequence of contacts, time interval and relevant background should be specified where the case information permits [93].

For legal practitioners, proposition-first reading provides an immediate test of relevance. Before relying on the magnitude of a DNA likelihood ratio, the report should be read against the disputed issue: does the statistic address who contributed the DNA, or the activity the court must decide? Where those questions differ, the evidential problem is not solved by repeating or emphasizing the source-level statistic.

9.2 Preserve the biological history of the exhibit, not only its possession history

A conventional chain of custody establishes continuity and accountability for an exhibit, but trace DNA interpretation often requires a more detailed biological history. Investigators should document the information that changes the probability of plausible transfer histories: ownership and habitual use; known legitimate handlers; close associates or co-users; the item's location before and after the event; cleaning, washing or laundering; environmental exposure; time intervals; subsequent use; and whether the item was shared, moved, folded, stacked or stored with other objects. For body sites and clothing, the exact sampled region and its expected contact history are equally important [4,77].

The post-event history requires comparable detail. Records should, where relevant, identify scene personnel and access, collection order, PPE and glove changes, tools used, packaging type, whether items were packaged together or allowed to contact packaging surfaces, transport conditions, laboratory receipt, opening and repackaging, shared equipment, and documented deviations or contamination events [22,23,47–49,77]. A possession log that states who held the evidence but omits how it was handled may demonstrate continuity while leaving important biological transfer opportunities unresolved.

These handling details are evidential metadata, not merely administrative records. Good documentation can exclude or weaken some proposed transfer routes; incomplete documentation leaves a wider range of post-event histories scientifically open. The objective is not to record every conceivable contact, but to preserve those most capable of changing the DNA distribution. For low-template, mixed, or spatially important findings, a concise record of glove sequence, folding, packaging, or an intervening examination may contribute more to activity-level evaluation than a generic statement that standard procedures were followed [53,77].

9.3 Sample for evidential discrimination, not simply for maximum DNA recovery

The most productive sampling location is not necessarily the most informative. Frequently touched areas such as handles, steering wheels, phone surfaces or garment cuffs may yield abundant DNA, but they may also have high expected background from owners, habitual users and legitimate contacts. By contrast, a less frequently touched or activity-specific region may yield less DNA but provide greater discrimination between competing activities. Sampling strategy should therefore consider both analytical yield and the expected evidential meaning of a result from that location [3,4].

Where spatial distribution is important, the integrity of location information should be preserved. Separate sampling of functionally distinct regions is preferable to indiscriminate pooling when the proposition concerns where contact occurred. Sampling plans may also benefit from appropriately chosen comparison or contextual locations, particularly when background prevalence is a material uncertainty. Recent work on contextual DNA samples shows that such sampling can inform case-specific background, but only when the locations, timing, number of samples and relationship to the questioned item are defensible [113]. Contextual sampling should answer a defined question rather than be selected retrospectively because it happens to produce a convenient comparison.

Negative findings remain part of the evidential pattern. Failure to detect the person of interest in one sample, a negative adjacent area beside a positive target area, or an unexpected contributor in a control can alter the relative probability of competing activities. More sampling is not automatically more informative; additional locations are valuable when they test a proposition-relevant prediction rather than simply increase the chance of another positive profile. The objective is a coherent spatial and contextual dataset, not the maximum number of positive swabs.

9.4 Reconstruct complete transfer histories before assigning meaning to the profile

Once the relevant observations and item history are available, the competing accounts should be translated into explicit transfer histories. A useful reconstruction begins before the alleged event and extends through collection and analysis. For each proposition, the examiner should consider who or what could initially carry the DNA, the order and nature of contacts, possible person- or object-mediated transfer, pre-existing background, persistence intervals, repeated use, cleaning, site-to-site movement, packaging, investigator handling and laboratory contamination [3,4]. **Fig. 2** provides the principal route categories, while **Fig. 3** illustrates why different histories may converge on the same source-level result.

Reconstructing explicit histories prevents two opposite errors: treating direct crime-related deposition as the default because it is narratively simple, and invoking secondary transfer, background DNA, or contamination as generic alternatives merely because they are scientifically possible. A useful competing history requires a plausible causal chain and, where quantitative evaluation is attempted, data relevant to the required steps. Physical possibility is necessary but not sufficient for evidential weight [3,15].

The histories also need not be mutually exclusive at the mechanistic level. An exhibit can contain habitual-user DNA before the offence, acquire event-related DNA during the offence, undergo secondary or site-to-site redistribution during later handling, and receive additional material during collection. Activity propositions may therefore generate mixed histories rather than single-route pathways. The evaluation should represent the complete observations produced by those histories, including unknown contributors and negative results, rather than forcing the case into a simple direct-versus-secondary dichotomy [46,54,108].

9.5 Evaluate the complete pattern of findings and their dependence

The evidential unit is rarely one isolated profile. Relevant observations may include DNA quantity, allele or locus recovery, contributor number, relative contribution, profile quality, the distribution of contributors across several sites, expected or unexpected background contributors, and non-detection. These observations should be considered jointly where the model and data permit. Selecting the strongest profile while disregarding neighbouring negative samples or an unexpected contributor can alter the apparent support for the competing histories [3,54,108].

Dependence between observations requires particular attention. DNA recovered from adjacent regions of one garment may share a common deposit or may have relocated during packaging. Several items may acquire the same contributor through one shared handler or surface. Repeated samples from the same transfer chain are not equivalent to independent transfer events. Taylor et al. demonstrated that site-to-site movement within a packaged exhibit can materially alter activity-level evaluation when DNA location is treated as crime-specific [46]. Accordingly, several matching DNA results do not automatically constitute several independent pieces of evidence, and likelihood ratios should not be multiplied unless the required independence assumptions are justified.

Unexpected contributors can also be informative. In experimental activity-level evaluations, the presence of an additional contributor has changed the likelihood ratio because it was more compatible with one transfer history than another [54,108]. Unknown DNA should therefore not be removed conceptually as 'noise' before considering whether its occurrence is predicted differently by the propositions. The same applies to absence: non-detection may support one history over another when the expected recovery probabilities differ, but it should not be converted into categorical proof that contact did not occur.

9.6 Ask what the likelihood ratio actually compares - and what data make it possible

For lawyers, investigators and courts, the most useful question about a reported likelihood ratio is not initially 'How large is it?' but 'What propositions does it compare?' A source-level LR may compare the proposition that Person A contributed the DNA with the proposition that an unknown unrelated person contributed it. An activity-level LR may instead compare, for example, direct use of an item during the alleged event with earlier legitimate use followed by persistence, or direct handling with a specified indirect-transfer route. The two statistics answer different questions and may differ by many orders of magnitude [3,54].

A defensible activity-level evaluation should make clear the proposition pair, the observations included, the conditioning information accepted, and the empirical or expert-assessment basis for the conditional probabilities. The relevance of the data should be interrogated against the case: donor structure, biological material, substrate, contact type, transfer sequence, elapsed time, background conditions, packaging, sampling method, laboratory workflow and outcome definition [3,15]. A transfer frequency from a highly controlled experiment is not a universal probability for all cases involving the same broad label.

Recent inter-laboratory studies make this issue concrete. The ReAct project identified substantial laboratory-to-laboratory differences in DNA recovery and dropout, and companion modelling showed that evidential values can change depending on whether pooled, hierarchical or laboratory-specific data are used [110–112]. Newer hierarchical activity-level frameworks likewise demonstrate that model structure, laboratory effects and data-selection strategies can materially change the numerical result [115,116]. Consequently, an activity-level LR should be accompanied by sufficient explanation of data relevance and sensitivity to uncertain assumptions. Apparent numerical precision is not a substitute for model validity.

When data are too sparse, poorly matched, or structurally incomplete to support a robust numerical LR, the appropriate response is not to manufacture precision. The expert can identify scientifically credible routes, explain which findings would be more or less expected under the competing histories, and state why reliable quantification is not possible [3,15,117]. For legal decision-makers, that limitation is substantive information: it defines where the available science ends.

9.7 Separate investigative utility from evidential proof

Trace DNA can be highly valuable during an investigation even when it cannot yet support a strong activity-level conclusion. A source-level association may generate a lead, identify a previously unknown person, reveal an associate, suggest a contact network, direct further sampling, or prompt comparison with elimination profiles. Those are legitimate investigative uses. The evidential question at trial may nevertheless be narrower and more demanding: once the person's identity or legitimate connection to the item is known, how well do the DNA findings distinguish the alleged activity from the alternative explanation?

Investigative follow-up should therefore examine contact history rather than stop at contributor identification. Relevant inquiries may include ownership, prior legitimate use, relationships between contributors, opportunities for indirect transfer, item sharing, cleaning, scene access, packaging history, and the identity of personnel who handled the evidence. When an alternative history is raised, testing its factual components is more informative than debating secondary transfer or background DNA in the abstract.

This approach also guards against confirmation bias in both directions. DNA should not be treated as conclusive merely because it identifies a suspect, but an alternative route should not be accepted simply because the literature shows that it can occur. Investigative utility concerns whether a result helps generate or prioritize inquiries; evidential value concerns how strongly the complete findings discriminate the propositions ultimately put before the court. Conflating the two can turn a useful lead into an overstated conclusion.

9.8 Treat contamination and quality records as case information

Contamination assessment should be integrated into the same reconstruction rather than left as a generic laboratory assurance statement. Relevant information includes who accessed the scene or exhibit, PPE and glove-change records where available, tools and shared surfaces, packaging and repackaging, negative controls, staff or police elimination comparisons, environmental monitoring, concurrent incidents, deviations and corrective actions [48,49,53,77]. Accreditation and SOP compliance reduce risk but do not demonstrate that a specific transfer route was impossible in a particular case.

The interpretation of quality information should remain symmetrical. A staff match may identify the contributor to a contamination event but not necessarily the immediate route by which the DNA reached the sample. Conversely, a negative blank or absence of a staff match does not exclude every contamination pathway because the suspected event

may have occurred before the control shared the relevant process, through an unprofiled person, or through an indirect chain. The useful question is whether the records support or weaken a specific post-event history, not whether the laboratory can be labelled 'contaminated' or 'contamination-free.'

Implementation reliability is therefore relevant to evidential reconstruction. A documented glove-change failure, unusual packaging event or interrupted workflow does not prove that contamination occurred, but it can identify a transfer opportunity that deserves evaluation. Conversely, contemporaneous records showing separation of items, appropriate glove changes, clean controls and no relevant elimination matches may reduce the plausibility of some routes. Quality-system evidence is most useful when linked to the actual chronology of the exhibit [53].

9.9 Communicate the conclusion at the same level as the evaluation

Reporting language is the final safeguard. If the analysis addresses contributor identity, the conclusion should remain at source or sub-source level. If an activity-level comparison has been performed, the report should identify the competing activities and state how much more or less probable the findings are under one than the other, together with material assumptions and limitations [3,117]. Neither form of opinion should be translated into the probability that the defendant performed the activity or committed the offence.

Legal professionals can test the scope of an opinion by asking four linked questions: what proposition level was evaluated; which competing proposition formed the denominator; what case information was conditioned upon; and what data or assumptions connect the proposed activities to the DNA findings. If any of these elements is unclear, the apparent certainty of the conclusion may be greater than its interpretive scope. If material conditioning information changes during the investigation or trial, the activity-level evaluation may also need to be reconsidered because its probabilities are conditional on that information [3,93].

Two stopping rules follow. First, a strong source-level result should not be escalated into an activity conclusion unless the additional transfer and contextual evaluation has actually been performed. Second, when proposition-relevant TPPR data are insufficient, the analysis should stop at the level supported by the evidence rather than force a numerical activity-level conclusion. These rules do not reduce the value of DNA; they prevent unsupported certainty while preserving strong evidence where the findings genuinely discriminate competing histories.

The framework can be reduced to seven linked stages: define the dispute; reconstruct the pre- and post-event history of the exhibit; select sampling locations for evidential discrimination; preserve handling and contamination information; evaluate the complete and potentially dependent pattern of findings; compare explicit propositions using sufficiently relevant data; and communicate the conclusion at the same inferential level. **Fig. 4** and **Table 4** operationalize this sequence. Section 10 considers the empirical and methodological gaps that still limit its routine application.

10 EVIDENCE GAPS AND FUTURE PRIORITIES

The central research gap in activity-level DNA interpretation is no longer proof that transfer, persistence, background DNA, redistribution, or contamination can occur; each is empirically established. The unresolved problem is whether sufficiently relevant data exist to estimate how probable the observed findings would be under the competing histories that matter in a case. Much of the literature establishes mechanism or feasibility under controlled conditions, whereas legal evaluation requires probabilities conditioned on realistic combinations of donor, substrate, contact sequence, prior use, elapsed time, background DNA, handling, packaging, recovery, and laboratory workflow [3,4]. Research priorities should therefore be set by uncertainties that materially change activity-level conclusions, not by repeated demonstrations that a pathway is physically possible.

10.1 Move from possibility studies to proposition-driven, realistic scenario data

Much transfer research relies on deliberately simplified systems: one or two donors, few contacts, standardized substrates, short transfer chains, and modest participant or replicate numbers. Such designs are valuable for isolating mechanisms, but their casework transportability is limited when the disputed history involves habitual use, prior legitimate contact, multiple intermediaries, cleaning, intervening activities, background contributors, or post-event handling. Earlier reviews identified small and sometimes unrepresentative participant samples as a recurring limitation and emphasized the need for larger studies capable of estimating probability distributions rather than single transfer frequencies [4]. That need becomes more important as activity-level models become more quantitative.

Future scenario studies should begin with explicit competing propositions. Experimental units, denominators, donor structure, repeated measures, negative outcomes, and dependencies should be defined before data collection, and the complete observation pattern should be retained rather than only detection of the person of interest. Particularly useful

designs combine realistic case features with controlled ground truth: habitual versus one-time use, direct versus specified indirect routes, sequential transfer with intervening activity, mixed biological backgrounds, realistic delays, cleaning or washing, and packaging or transport. Case-specific re-enactments may be informative but are difficult to scale. Modular multicentre datasets that study common scenario components systematically would provide a more sustainable basis for transparent probabilistic models [4,15].

10.2 Study TPPR as a connected process, not as isolated variables

Transfer, persistence, prevalence/background, and recovery are often studied separately even though they operate sequentially and interact in casework. That separation creates an interpretive weakness when a probability estimated for one stage is applied as though the remaining stages were fixed or independent. Real exhibits rarely meet that assumption. DNA may be deposited onto an already DNA-bearing surface, added to or removed by later handling, relocated during packaging, and only partly recovered at sampling. The final profile therefore reflects a connected process rather than a single transfer event.

Priority should be given to longitudinal and full-pathway experiments that preserve this causal structure. Data are needed on how contributor quantity, mixture proportion, profile quality, spatial distribution, and non-detection evolve jointly across repeated contacts and multiple sampling sites. Particular attention is required where observations are likely to be dependent, including adjacent garment regions, co-packaged exhibits, repeated samples from one transfer chain, and multiple objects contacted by the same intermediary. Site-to-site transfer modelling has already shown that allowing for redistribution within a packaged exhibit can change activity-level evaluation [46]. Comparable empirical work is required across a broader range of exhibit classes and handling histories. Sensitivity analysis should then be used to identify which poorly characterized parameters most influence the likelihood ratio, so that research effort is directed toward decision-critical uncertainty rather than variables with little effect on the conclusion [114–116].

10.3 Characterize background DNA and temporal context in the environments where cases occur

Background and prevalent DNA are among the least portable activity-level parameters because they are strongly shaped by local occupancy, ownership, co-users, cleaning, social networks, and sampling location. A generic literature estimate of 'background DNA' may therefore be less informative than data from the relevant environment. Contextual sampling can provide local prevalence information, but its value depends on sampling design, the number and location of samples, collection timing, and uncertainty from small samples [113]. Protocols for when contextual samples should be collected, which surfaces should be sampled, and how those observations should enter activity-level models require further validation.

The temporal component is similarly underdeveloped. Conventional STR quantity and profile completeness do not provide a universal time-since-deposition clock, and elapsed time cannot be interpreted independently of substrate, environmental exposure, cleaning, later use, and recovery. Future work should therefore focus less on assigning a single age to a trace and more on comparing defined temporal histories: recent event-related deposition versus earlier legitimate use, persistence followed by later handling, or recent relocation of older biological material. Shared environments, clothing, vehicles, body surfaces, fingernails, outdoor scenes, and routinely cleaned objects are particularly important because they combine persistence with repeated opportunities for acquisition and redistribution. These settings are also those in which intuitive assumptions about recency are most likely to be legally persuasive despite weak scientific support.

10.4 Make transfer and recovery data portable across laboratories

Well-designed transfer data are not automatically portable across laboratories when recovery and analytical performance differ. The ReAct project demonstrated substantial inter-laboratory variation in DNA recovery and dropout across 23 laboratories, and subsequent modelling showed that evidential values can change depending on whether pooled, hierarchical, or laboratory-specific data are used [110–112]. Recovery is therefore an interpretive parameter, not merely a methodological detail. Further work is needed to quantify recovery efficiency across relevant combinations of trace type, collection device, extraction method, quantification system, profiling workflow, and mixture interpretation, and to define when external data can be transported to a laboratory with different performance characteristics.

Recent FSI: Genetics minimum requirements provide a foundation for such portability by requiring standardized sample-level reporting of contributor identifiers, mixture proportions, quantification values, total DNA recovery, elution volume, sub-source likelihood ratios, analytical settings, and sufficiently detailed sampling methods, while discouraging pre-publication filtering based on laboratory-specific reporting criteria [15]. The next priority is implementation at scale through multi-laboratory replication, recovery calibration, transparent uncertainty estimates, and interoperable open datasets. Negative and low-level outcomes must remain in shared datasets; systematic exclusion inflates apparent transfer or recovery success and weakens the denominators needed for activity-level evaluation [15].

10.5 Quantify post-event contamination and implementation reliability under realistic workflows

Contamination research has established numerous mechanisms by which DNA can be introduced or relocated after an event, but the probability of those pathways under routine operational conditions remains incompletely characterized. Detected contamination rates depend on elimination-database coverage, environmental monitoring, reporting thresholds, and the ability to recognize indirect transfer, making institutional rates difficult to compare directly. Future studies should move beyond demonstrations that gloves, tools, packaging, or work surfaces can carry DNA and quantify how specific workflow sequences alter the probability and composition of transfer. Prospective studies linking glove-change points, packaging transitions, shared equipment, scene access, cleaning, and staff movement to sample-level DNA outcomes would provide more useful parameters for evaluating concrete contamination histories.

Human and organizational factors should be incorporated with similar care. Workload, fatigue, interruption, staffing, communication, and layout can influence implementation reliability, but they should not be treated as direct causes of an individual contamination event without a demonstrated transfer pathway. The research need is therefore for designs that connect observable process conditions to measurable deviations, transfer opportunities, contamination outcomes, and detection by quality systems. Near-miss records, elimination matches, environmental monitoring, corrective actions, and contemporaneous handling data could provide a richer operational evidence base than retrospective attribution of incidents to generic 'human error' [53].

10.6 Treat legal implementation and communication as part of the research agenda

A final gap concerns implementation. Scientific frameworks for activity-level evaluation have advanced more rapidly than their consistent use across jurisdictions. In a global survey of 162 forensic DNA practitioners, major barriers included limited case-relevant TPPR data, insufficient education and training among forensic and legal stakeholders, lack of validated and standardized reporting frameworks, and uncertainty about legal acceptance [10]. Better experiments alone will therefore not ensure better interpretation in court.

Future work should therefore evaluate how investigators, lawyers, judges, and jurors understand source-level and activity-level conclusions, likelihood ratios, non-detection, alternative transfer histories, and model limitations. Reporting formats should be tested for whether they preserve the direction of conditioning and the level of proposition rather than merely for readability. Training and competency assessment should also treat activity-level interpretation as a distinct expertise, requiring proficiency in proposition formulation, TPPR evidence, probabilistic reasoning, data relevance, sensitivity analysis, and communication of uncertainty [3,4,10,117]. Decision-support tools may improve consistency [119], but their assumptions, data sources, dependence structures, and stopping rules must remain visible to the scientist and capable of scrutiny by the opposing party and the court. Recent work on survivor experiences after sexual assault also highlights the importance of clear, sensitive communication of forensic findings throughout the justice process [120].

The most consequential future work is therefore not simply to detect smaller quantities of DNA, but to improve the evidential meaning assigned to what is detected. Priorities include realistic proposition-driven datasets, joint modelling of TPPR processes, case-relevant background and temporal information, calibrated inter-laboratory recovery data, quantified post-event transfer pathways, open and reusable reporting standards, and validated communication to legal decision-makers. These advances would not remove uncertainty; they would make it more measurable, transparent, and correctly located within the inferential chain from DNA detection to crime-level reasoning.

11 CONCLUSION

The principal interpretive challenge in forensic DNA evidence is not whether modern profiling can associate biological material with a person, but how far that association can legitimately support reconstruction of an event. A profile may provide extremely strong support for contributor attribution while remaining much less informative about the route, timing, or activity responsible for deposition. Direct crime-related contact, earlier legitimate use, indirect or subsequent transfer, persistence of pre-existing DNA, background DNA, redistribution during handling or packaging, and post-event contamination can produce overlapping laboratory observations. Positive and negative findings are therefore endpoints of a transfer-persistence-prevalence-recovery history rather than direct records of the event itself.

DNA quantity, profile completeness, contributor rank, mixture composition, spatial location, and non-detection can all contribute to evaluation, but none independently establishes directness, recency, or crime-related deposition. When activity is disputed, the findings should be compared under explicit competing propositions using data sufficiently relevant to the biological material, substrate, contact sequence, elapsed time, background conditions, packaging, recovery, and laboratory workflow. The inferential direction remains the probability of the findings given the competing activities, not the probability that an activity occurred given the DNA result. Where proposition-relevant data are insufficient, a limited or qualitative opinion is more defensible than unsupported numerical precision.

Operationally, the same inferential discipline should extend from scene to courtroom. Investigators should preserve the biological history of an exhibit alongside its chain of custody, including ownership, prior use, cleaning, environmental exposure, sampling location, handling sequence, packaging, and potential contamination opportunities. Forensic scientists should evaluate the complete pattern of findings, including negative results, unexpected contributors, spatial relationships, and dependencies between samples. Lawyers and courts should ask which proposition a reported statistic addresses and whether the conclusion remains at the inferential level actually evaluated. These distinctions protect, rather than diminish, the probative value of a strong source-level result.

Progress will depend on realistic proposition-driven datasets, integrated TPPR research, better characterization of background and temporal context, calibrated inter-laboratory recovery data, quantified post-event transfer pathways, transparent reporting standards, and stronger activity-level training across forensic and legal disciplines. As analytical sensitivity increases, the scientific task is not only to detect more DNA but to assign the correct evidential meaning to what is detected. DNA at a scene can provide compelling evidence of biological association. Whether it is DNA from the crime remains a separate question that must be evaluated from the complete transfer history and competing case propositions rather than assumed from the profile alone.

STATEMENTS ON COMPLIANCE WITH ETHICAL STANDARDS

Acknowledgments

The author acknowledges the institutional and professional setting that supported preparation of this review and is grateful to forensic-science colleagues for general scientific discussions that helped refine its scope and interpretation.

Disclosure of conflict of interest

The author declares that there are no conflicts of interest.

Author Contributions

Salem K. Alketbi conceived the review, developed its methodological and interpretive framework, conducted the literature search and study selection, performed data extraction and cross-study synthesis, developed the figures and tables, and drafted and revised the manuscript.

Data Availability Statement

No new dataset was generated for this review; data availability is therefore not applicable.

REFERENCES

[1] Cook R, Evett IW, Jackson G, Jones PJ, Lambert JA. A hierarchy of propositions: deciding which level to address in casework. Sci Justice. 1998;38(4):231-239.

[2] Gill P, Hicks T, Butler JM, Connolly E, Gusmão L, Kokshoorn B, et al. DNA Commission of the International Society for Forensic Genetics: Assessing the value of forensic biological evidence - Guidelines highlighting the importance of propositions. Part I: evaluation of DNA profiling comparisons given (sub-) source propositions. Forensic Sci Int Genet. 2018;36:189-202. https://doi.org/10.1016/j.fsigen.2018.07.003.

[3] Gill P, Hicks T, Butler JM, Connolly E, Gusmão L, Kokshoorn B, et al. DNA Commission of the International Society for Forensic Genetics: Assessing the value of forensic biological evidence - Guidelines highlighting the importance of propositions. Part II: evaluation of biological traces considering activity-level propositions. Forensic Sci Int Genet. 2020;44:102186. https://doi.org/10.1016/j.fsigen.2019.102186.

[4] van Oorschot RAH, Szkuta B, Meakin GE, Kokshoorn B, Goray M. DNA transfer in forensic science: A review. Forensic Sci Int Genet. 2019;38:140-166. https://doi.org/10.1016/j.fsigen.2018.10.014.

[5] Alketbi SK. The role of DNA in forensic science: A comprehensive review. Int J Sci Res Arch. 2023;9(2):814-829. https://doi.org/10.30574/ijsra.2023.9.2.0624.

[6] Alketbi SK, Goodwin W, Alghanim HJ, Abdullahi AA, Aidarous NI, Alawadhi HM, et al. Trace DNA Recovery: Insights from Dubai Police Casework. Perspect Leg Forensic Sci. 2025;2:10001. https://doi.org/10.70322/plfs.2025.10001.

[7] Hoffmann R, Roux C, Meakin GE, Daubney J, Nadort A, Sears A, Morelato M. The added value of trace DNA in an investigative context. Forensic Sci Int. 2026;388:113070. https://doi.org/10.1016/j.forsciint.2026.113070.

[8] Taylor D, Kokshoorn B, Biedermann A. Evaluation of forensic genetics findings given activity level propositions: A review. Forensic Sci Int Genet. 2018;36:34-49. https://doi.org/10.1016/j.fsigen.2018.06.001.

[9] Gill P. DNA evidence and miscarriages of justice. Forensic Sci Int. 2019;294:e1-e3. https://doi.org/10.1016/j.forsciint.2018.12.003.

[10] Prinz M, Pirtle D, Oldoni F. Global survey on evaluative reporting on DNA evidence with regard to activity-level propositions. J Forensic Sci. 2024;69(3):798-813. https://doi.org/10.1111/1556-4029.15488.

[11] Alketbi SK. The Affecting Factors of Touch DNA. J Forensic Res. 2018;9(3):424. https://doi.org/10.4172/2157-7145.1000424.

[12] Alketbi SK, Goodwin W. The effect of surface type, collection and extraction methods on touch DNA. Forensic Sci Int Genet Suppl Ser. 2019;7:704-706. https://doi.org/10.1016/j.fsigss.2019.10.145.

[13] Verdon TJ, Mitchell RJ, van Oorschot RAH. The influence of substrate on DNA transfer and extraction efficiency. Forensic Sci Int Genet. 2013;7(1):167-175.

[14] National Institute of Standards and Technology. Forensic DNA Interpretation and Human Factors: Improving the Practice Through a Systems Approach. NIST IR 8503. 2024. https://doi.org/10.6028/nist.ir.8503.

[15] Gill P, Hicks T, Kokshoorn B, van Oorschot RAH, Taylor D, Parson W. Minimum FSI: Genetics requirements for publishing data on DNA transfer and recovery, given activities. Forensic Sci Int Genet. 2026;80:103330. https://doi.org/10.1016/j.fsigen.2025.103330.

[16] van Oorschot RAH, Meakin GE, Kokshoorn B, Goray M, Szkuta B. DNA Transfer in Forensic Science: Recent Progress towards Meeting Challenges. Genes (Basel). 2021;12(11):1766. https://doi.org/10.3390/genes12111766.

[17] Butler JM, et al. DNA Mixture Interpretation: A NIST Scientific Foundation Review. NIST IR 8351. 2024.

[18] European Network of Forensic Science Institutes (ENFSI). ENFSI Guideline for Evaluative Reporting in Forensic Science. Approved version 3.0. 2015.

[19] European Network of Forensic Science Institutes (ENFSI). Best Practice Manual for the Forensic Examination of DNA. ENFSI-BPM-DNA-03. 2022.

[20] Taylor D, Biedermann A, Samie L, Pun KM, Hicks T, Champod C. Helping to distinguish primary from secondary transfer events for trace DNA. Forensic Sci Int Genet. 2017;28:155-177. https://doi.org/10.1016/j.fsigen.2017.02.008.

[21] Fonneløp AE, Ramse M, Egeland T, Gill P. The implications of shedder status and background DNA on direct and secondary transfer in an attack scenario. Forensic Sci Int Genet. 2017;29:48-60. https://doi.org/10.1016/j.fsigen.2017.03.019.

[22] Goray M, van Oorschot RAH, Mitchell RJ. DNA transfer within forensic exhibit packaging: potential for DNA loss and relocation. Forensic Sci Int Genet. 2012;6(2):158-166. https://doi.org/10.1016/j.fsigen.2011.03.013.

[23] Fonneløp AE, Johannessen H, Egeland T, Gill P. Contamination during criminal investigation: Detecting police contamination and secondary DNA transfer from evidence bags. Forensic Sci Int Genet. 2016;23:121-129. https://doi.org/10.1016/j.fsigen.2016.04.003.

[24] Szkuta B, Ballantyne KN, Kokshoorn B, van Oorschot RAH. Transfer and persistence of non-self DNA on hands over time: Using empirical data to evaluate DNA evidence given activity level propositions. Forensic Sci Int Genet. 2018;33:84-97. https://doi.org/10.1016/j.fsigen.2017.11.017.

[25] Meakin GE, Butcher EV, van Oorschot RAH, Morgan RM. Trace DNA evidence dynamics: An investigation into the deposition and persistence of directly- and indirectly-transferred DNA on regularly-used knives. Forensic Sci Int Genet. 2017;29:38-47. https://doi.org/10.1016/j.fsigen.2017.03.016.

[26] Lehmann VJ, Mitchell RJ, Ballantyne KN, van Oorschot RAH. Following the transfer of DNA: How does the presence of background DNA affect the transfer and detection of a target source of DNA? Forensic Sci Int Genet. 2015;19:68-75. https://doi.org/10.1016/j.fsigen.2015.05.002.

[27] Alketbi SK, Ahmed SR. Influence of physiological activation on Touch DNA deposition and STR profile quality during competitive computer gaming: a forensic pilot study. Forensic Sci Int Genet. 2027;87:103599. https://doi.org/10.1016/j.fsigen.2026.103599.

[28] Biedermann A, Champod C, Jackson G, Gill P, Taylor D, Butler J, et al. Evaluation of forensic DNA traces when propositions of interest relate to activities: analysis and discussion of recurrent concerns. Front Genet. 2016;7:215.

[29] McCrane SM, Mulligan CJ. An innovative transfer DNA experimental design and qPCR assay to identify primary, secondary, and tertiary DNA transfer. J Forensic Sci. 2024;69(2):618-630. https://doi.org/10.1111/1556-4029.15444.

[30] Goray M, Mitchell RJ, van Oorschot RAH. Investigation of secondary DNA transfer of skin cells under controlled test conditions. Leg Med (Tokyo). 2010;12(3):117-120. https://doi.org/10.1016/j.legalmed.2010.01.003.

[31] Fonneløp AE, Egeland T, Gill P. Secondary and subsequent DNA transfer during criminal investigation. Forensic Sci Int Genet. 2015;17:155-162. https://doi.org/10.1016/j.fsigen.2015.05.009.

[32] Carson S, Volgin L, Abarno D, Taylor D. The potential for investigator-mediated contamination to occur during routine search activities. Forensic Sci Med Pathol. 2022;18(3):299-310. https://doi.org/10.1007/s12024-022-00465-6.

[33] Henry L, Zieger M. Self- and non-self-DNA on hands and sleeve cuffs. Int J Legal Med. 2024;138:757-766. https://doi.org/10.1007/s00414-023-03124-9.

[34] Alketbi SK, Goodwin W. Temporal Assessment of DNA Shedding from Human Hands After Handwashing: Implications for Touch DNA Recovery. Biomed J Sci Tech Res. 2024;59(5). https://doi.org/10.26717/bjstr.2024.59.009365.

[35] Jansson L, Swensson M, Gifvars E, Hedell R, Forsberg C, Ansell R, et al. Individual shedder status and the origin of touch DNA. Forensic Sci Int Genet. 2022;56:102626. https://doi.org/10.1016/j.fsigen.2021.102626.

[36] Alketbi SK. Fingernail Samples as DNA Reservoirs: Implications for Forensic Interpretation. World J Adv Res Rev. 2026;30(1):1154-1185. https://doi.org/10.30574/wjarr.2026.30.1.0913.

[37] Onofri M, Tommolini F, Severini S, Gambelunghe C, Lancia M, Carlini L, Carnevali E. Trace DNA transfer in co-working spaces: The importance of background DNA analysis. International Journal of Molecular Sciences. 2024;25(4):2207. https://doi.org/10.3390/ijms25042207.

[38] Zacher M, van Oorschot RAH, Handt O, Goray M. Transfer and persistence of intruder DNA within an office after reuse by owner. Forensic Sci Int Genet. 2024;73:103130. https://doi.org/10.1016/j.fsigen.2024.103130.

[39] Szkuta B, Ansell R, Boiso L, Connolly E, Kloosterman AD, Kokshoorn B, McKenna LG, Steensma K, van Oorschot RAH. Assessment of the transfer, persistence, prevalence and recovery of DNA traces from clothing: an inter-laboratory study on worn upper garments. Forensic Sci Int Genet. 2019;42:56-68. https://doi.org/10.1016/j.fsigen.2019.06.011.

[40] Alketbi SK, Carta L. Uncovering the Persistence of Touch DNA on Human Skin and Its Implications for Violent Crime Investigations. World J Biol Pharm Health Sci. 2025;21(3):234-244. https://doi.org/10.30574/wjbphs.2025.21.3.0270.

[41] Goray M, Pirie E, van Oorschot RAH. DNA transfer: DNA acquired by gloves during casework examinations. Forensic Sci Int Genet. 2019;38:167-174. https://doi.org/10.1016/j.fsigen.2018.10.018.

[42] Otten L, Banken S, Schürenkamp M, Schulze-Johann K, Sibbing U, Pfeiffer H, Vennemann M. Secondary DNA transfer by working gloves. Forensic Sci Int Genet. 2019;43:102126. https://doi.org/10.1016/j.fsigen.2019.07.005.

[43] Tanzhaus K, Reiß MT, Zaspel T. "I've never been at the crime scene!"-gloves as carriers for secondary DNA transfer. Int J Legal Med. 2021;135(4):1385-1393. https://doi.org/10.1007/s00414-021-02597-w.

[44] Mehta AA, Alketbi SK. Touching Without Contact: Glove-Mediated Secondary DNA Transfer in Forensic Casework. J Forensic Allied Sci. 2025;1(1):56-72. https://doi.org/10.64475/jfas.vol.1.issue1.8.

[45] Noël S, Lagacé K, Rogic A, Granger D, Bourgoin S, Jolicoeur C, Séguin D. DNA transfer during laundering may yield complete genetic profiles. Forensic Sci Int Genet. 2016;23:240-247. https://doi.org/10.1016/j.fsigen.2016.05.004.

[46] Taylor D, Volgin L, Kokshoorn B. Accounting for site-to-site DNA transfer on a packaged exhibit in an evaluation given activity level propositions. Forensic Sci Int Genet. 2024;73:103122. https://doi.org/10.1016/j.fsigen.2024.103122.

[47] Stella CJ, Goray M, Meakin GE, van Oorschot RAH. DNA transfer in packaging: Investigation of mitigation strategies. J Forensic Sci. 2026;71:197-210. https://doi.org/10.1111/1556-4029.70217.

[48] Pickrahn I, Kreindl G, Müller E, Dunkelmann B, Zahrer W, Cemper-Kiesslich J, Neuhuber F. Contamination incidents in the pre-analytical phase of forensic DNA analysis in Austria-Statistics of 17 years. Forensic Sci Int Genet. 2017;31:12-18. https://doi.org/10.1016/j.fsigen.2017.07.012.

[49] Basset P, Castella V. Lessons from a study of DNA contaminations from police services and forensic laboratories in Switzerland. Forensic Sci Int Genet. 2018;33:147-154. https://doi.org/10.1016/j.fsigen.2017.12.012.

[50] Alketbi SK. DNA Contamination in Crime Scene Investigations: Common Errors, Best Practices, and Insights from a Survey Study. Biomed J Sci Tech Res. 2024;58(5). https://doi.org/10.26717/bjstr.2024.58.009223.

[51] Basset P, Castella V. Positive impact of DNA contamination minimization procedures taken within the laboratory. Forensic Sci Int Genet. 2019;38:232-235. https://doi.org/10.1016/j.fsigen.2018.11.013.

[52] Vandewoestyne M, Van Hoofstat D, De Groote S, Van Thuyne N, Haerinck S, Van Nieuwerburgh F, et al. Sources of DNA Contamination and Decontamination Procedures in the Forensic Laboratory. J Forensic Res. 2011;S2:001. https://doi.org/10.4172/2157-7145.s2-001.

[53] Abdullahi AA, Alketbi SK. Implementation reliability in forensic DNA contamination prevention: a human-factor quality-systems mini review. Med Res Arch. 2026;14(7):1-18. https://doi.org/10.18103/mra.2026.0388.

[54] Onofri M, Altomare C, Severini S, Tommolini F, Lancia M, Carlini L, et al. Direct and secondary transfer of touch DNA on a credit card: Evidence evaluation given activity level propositions and application of Bayesian networks. Genes (Basel). 2023;14(5):996. https://doi.org/10.3390/genes14050996.

[55] Cahill A, Volgin L, van Oorschot RAH, Taylor D, Goray M. Where did it go? A study of DNA transfer in a social setting. Forensic Sci Int Genet. 2024;73:103101. https://doi.org/10.1016/j.fsigen.2024.103101.

[56] Szkuta B, Ballantyne KN, van Oorschot RAH. Transfer and persistence of DNA on the hands and the influence of activities performed. Forensic Sci Int Genet. 2017;28:10-20. https://doi.org/10.1016/j.fsigen.2017.01.006.

[57] Cale CM, Earll ME, Latham KE, Bush GL. Could secondary DNA transfer falsely place someone at the scene of a crime? J Forensic Sci. 2016;61(1):196-203. https://doi.org/10.1111/1556-4029.12894.

[58] Jansson L, Siti C, Hedell R, Forsberg C, Ansell R, Hedman J. Assessing the consistency of shedder status under various experimental conditions. Forensic Sci Int Genet. 2024;69:103002. https://doi.org/10.1016/j.fsigen.2023.103002.

[59] Kanokwongnuwut P, Martin B, Kirkbride KP, Linacre A. Shedding light on shedders. Forensic Sci Int Genet. 2018;36:20-25. https://doi.org/10.1016/j.fsigen.2018.06.004.

[60] Szkuta B, Harvey ML, Ballantyne KN, van Oorschot RAH. DNA transfer by examination tools - a risk for forensic casework? Forensic Sci Int Genet. 2015;16:246-254. https://doi.org/10.1016/j.fsigen.2015.02.004.

[61] Zoppis S, Muciaccia B, D'Alessio A, Ziparo E, Vecchiotti C, Filippini A. DNA fingerprinting secondary transfer from different skin areas: morphological and genetic studies. Forensic Sci Int Genet. 2014;11:137-143. https://doi.org/10.1016/j.fsigen.2014.03.005.

[62] Singh HP, Alketbi SK. Influence of Non-Porous Surface Morphology on DNA Recovery Efficiency and STR Profile Quality Using Common Forensic Swabbing Techniques. Biomed J Sci Tech Res. 2026;65(5). https://doi.org/10.26717/bjstr.2026.65.010242.

[63] Alketbi SK, Goodwin W. The impact of deposition area and time on Touch DNA collected from fabric. Forensic Sci Int Genet Suppl Ser. 2022;8:45-47. https://doi.org/10.1016/j.fsigss.2022.09.017.

[64] Alketbi SK, Goodwin W. The Impact of Area Size and Fabric Type on Touch DNA Collected from Fabric. J Forensic Sci Criminol Investig. 2022;16(1):555926. https://doi.org/10.19080/jfsci.2022.16.555926.

[65] Alketbi SK. The Impact of Collection Method on Touch DNA Collected from Fabric. J Forensic Sci Criminol Investig. 2022;15(5):555923. https://doi.org/10.19080/jfsci.2022.15.555923.

[66] Alketbi SK, Ali MS, Khan SA. Managing Porous Substrate Wicking in Trace DNA Collection: Impact of Swab Wetting Volume on Fabric Evidence. Med Res Arch. 2026;14(2). https://doi.org/10.18103/mra.v14i2.6610.

[67] Alketbi SK. Collection techniques of touch DNA deposited on human skin following a strangulation scenario. Int J Legal Med. 2023;137:1357-1362. https://doi.org/10.1007/s00414-023-03036-8.

[68] Alketbi SK, Goodwin W. The effect of time and environmental conditions on Touch DNA. Forensic Sci Int Genet Suppl Ser. 2019;7:701-703. https://doi.org/10.1016/j.fsigss.2019.10.144.

[69] Chahal RB, Alketbi SK. Touch DNA on wood: Effects of surface morphology, humidity, and adaptive recovery strategies on forensic DNA yield. Int J Forens Sci. 2026;11(1):000453. https://doi.org/10.23880/ijfsc-16000453.

[70] Alketbi SK, Goodwin W. The Effect of Sandy Surfaces on Touch DNA. J Forensic Leg Investig Sci. 2019;5:034. https://doi.org/10.24966/flis-733x/100034.

[71] Alketbi SK, Goodwin W. Evaluating the impact of sandy surface contamination on trace DNA recovery from wearable fabrics: A comparative study of collection methods and extraction kits. World J Adv Res Rev. 2025;26(3):2399-2410. https://doi.org/10.30574/wjarr.2025.26.3.2441.

[72] Alketbi SK. Collection of Touch DNA from Rotten Banana Skin. Int J Forens Sci. 2020;5(4):000204. https://doi.org/10.23880/ijfsc-16000204.

[73] Salleh HM, Alketbi SK. Touch DNA Recovery from Edible Surfaces: Forensic Implications for Crime Scene Evidence Collection. J Forensic Allied Sci. 2026;2(1):001-016. https://doi.org/10.64475/jfas.vol.2.issue1.1.

[74] Singh VS, Alketbi SK, Sharma PA. Influence of Surface Material, Cleaning Frequency and Swab Type on Touch DNA Recovery from Entrance Door Handles: A Simulated Study. Int J Forens Sci. 2025;10(4):000449. https://doi.org/10.23880/ijfsc-16000449.

[75] Alketbi SK, Carta L. Safeguarding DNA Integrity: The Critical Role of PPE in Preventing Contamination in Forensic Laboratories. J Forensic Sci Crim Investig. 2025;19(2):556010. https://doi.org/10.19080/jfsci.2025.19.556010.

[76] Alketbi SK. Preventing DNA Contamination in Forensic Laboratories: An Illustrated Review of Best Practices. Am J Biomed Sci Res. 2024;24(1). https://doi.org/10.34297/ajbsr.2024.24.003153.

[77] Alketbi SK. Maintaining the chain of custody: Anti-contamination measures for trace DNA evidence. Int J Sci Res Arch. 2023;8(2):457-461. https://doi.org/10.30574/ijsra.2023.8.2.0257.

[78] Kloosterman A, Sjerps M, Quak A. Error rates in forensic DNA analysis: Definition, numbers, impact and communication. Forensic Sci Int Genet. 2014;12:77-85. https://doi.org/10.1016/j.fsigen.2014.04.014.

[79] Jeanguenat AM, Budowle B, Dror IE. Strengthening forensic DNA decision making through a better understanding of the influence of cognitive bias. Sci Justice. 2017;57(6):415-420. https://doi.org/10.1016/j.scijus.2017.07.005.

[80] Dror IE, Hampikian G. Subjectivity and bias in forensic DNA mixture interpretation. Sci Justice. 2011;51(4):204-208. https://doi.org/10.1016/j.scijus.2011.08.004.

[81] Alketbi SK, Goodwin W. Validating Touch DNA Collection Techniques Using Cotton Swabs. J Forensic Res. 2019;10(3):445. Available at SSRN: https://ssrn.com/abstract=4368453.

[82] Alketbi SK, Goodwin W. Touch DNA Collection Techniques for Non-Porous Surfaces Using Cotton and Nylon Swabs. Biomed J Sci Tech Res. 2021;36(3). https://doi.org/10.26717/bjstr.2021.36.005863.

[83] Alketbi SK. An Evaluation of the Performance of Two Quantification Methods for Trace DNA Casework Samples. J Forensic Sci Criminol Investig. 2023;16(5):555950. https://doi.org/10.19080/jfsci.2023.16.555950.

[84] Alketbi SK. Analysis of Touch DNA [doctoral thesis]. University of Lancashire; 2023. Available from: https://knowledge.lancashire.ac.uk/id/eprint/46154/ (accessed 7 May 2026).

[85] Alketbi SK, Goodwin W. Evaluation of microFLOQ™ Direct Swab for Touch DNA Recovery. J Forensic Leg Investig Sci. 2024;10:093. https://doi.org/10.24966/flis-733x/100093.

[86] Aljanahi NS, Alketbi SK, Almheiri MM, Alshehhi SA, Sanqoor AN, Alghanim HJ. Enhancing trace DNA profile recovery in forensic casework using the amplicon RX post-PCR clean-up kit. Sci Rep. 2025;15:3324. https://doi.org/10.1038/s41598-025-88164-4.

[87] Alketbi SK, Goodwin W, Alghanim HJ, Sanqoor SH, Alshehhi SA, Almheiri MM, et al. Comparing Extraction and Direct Amplification Methods for Enhanced Touch DNA Profiling. In: 30th Congress of the International Society for Forensic Genetics. Universidade de Santiago de Compostela; 2025. p. 1035-1042. https://doi.org/10.15304/cc.2025.1869.

[88] Alketbi SK, Goodwin W. Enhancing trace DNA recovery from disposable face masks: insights from the COVID-19 era and beyond. Int J Legal Med. 2025;139:1529-1536. https://doi.org/10.1007/s00414-025-03435-z.

[89] Alketbi SK. An Innovative Solution to Collect Touch DNA for Direct Amplification. J Forensic Sci Criminol Investig. 2022;16(1):555928. https://doi.org/10.19080/jfsci.2022.16.555928.

[90] Alketbi SK, Alsoofi S. Dual Recovery of DNA and Fingerprints using Minitapes. J Forensic Sci Criminol Investig. 2022;16(1):555929. https://doi.org/10.19080/jfsci.2022.16.555929.

[91] Alketbi SK, Goodwin W. Collection Methods for Touch DNA Direct Amplification. J Forensic Leg Investig Sci. 2023;9:072. https://doi.org/10.24966/flis-733x/100072.

[92] Aidarous NI, Alketbi SK, Abdullahi AA, Alghanim HJ, Alawadhi HM, Alrazouqi AM, et al. Investigating Touch DNA Success Rates in Vehicle Sites for Hit-and-Run Casework. Perspect Leg Forensic Sci. 2025;2:10008. https://doi.org/10.70322/plfs.2025.10008.

[93] Kokshoorn B, Blankers BJ, de Zoete J, Berger CEH. Activity level DNA evidence evaluation: On propositions addressing the actor or the activity. Forensic Sci Int. 2017;278:115-124. https://doi.org/10.1016/j.forsciint.2017.06.029.

[94] Burrill J, Daniel B, Frascione N. A review of trace "Touch DNA" deposits: variability factors and an exploration of cellular composition. Forensic Sci Int Genet. 2019;39:8-18. https://doi.org/10.1016/j.fsigen.2018.11.019.

[95] Raymond JJ, van Oorschot RAH, Gunn PR, Walsh SJ, Roux C. Trace evidence characteristics of DNA: a preliminary investigation of the persistence of DNA at crime scenes. Forensic Sci Int Genet. 2009;4:26-33. https://doi.org/10.1016/j.fsigen.2009.04.002.

[96] Kaesler T, Kirkbride KP, Linacre AMT. Persistence of touch DNA on commonly encountered substrates in different storage conditions. Forensic Sci Int. 2023;348:111728. https://doi.org/10.1016/j.forsciint.2023.111728.

[97] Arsenault H, Kuffel A, Dugard P, Nic Daeid N, Gray A. Trace DNA and its persistence on various surfaces: a long term study investigating the influence of surface type and environmental conditions - Part two, non-metals. Forensic Sci Int Genet. 2025;74:103151. https://doi.org/10.1016/j.fsigen.2024.103151.

[98] Bowman ZE, Mosse KSA, Sungaila AM, van Oorschot RAH, Hartman D. Detection of offender DNA following skin-to-skin contact with a victim. Forensic Sci Int Genet. 2018;37:252-259. https://doi.org/10.1016/j.fsigen.2018.09.005.

[99] Pfeifer CM, Wiegand P. Persistence of touch DNA on burglary-related tools. Int J Legal Med. 2017;131:941-953. https://doi.org/10.1007/s00414-017-1551-4.

[100] Atkinson K, Arsenault H, Taylor C, Volgin L, Millman J. Transfer and persistence of DNA on items routinely encountered in forensic casework following habitual and short-duration one-time use. Forensic Sci Int Genet. 2022;60:102737. https://doi.org/10.1016/j.fsigen.2022.102737.

[101] Sallows G, Taylor D, van Oorschot RAH, Goray M. Contacting surfaces are rarely DNA free: another look at transfer when both surfaces have DNA. Sci Justice. 2025;65:101248. https://doi.org/10.1016/j.scijus.2025.101248.

[102] Sorg A, Gouy A, Tièche CC, Zieger M. Human background DNA on stones in an urban environment. Forensic Sci Int Genet. 2023;65:102880. https://doi.org/10.1016/j.fsigen.2023.102880.

[103] Sessa F, Salerno M, Bertozzi G, Messina G, Ricci P, Ledda C, Rapisarda V, Cantatore S, Turillazzi E, Pomara C. Touch DNA: impact of handling time on touch deposit and evaluation of different recovery techniques: an experimental study. Sci Rep. 2019;9:9542. https://doi.org/10.1038/s41598-019-46051-9.

[104] Matte M, Williams L, Frappier R, Newman J. Prevalence and persistence of foreign DNA beneath fingernails. Forensic Sci Int Genet. 2012;6(2):236-243. https://doi.org/10.1016/j.fsigen.2011.05.008.

[105] Rutty GN, Hopwood A, Tucker V. The effectiveness of protective clothing in the reduction of potential DNA contamination of the scene of crime. Int J Legal Med. 2003;117(3):170-174. https://doi.org/10.1007/s00414-002-0348-1.

[106] Mercer C, Taylor D, Henry J, Linacre A. DNA accumulation and transfer within an operational forensic exhibit storeroom. Forensic Sci Int Genet. 2023;62:102799. https://doi.org/10.1016/j.fsigen.2022.102799.

[107] Taylor D, Biedermann A, Hicks T, Champod C. A template for constructing Bayesian networks in forensic biology cases when considering activity level propositions. Forensic Sci Int Genet. 2018;33:136-146. https://doi.org/10.1016/j.fsigen.2017.12.006.

[108] Fonnelop AE, Faria S, Shanthan G, Gill P. Who packed the drugs? Application of Bayesian networks to address questions of DNA transfer, persistence, and recovery from plastic bags and tape. Genes. 2022;13(1):18. https://doi.org/10.3390/genes13010018.

[109] Taylor D, Volgin L, Kokshoorn B, Champod C. The importance of considering common sources of unknown DNA when evaluating findings given activity level propositions. Forensic Sci Int Genet. 2021;53:102518. https://doi.org/10.1016/j.fsigen.2021.102518.

[110] Gill P, Fonnelop AE, Hicks T, et al. The ReAct project: analysis of data from 23 different laboratories to characterise DNA recovery given two sets of activity level propositions. Forensic Sci Int Genet. 2025;76:103222. https://doi.org/10.1016/j.fsigen.2025.103222.

[111] Gill P, Hicks T, Carracedo A, et al. The ReAct project: Bayesian networks for assessing the value of the results given activity level propositions. Forensic Sci Int Genet. 2025;76:103223. https://doi.org/10.1016/j.fsigen.2025.103223.

[112] Taylor D, Volgin L, Gill P, Kokshoorn B. Accounting for inter-laboratory DNA recovery data variability when performing evaluations given activities. Forensic Sci Int Genet. 2025;78:103283. https://doi.org/10.1016/j.fsigen.2025.103283.

[113] Goedhart YR, de Koeijer JA, Aarts LHJ, de Poot CJ, Kokshoorn B. Contextual DNA samples in evaluations given activity level propositions. Forensic Sci Int Genet. 2026;84:103452. https://doi.org/10.1016/j.fsigen.2026.103452.

[114] Gill P, Bleka O, Roseth A, Fonnelop AE. An LR framework incorporating sensitivity analysis to model multiple direct and secondary transfer events on skin surface. Forensic Sci Int Genet. 2021;53:102509. https://doi.org/10.1016/j.fsigen.2021.102509.

[115] Gill P, Bleka O. Likelihood ratios given activity-level propositions for DNA transfer evidence: theoretical foundations of the HaloGen framework (Part I). Forensic Sci Int Genet. 2026;103570. Online ahead of print. https://doi.org/10.1016/j.fsigen.2026.103570.

[116] Gill P, Bleka O. Likelihood ratios given activity-level propositions for DNA transfer evidence: practical implementation and simulation studies using the HaloGen engine (Part II). Forensic Sci Int Genet. 2026;103571. Online ahead of print. https://doi.org/10.1016/j.fsigen.2026.103571.

[117] Buckleton J, Taylor D, Allen PS, Curran J, Kalafut T. Reporting the value of biological findings given activity level propositions: a discussion of published recommendations. J Forensic Sci. 2025;70(5):1670-1686. https://doi.org/10.1111/1556-4029.70112.

[118] Khan AA, Alketbi SK. Integrating DNA and Chemical Profiling to Trace Illicit Drug Manufacture and Distribution. Perspect Leg Forensic Sci. 2025;2:10009. https://doi.org/10.70322/plfs.2025.10009.

[119] Alketbi SK. Emerging Technologies in Forensic DNA Analysis. Perspect Leg Forensic Sci. 2024;1(1):10007. https://doi.org/10.70322/plfs.2024.10007.

[120] Abdelrahman SR, Alketbi SK. Survivor experiences of forensic and legal processes after sexual assault: an exploratory mixed-methods study of participants recruited through Middle Eastern support networks. Forensic Sci Med Pathol. 2026. https://doi.org/10.1007/s12024-026-01342-2.